Datasheet for ABIN3090435

ARNTL Protein (AA 1-626) (Strep Tag)

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Overview

Quantity:	250 µg
Target:	ARNTL
Protein Characteristics:	AA 1-626
Origin:	Human
Source:	Cell-free protein synthesis (CFPS)
Protein Type:	Recombinant
Purification tag / Conjugate:	This ARNTL protein is labelled with Strep Tag.
Application:	Western Blotting (WB), SDS-PAGE (SDS), ELISA

Product Details

Brand:	AliCE®
Sequence:	MADQRMDISS TISDFMSPGP TDLLSSSLGT SGVDCNRKRK GSSTDYQESM DTDKDDPHGR LEYTEHQGRI KNAREAHSQI EKRRRDKMNS FIDELASLVP TCNAMSRKLD KLTVLRMAVQ HMKTLRGATN PYTEANYKPT FLSDDELKHL ILRAADGFLF VVGCDRGKIL FVSESVFKIL NYSQNDLIGQ SLFDYLHPKD IAKVKEQLSS SDTAPRERLI DAKTGLPVKT DITPGPSRLC SGARRSFFCR MKCNRPSVKV EDKDFPSTCS KKKADRKSFC TIHSTGYLKS WPPTKMGLDE DNEPDNEGCN LSCLVAIGRL HSHVVPQPVN GEIRVKSMEY VSRHAIDGKF VFVDQRATAI LAYLPQELLG TSCYEYFHQD DIGHLAECHR QVLQTREKIT TNCYKFKIKD GSFITLRSRW FSFMNPWTKE VEYIVSTNTV VLANVLEGGD PTFPQLTASP HSMDSMLPSG EGGPKRTHPT VPGIPGGTRA GAGKIGRMIA EEIMEIHRIR GSSPSSCGSS PLNITSTPPP DASSPGGKKI LNGGTPDIPS SGLLSGQAQE NPGYPYSDSS SILGENPHIG IDMIDNDQGS SSPSNDEAAM AVIMSLLEAD AGLGGPVDFS DLPWPL

Product Details

	Sequence without tag. The proposed Strep-Tag is based on experience s with the expression system, a different complexity of the protein could make another tag necessary. In case you have a special request, please contact us.
Characteristics:	Key Benefits: • Made in Germany - from design to production - by highly experienced protein experts. • Protein expressed with ALiCE® and purified in one-step affinity chromatography • These proteins are normally active (enzymatically functional) as our customers have reported (not tested by us and not guaranteed). • State-of-the-art algorithm used for plasmid design (Gene synthesis). This protein is a **made-to-order protein** and will be made for the first time for your order. Our experts in the lab try to ensure that you receive soluble protein. The big advantage of ordering our **made-to-order proteins** in comparison to ordering custom made proteins from other companies is that there is no financial obligation in case the protein cannot be expressed or purified. Expression System: • ALiCE®, our Almost Living Cell-Free Expression System is based on a lysate obtained from Nicotiana tabacum c.v.. This contains all the protein expression machinery needed to produce even the most difficult-to-express proteins, including those that require post-translational modifications. • During lysate production, the cell wall and other cellular components that are not required for protein production are removed, leaving only the protein production machinery and the mitochondria to drive the reaction. During our lysate completion steps, the additional components needed for protein production (amino acids, cofactors, etc.) are added to produce something that functions like a cell, but without the constraints of a living system - all that's needed is the DNA that codes for the desired protein! Concentration: • The concentration of our recombinant proteins is measured using the absorbance at 280nm. • The protein's absorbance will be measured against its specific reference buffer. • We use the Expasy's ProtParam tool to determine the absorption coefficient of each protein.
Purification:	One-step Strep-tag purification of proteins expressed in Almost Living Cell-Free Expression System (AliCE®).
Purity:	> 70-80 % as determined by SDS PAGE, Western Blot and analytical SEC (HPLC).

Product Details

Grade:	custom-made

Target Details

Target:	ARNTL
Alternative Name:	BMAL1 (ARNTL Products)
Background:	Basic helix-loop-helix ARNT-like protein 1 (Aryl hydrocarbon receptor nuclear translocator-like protein 1) (Basic-helix-loop-helix-PAS protein MOP3) (Brain and muscle ARNT-like 1) (Class E basic helix-loop-helix protein 5) (bHLHe5) (Member of PAS protein 3) (PAS domain-containing protein 3) (bHLH-PAS protein JAP3),FUNCTION: Transcriptional activator which forms a core component of the circadian clock. The circadian clock, an internal time-keeping system, regulates various physiological processes through the generation of approximately 24 hour circadian rhythms in gene expression, which are translated into rhythms in metabolism and behavior. It is derived from the Latin roots 'circa' (about) and 'diem' (day) and acts as an important regulator of a wide array of physiological functions including metabolism, sleep, body temperature, blood pressure, endocrine, immune, cardiovascular, and renal function. Consists of two major components: the central clock, residing in the suprachiasmatic nucleus (SCN) of the brain, and the peripheral clocks that are present in nearly every tissue and organ system. Both the central and peripheral clocks can be reset by environmental cues, also known as Zeitgebers (German for 'timegivers'). The predominant Zeitgeber for the central clock is light, which is sensed by retina and signals directly to the SCN. The central clock entrains the peripheral clocks through neuronal and hormonal signals, body temperature and feeding-related cues, aligning all clocks with the external light/dark cycle. Circadian rhythms allow an organism to achieve temporal homeostasis with its environment at the molecular level by regulating gene expression to create a peak of protein expression once every 24 hours to control when a particular physiological process is most active with respect to the solar day. Transcription and translation of core clock components (CLOCK, NPAS2, BMAL1, BMAL2, PER1, PER2, PER3, CRY1 and CRY2) plays a critical role in rhythm generation, whereas delays imposed by post-translational modifications (PTMs) are important for determining the period (tau) of the rhythms (tau refers to the period of a rhythm and is the length, in time, of one complete cycle). A diurnal rhythm is synchronized with the day/night cycle, while the ultradian and infradian rhythms have a period shorter and longer than 24 hours, respectively. Disruptions in the circadian rhythms contribute to the pathology of cardiovascular diseases, cancer, metabolic syndromes and aging. A transcription/translation feedback loop (TTFL) forms the core of the molecular circadian clock mechanism. Transcription factors, CLOCK or NPAS2 and BMAL1 or BMAL2, form the positive limb of the feedback loop, act in the form of a heterodimer

and activate the transcription of core clock genes and clock-controlled genes (involved in key metabolic processes), harboring E-box elements (5'-CACGTG-3') within their promoters. The core clock genes: PER1/2/3 and CRY1/2 which are transcriptional repressors form the negative limb of the feedback loop and interact with the CLOCK|NPAS2-BMAL1|BMAL2 heterodimer inhibiting its activity and thereby negatively regulating their own expression. This heterodimer also activates nuclear receptors NR1D1/2 and RORA/B/G, which form a second feedback loop and which activate and repressBMAL1 transcription, respectively.BMAL1 positively regulates myogenesis and negatively regulates adipogenesis via the transcriptional control of the genes of the canonical Wnt signaling pathway. Plays a role in normal pancreatic beta-cell function, regulates glucose-stimulated insulin secretion via the regulation of antioxidant genes NFE2L2/NRF2 and its targets SESN2, PRDX3, CCLC and CCLM. Negatively regulates the mTORC1 signaling pathway, regulates the expression of MTOR and DEPTOR. Controls diurnal oscillations of Ly6C inflammatory monocytes, rhythmic recruitment of the PRC2 complex imparts diurnal variation to chemokine expression that is necessary to sustain Ly6C monocyte rhythms. Regulates the expression of HSD3B2, STAR, PTGS2, CYP11A1, CYP19A1 and LHCGR in the ovary and also the genes involved in hair growth. Plays an important role in adult hippocampal neurogenesis by regulating the timely entry of neural stem/progenitor cells (NSPCs) into the cell cycle and the number of cell divisions that take place prior to cell-cycle exit. Regulates the circadian expression of CIART and KLF11. The CLOCK-BMAL1 heterodimer regulates the circadian expression of SERPINE1/PAI1, VWF, B3, CCRN4L/NOC, NAMPT, DBP, MYOD1, PPARGC1A, PPARGC1B, SIRT1, GYS2, F7, NGFR, GNRHR, BHLHE40/DEC1, ATF4, MTA1, KLF10 and also genes implicated in glucose and lipid metabolism. Promotes rhythmic chromatin opening, regulating the DNA accessibility of other transcription factors. The NPAS2-BMAL1 heterodimer positively regulates the expression of MAOA, F7 and LDHA and modulates the circadian rhythm of daytime contrast sensitivity by regulating the rhythmic expression of adenylate cyclase type 1 (ADCY1) in the retina. The preferred binding motif for the CLOCK-BMAL1 heterodimer is 5'-CACGTGA-3', which contains a flanking adenine nucleotide at the 3-prime end of the canonical 6-nucleotide E-box sequence (PubMed:23229515). CLOCK specifically binds to the half-site 5'-CAC-3', while BMAL1 binds to the half-site 5'-GTGA-3' (PubMed:23229515). The CLOCK-BMAL1 heterodimer also recognizes the non-canonical E-box motifs 5'-AACGTGA-3' and 5'-CATGTGA-3' (PubMed:23229515). Essential for the rhythmic interaction of CLOCK with ASS1 and plays a critical role in positively regulating CLOCK-mediated acetylation of ASS1 (PubMed:28985504). Plays a role in protecting against lethal sepsis by limiting the expression of immune checkpoint protein CD274 in macrophages in a PKM2-dependent manner (By similarity). Regulates the diurnal rhythms of skeletal muscle metabolism via transcriptional activation of genes promoting triglyceride synthesis (DGAT2)

Target Details

	and metabolic efficiency (COQ10B) (By similarity). {ECO:0000250|UniProtKB:Q9WTL8, ECO:0000269|PubMed:11441146, ECO:0000269|PubMed:12738229, ECO:0000269|PubMed:18587630, ECO:0000269|PubMed:23785138, ECO:0000269|PubMed:23955654, ECO:0000269|PubMed:24005054, ECO:0000269|PubMed:28985504}., FUNCTION: (Microbial infection) Regulates SARS coronavirus-2/SARS-CoV-2 entry and replication in lung epithelial cells probably through the post-transcriptional regulation of ACE2 and interferon-stimulated gene expression. {ECO:0000269|PubMed:34545347}.
Molecular Weight:	68.8 kDa
UniProt:	O00327
Pathways:	Regulation of Lipid Metabolism by PPARalpha, Protein targeting to Nucleus, Warburg Effect

Application Details

Application Notes:	In addition to the applications listed above we expect the protein to work for functional studies as well. As the protein has not been tested for functional studies yet we cannot offer a guarantee though.
Comment:	ALiCE®, our Almost Living Cell-Free Expression System is based on a lysate obtained from Nicotiana tabacum c.v.. This contains all the protein expression machinery needed to produce even the most difficult-to-express proteins, including those that require post-translational modifications. During lysate production, the cell wall and other cellular components that are not required for protein production are removed, leaving only the protein production machinery and the mitochondria to drive the reaction. During our lysate completion steps, the additional components needed for protein production (amino acids, cofactors, etc.) are added to produce something that functions like a cell, but without the constraints of a living system - all that's needed is the DNA that codes for the desired protein!
Restrictions:	For Research Use only

Handling

Format:	Liquid
Buffer:	The buffer composition is at the discretion of the manufacturer. Standard Storage Buffer: PBS pH 7.4, 10 % Glycerol **Might differ depending on protein.**

Handling

Handling Advice:	Avoid repeated freeze-thaw cycles.
Storage:	-80 °C
Storage Comment:	Store at -80°C.
Expiry Date:	12 months

