**Anti-Human ARID3A, monoclonal**

Alternate Names: AT-rich interactive domain-containing protein 3A

Cat. No. 13-034

**FOR RESEARCH USE ONLY**

**UniProt Summary**

| Primary Accession: | Q99856 |

Transcription factor which may be involved in the control of cell cycle progression by the RB1/E2F1 pathway and in B-cell differentiation. Homodimer. Heterodimer with ARID3B. Interacts with E2F1, interacts with GTF2I and BTK. Q06187:BTK; NbExp=3; IntAct=EBI-5458244, EBI-624835; Nucleus. Cytoplasm. Note=Shuttles between nucleus and cytoplasm. Widely expressed, with highest expression in skeletal muscle, thalamus, and colon. By p53/TP53 following DNA damage. Contains 1 ARID domain. Contains 1 REKLES domain. Sequence=AAW30734.1; Type=Frameshift; Positions=498;

**Physical Characteristics**

- **Quantity:** 1 ml (culture supernatant) or 100μg at 1mg/ml (purified)
- **Format:** culture supernatant or purified material
- **Host/Isotype:** mouse IgG1
- **Clonality:** monoclonal; ID R21.1.1E9

**Formulation:** culture supernatant contains 0.02% NaN3. Purified material contains 30% glycerol, PBS and 0.02% NaN3

**Specificity:** monospecific for human ARID3A ; see "Microarray Analysis" below

**Reactivity:** human; not tested for cross reactivity in other species

**Stability/Storage:** 12 months long term: -20°C; short term: 4°C; avoid freeze-thaw cycles; aliquot as required

**Handling Notes:** small volumes of antibody may occasionally become entrapped in the seal of the product vial during shipment and storage; briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container cap

**Tested Research Applications**

- Western Immunoblotting - PASS by SOP
- Immunoprecipitation - PASS by SOP
- SPR - PASS
- ChIP-Seq - PASS in HepG2 cell line(s). and did not pass in K562 cell line(s).

  - View raw alignment peaks
  - View MACS peak alignment

Antibody tested as purified IgG. Optimal dilution to be determined by user.

**Quality Assurance**

**Notes:**

1. Please refer to the SOP manual [click here](#) to for detailed explanation of the experimental setup and thresholds used to evaluate the results shown below.

2. Predicted MW of the target protein expressed in the western immunoblotting (WB) and immunoprecipitation (IP) experiment is **65.34kDa** and the three fusion tags (venus, 3xFLAG, V5) adds another **38.7kDa** to this protein. Therefore the protein is expected to migrate ~104.04kDa in a denatured SDS-PAGE gel.

3. See results below for any applicable cautionary notes.
About Z and S Scores: The z-score represents the strength of a signal that a mAb (in combination with a fluorescently-tagged anti-IgG secondary antibody) produces when binding to a particular protein on the HuProt™ array. Z-scores are described in units of standard deviations (SDs) above the mean value of all signals generated on that array. To be considered a definite binding event between a mAb and a protein target, the z-score must have a value of at least 2.5 (SDs above the mean). The s-score represents the relative target specificity of a mAb, and is the difference (also in units of SDs) between the z-score a mAb generates upon binding to one protein and the next highest z-score that the mAb generates against another protein. For example, if a mAb binds to protein X with a z-score of 43 and to protein Y with a z-score of 14, then the s-score for the binding of that mAb to protein X is equal to 29.

Affinity Measurements

Binding affinity measure by OIRD

Association constant – \( K_{on} \) (1/ms): \( 2.09 \times 10^5 \)

Dissociation constant - \( K_{off} \) (1/s): \( 5.19 \times 10^3 \)

Equilibrium binding constant - \( K_d \) (M): \( 2.05 \times 10^{-8} \)
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**Quality Assurance (continued)**

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**IMMUNOPRECIPITATION - Predicted MW 104.04kDa**

Tet-ON HeLa cells were transfected with construct encoding ARID3A (BC068286.1) with an N-terminal fusion of FLAG, YFP (Venus) and VS tags under a tetr-insducible promoter. These cells were stimulated with 0, 50 or 1000 ng/ml doxycycline. Immunoprecipitation (IP) was carried out using 5μg of either IgG, CDI mAb Anti-ARID3A (cloneID# R21.1.1E9) or 1 μg of FLAG-M2. Immunoblotting was performed using rabbit Anti-FLAG (1:1000, Cell Signalling #2368).
CHIP SEQ

The ChIP was performed with chromatin from 10 million HepG2 cells and 3 µg of Anti-ARID3A (cloneID #R21.1.1E9) antibody. The ChIP DNA was sequenced on an Illumina HiSeq platform and read counts were calculated at consecutive 100 bp bins across the human genome hg19. Normalized read-count levels for ChIP-seq of ARID3A (R21.1.1E9_ChIP) and control (R21.1.1E9_IN) around the ID2, IFT88, SPATA13 and LIMK2 loci are displayed in the CisGenome browser.
Quality Assurance (continued)

Western Blot

Pending data
ELISA performed by NCI. For protocol information click here.
SPR performed by NCI. For protocol information click [here](#).