SANTA CRUZ BIOTECHNOLOGY, INC.

Mi2 (B-4): sc-55606

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

In the intact cell, DNA closely associates with histones and other nuclear proteins to form chromatin. The remodeling of chromatin is believed to be a critical component of transcriptional regulation and a major source of this remodeling is brought about by the acetylation of nucleosomal histones. Acetylation of lysine residues in the amino-terminal tail domain of histone results in an allosteric change in the nucleosomal conformationdditional species, including equine, canine and porcine. and an increased accessibility to transcription factors by DNA. Conversely, the deacetylation of histones is associated with transcriptional silencing. Chromatin structure alteration may be brought about by the action of ATP-dependent multiprotein complexes. One such complex is the mSin3 corepressor complex, which contains mSin3, the histone deacetylases HDAC1 and HDAC2, the associated proteins SAP 30 and SAP 18, and the autoantigens Mi2-α and Mi2-β.

REFERENCES

1. Lee, D.Y., et al. 1993. A positive role for histone acetylation in transcription factor access to nucleosomal DNA. Cell 72: 73-82.
2. Braunstein, M., et al. 1993. Transcriptional silencing in yeast is associated with reduced nucleosome acetylation. Genes Dev. 7: 592-604.
3. Bauer, W.R., et al. 1994. Nucleosome structural changes due to acetylation. J. Mol. Biol. 236: 685-690.

CHROMOSOMAL LOCATION

Genetic locus: CHD3 (human) mapping to 17p13.1, CHD4 (human) mapping to 12p13.31; Chd3 (mouse) mapping to 11 B3, Chd4 (mouse) mapping to 6 F2.

SOURCE

Mi2 (B-4) is a mouse monoclonal antibody raised against amino acids 1671-1912 of Mi2 of human origin.

PRODUCT

Each vial contains 200 µg IgA kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

APPLICATIONS

Mi2 (B-4) is recommended for detection of Mi2-α and Mi2-β of mouse, rat and human origin by Western Blotting (starting dilution 1:100, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500), immunohistochemistry (including paraffin-embedded sections) (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Mi2 (B-4) is also recommended for detection of Mi2-α and Mi2-β in additional species, including equine, canine and porcine.

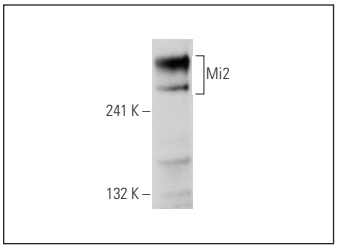
Molecular Weight of Mi2: 218 kDa.

Positive Controls: K-562 whole cell lysate: sc-2203 or K-562 nuclear extract: sc-2130.

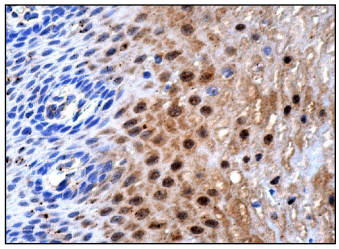
RECOMMENDED SUPPORT REAGENTS

To ensure optimal results, the following support reagents are recommended: 1) Western Blotting: use m-IgGκ BP-HRP: sc-516102 or m-IgGκ BP-HRP (Cruz Marker): sc-516102-CM (dilution range: 1:1000-1:10000), Cruz Marker™ Molecular Weight Standards: sc-2035, UltraCruz® Blocking Reagent: sc-516214 and Western Blotting Luminol Reagent: sc-2048. 2) Immunoprecipitation: use Protein L-Agarose: sc-2336 (0.5 ml agarose/2.0 ml). 3) Immunofluorescence: use m-IgGκ BP-FITC: sc-516140 or m-IgGκ BP-PE: sc-516141 (dilution range: 1:50-1:200) with UltraCruz® Mounting Medium: sc-24941 or UltraCruz® Hard-set Mounting Medium: sc-359850. 4) Immunohistochemistry: use m-IgGκ BP-HRP: sc-516102 with DAB, 50X: sc-24982 and Immunohistomount: sc-45086, or Organo/Limonene Mount: sc-45087.

DATA



Mi2 (B-4): sc-55606. Western blot analysis of Mi2 expression in K-562 whole cell lysate.



Mi2 (B-4): sc-55606. Immunoperoxidase staining of formalin fixed, paraffin-embedded human esophagus tissue showing nuclear and cytoplasmic staining of squamous epithelial cells.

SELECT PRODUCT CITATIONS

1. Verstappen G,, et al. 2008. Atypical Mowat-Wilson patient confirms the importance of the novel association between ZFHX1B/SIP1 and NuRD corepressor complex. Hum. Mol. Genet. 17: 1175-1183.
2. Qi, W., et al. 2015. Acetyltransferase p300 collaborates with chromodomain helicase DNA-binding protein 4 (CHD4) to facilitate DNA double-strand break repair. Mutagenesis 31: 193-203.
3. Blank, M.F., et al. 2017. SIRT7-dependent deacetylation of CDK9 activates RNA polymerase II transcription. Nucleic Acids Res. 45: 2675-2686.
4. Connelly, K.E., et al. 2018. Analysis of human nuclear protein complexes by quantitative mass spectrometry profiling. Proteomics 14: e1700427.

STORAGE

Store at 4° C, **DO NOT FREEZE**. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

RESEARCH USE

For research use only, not for use in diagnostic procedures.

PROTOCOLS

See our web site at www.scbt.com for detailed protocols and support products.