abcam

Product datasheet

Recombinant Human Daxx protein ab131785

1 Image

Description

Product name	Recombinant Human Daxx protein
Expression system	Wheat germ
Accession	**Q9UER7**
Protein length	Full length protein
Animal free	No
Nature	Recombinant
Species	Human
Sequence	MATANSIIVLDDDDEDEAAAQPGPSHPLPNAASPGAEAP SSSEPHGARGS SSSGGKKCYKLENEKLFEEFLELCKMQTADHPEVVPFLY NRQQRAHSLFL ASAEFCNILSRVLSRARSRPAKLYVYINELCTVLKAHSAKK KLNLAPAAT TSNEPSGNNPPTHLSLDPTNAENTASQSPRTRGSRRQIQR LEQLLALYVA EIRRLQEKELDLSELDDPDSAYLQEARLKRKLIRLFGRLCE LKDCSSLTG RVIEQRIPYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLRA VEKAAARH SLGLPRQQLQLMAQDAFRDVGIRLQERRHLDLIYNFGCHL TDDYRPGVDP ALSDPVLARRLRENRSLAMSRLDEVISKYAMLQDKSEEG ERKKRRARLQG TSSHSADTPEASLDSGEGPSGMASQGCPSASRAETDDE DDEESDEEEEEE EEEEEEEATDSEEEEDLEQMQEGQEDDEEEDEEEEAAA GKDGDKSPMSSL QISNEKNLEPGKQISRSSGEQQNKGRIVSPSLLSEEPLAP SSIDAESNGE QPEELTLEEESPVSQLFELEIEALPLDTPSSVETDISSSRK QSEEPFTTV LENGAGMVSSTSFNGGVSPHNWGDSGPPCKKSRKEKK QTGSGPLGNSYVE RQRSVHEKNGKKICTLPSPPSPLASLAPVADSSTRVDSP SHGLVTSSLCI

PSPARLSQTPHSQPPRPGTCKTSVATQCDPEEIIVLSDSD

Predicted molecular weight	108 kDa including tags
Amino acids	1 to 740

Specifications

Our **Abpromise guarantee** covers the use of **ab131785** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications	ELISA Western blot SDS-PAGE
Form	Liquid

Preparation and Storage

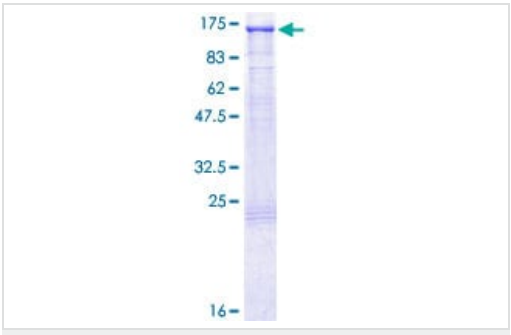
Stability and Storage	Shipped on dry ice. Upon delivery aliquot and store at -80ºC. Avoid freeze / thaw cycles. pH: 8.00 Constituents: 0.31% Glutathione, 0.79% Tris HCl

General Info

Function	Transcription corepressor known to repress transcriptional potential of several sumoylated transcription factors. Down-regulates basal and activated transcription. Its transcription repressor activity is modulated by recruiting it to subnuclear compartments like the nucleolus or PML/POD/ND10 nuclear bodies through interactions with MCSR1 and PML, respectively. Seems to regulate transcription in PML/POD/ND10 nuclear bodies together with PML and may influence TNFRSF6-dependent apoptosis thereby. Inhibits transcriptional activation of PAX3 and ETS1 through direct protein-protein interactions. Modulates PAX5 activity; the function seems to involve CREBBP. Acts as an adapter protein in a MDM2-DAXX-USP7 complex by regulating the RING-finger E3 ligase MDM2 ubiquitination activity. Under non-stress condition, in association with the deubiquitinating USP7, prevents MDM2 self-ubiquitination and enhances the intrinsic E3 ligase activity of MDM2 towards TP53, thereby promoting TP53 ubiquitination and subsequent proteasomal degradation. Upon DNA damage, its association with MDM2 and USP7 is disrupted, resulting in increased MDM2 autoubiquitination and consequently, MDM2 degradation, which leads to TP53 stabilization. Acts as histone chaperone that facilitates deposition of histone H3.3. Acts as targeting component of the chromatin remodeling complex ATRX:DAXX which has ATP-dependent DNA translocase activity and catalyzes the replication-independent deposition of histone H3.3 in pericentric DNA repeats outside S-phase and telomeres, and the in vitro remodeling of H3.3-containing nucleosomes. Does not affect the ATPase activity of ATRX but alleviates its transcription repression activity. Upon neuronal activation associates with regulatory elements of selected immediate early genes where it promotes deposition of histone H3.3 which may be linked to transcriptional induction of these genes. Required for the recruitment of histone H3.3:H4 dimers to PML-nuclear bodies (PML-NBs); the process is independent of ATRX and facilitated by ASF1A; PML-NBs are suggested to function as regulatory sites for the incorporation of newly synthesized histone H3.3 into chromatin. In case of overexpression of centromeric histone variant CENPA (as found in various tumors) is involved in its mislocalization to chromosomes; the ectopic localization involves a heterotypic tetramer containing CENPA, and

	histones H3.3 and H4 and decreases binding of CTCF to chromatin. Proposed to mediate activation of the JNK pathway and apoptosis via MAP3K5 in response to signaling from TNFRSF6 and TGFBR2. Interaction with HSPB1/HSP27 may prevent interaction with TNFRSF6 and MAP3K5 and block DAXX-mediated apoptosis. In contrast, in lymphoid cells JNC activation and TNFRSF6-mediated apoptosis may not involve DAXX. Shows restriction activity towards human cytomegalovirus (HCMV).
Tissue specificity	Ubiquitous.
Sequence similarities	Belongs to the DAXX family.
Domain	The Sumo interaction motif mediates Sumo binding, and is required both for sumoylation and binding to sumoylated targets.
Post-translational modifications	Sumoylated with SUMO1 on multiple lysine residues. Phosphorylated by HIPK1 upon glucose deprivation. Polyubiquitinated; which is promoted by CUL3 and SPOP and results in proteasomal degradation. Ubiquitinated by MDM2; inducing its degradation. Deubiquitinated by USP7; leading to stabilize it.
Cellular localization	Nucleus. Diffuse nuclear distribution pattern and no comparable dot-like accumulation of isoform 1 and Cytoplasm. Nucleus, nucleoplasm. Nucleus, PML body. Nucleus, nucleolus. Chromosome, centromere. Dispersed throughout the nucleoplasm, in PML/POD/ND10 nuclear bodies, and in nucleoli (Probable). Colocalizes with histone H3.3, ATRX, HIRA and ASF1A at PML-nuclear bodies (PubMed:12953102, PubMed:14990586, PubMed:23222847, PubMed:24200965). Colocalizes with a subset of interphase centromeres, but is absent from mitotic centromeres (PubMed:9645950). Detected in cytoplasmic punctate structures (PubMed:11842083). Translocates from the nucleus to the cytoplasm upon glucose deprivation or oxidative stress (PubMed:12968034). Colocalizes with RASSF1 in the nucleus (PubMed:18566590). Colocalizes with USP7 in nucleoplasma with accumulation in speckled structures (PubMed:16845383).

Images



SDS-PAGE - Recombinant Human Daxx protein (ab131785)

12.5% SDS-PAGE analysis of ab131785 stained with Coomassie Blue.

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