

## Daxx (Phospho Ser668) Rabbit pAb

CatalogNo: YP0625 **Orthogonal Validated** 

### Key Features

#### Host Species

- Rabbit

#### Reactivity

- Human, Mouse, Rat

#### Applications

- WB, IHC, IF, ELISA

#### MW

- 85-115kD (Observed)

#### Isotype

- IgG

### Storage

**Storage\*** -15°C to -25°C/1 year (Do not lower than -25°C)**Formulation** Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.

### Recommended Dilution Ratios

**WB 1:500-1:2000****IHC 1:100-1:300****ELISA 1:10000****IF 1:50-200**

### Basic Information

**Clonality** Polyclonal

### Immunogen Information

**Immunogen** The antiserum was produced against synthesized peptide derived from human Daxx around the phosphorylation site of Ser668. AA range: 634-683

**Specificity**

Phospho-Daxx (S668) Polyclonal Antibody detects endogenous levels of Daxx protein only when phosphorylated at S668. The name of modified sites may be influenced by many factors, such as species (the modified site was not originally found in human samples) and the change of protein sequence (the previous protein sequence is incomplete, and the protein sequence may be prolonged with the development of protein sequencing technology). When naming, we will use the "numbers" in historical reference to keep the sites consistent with the reports. The antibody binds to the following modification sequence (lowercase letters are modification sites):LPsPP

## | Target Information

**Gene name** DAXX

**Protein Name** Death domain-associated protein 6

| Organism | Gene ID                 | UniProt ID               |
|----------|-------------------------|--------------------------|
| Human    | <a href="#">1616</a> ;  | <a href="#">Q9UER7</a> ; |
| Mouse    | <a href="#">13163</a> ; | <a href="#">Q35613</a> ; |
| Rat      |                         | <a href="#">Q8VIB2</a> ; |

**Cellular Localization**

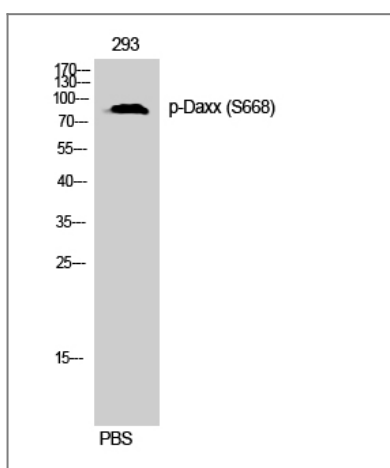
Cytoplasm . Nucleus, nucleoplasm . Nucleus, PML body . Nucleus, nucleolus . Chromosome, centromere . Dispersed throughout the nucleoplasm, in PML/POD/ND10 nuclear bodies, and in nucleoli (Probable). Colocalizes with histone H3.3, ATRX, HIRA and ASF1A at PML-nuclear bodies (PubMed:12953102, PubMed:14990586, 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 nucleoplasm with accumulation in speckled structures (PubMed:16845383). .; [Isoform beta]: Nucleus . Diffuse nuclear distribution pattern and no comparable dot-like accumulation of isoform 1. .; [Isoform gamma]: Nucleus . Diffuse nuclear distribution pattern and no comparable dot-like accumulation of isoform 1.

**Tissue specificity** Ubiquitous.

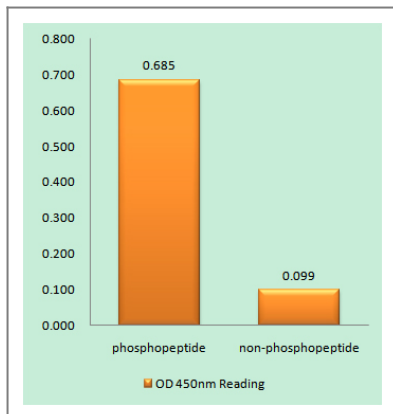
## Function

Function: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. Seems to regulate transcription in PML/POD/ND10 nuclear bodies together with PML and may influence TNFRSF6-dependent apoptosis thereby. Down-regulates basal and activated transcription. Seems to act as a transcriptional co-repressor and inhibits PAX3 and ETS1 through direct protein-protein interaction. Modulates PAX5 activity. 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.,induction:Upon mitogenic stimulation by concanavalin A.,PTM:Phosphorylated upon DNA damage, probably by ATM or ATR. Phosphorylated by HIPK1 upon glucose deprivation.,PTM:Polyubiquitinated; which is promoted by CUL3 and SPOP and results in proteasomal degradation.,PTM:Sumoylated.,similarity:Belongs to the DAXX family.,subcellular location:Dispersed throughout the nucleoplasm, in PML/POD/ND10 nuclear bodies, and in nucleoli. Colocalizes with a subset of interphase centromeres, but is absent from mitotic centromeres. Detected in cytoplasmic punctate structures. Translocates from the nucleus to the cytoplasm upon glucose deprivation or oxidative stress.,subunit:Homomultimer. Binds to the TNFRSF6 death domain via its C-terminus and to PAX5. Binds to SLC2A4/GLUT4, MAP3K5, TGFBR2, phosphorylated dimeric HSPB1/HSP27, CENPC1, ETS1, sumoylated PML, UBE2I and MCSR1. Is part of a complex containing PAX5 and CREBBP. Interacts with HIPK2 and HIPK3 via its N-terminus. Interacts with HIPK1, which induces translocation from PML/POD/ND10 nuclear bodies to chromatin and enhances association with HDAC1 (By similarity). The non-phosphorylated form binds to PAX3, PAX7, DEK, HDAC1, HDAC2, HDAC3, acetylated histone H4 and histones H2A, H2B, H3 and H4. Interacts with SPOP. Part of a complex consisting of DAXX, CUL3 and SPOP. Interacts with CBP; the interaction is dependent the sumoylation of CBP and suppresses CBP transcriptional activity via recruitment of HDAC2 (By similarity). Interacts with HCMV tegument phosphoprotein pp71.,tissue specificity:Ubiquitous.,

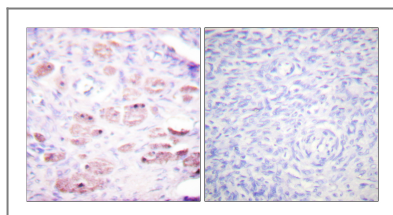
## Validation Data



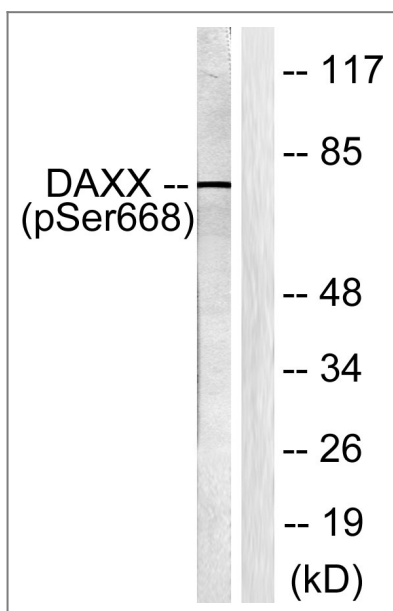
Western Blot analysis of 293 cells using Phospho-Daxx (S668) Polyclonal Antibody



Enzyme-Linked Immunosorbent Assay (Phospho-ELISA) for Immunogen Phosphopeptide (Phospho-left) and Non-Phosphopeptide (Phospho-right), using Daxx (Phospho-Ser668) Antibody



Immunohistochemistry analysis of paraffin-embedded human ovary, using Daxx (Phospho-Ser668) Antibody. The picture on the right is blocked with the phospho peptide.



Western blot analysis of lysates from 293 cells treated with PBS 60', using Daxx (Phospho-Ser668) Antibody. The lane on the right is blocked with the phospho peptide.

## Contact information

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