SANTA CRUZ BIOTECHNOLOGY, INC.

HoxB6 (S-20): sc-17171

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

Hox genes play a fundamental role in the development of the vertebrate central nervous system, heart, axial skeleton, limbs, gut, urogenital tract and external genitalia. There are multiple transcripts of the HoxB3 gene, and the anterior boundaries of its expression vary at different stages of development. HoxB3 plays a role in the proliferation and differentiation of both early myeloid and lymphoid developmental pathways. HoxB3 also has overlapping function in mediating the migration of pharyngeal organ primordia and is expressed in very restricted domains in the future hindbrain. HoxB6 controls the generation, proliferation and survival of erythroid progenitor cells. The HoxB6 protein is expressed in the suprabasal layer of the early developing epidermis and throughout the upper layers of late fetal and adult human skin. HoxB6 is cytoplasmically expressed throughout fetal epidermal development, but displays nuclear expression in normal adult skin. HoxB6 protein also has nuclear expression in hyperproliferative skin conditions, but appears to be localized in the cytoplasm in basal and squamous cell carcinomas. HoxB6 genes are also expressed in normal adult lung.

REFERENCES

1. Godsave, S., et al. 1994. Expression patterns of Hoxb genes in the *Xenopus* embryo suggest roles in anteroposterior specification of the hindbrain and in dorsoventral patterning of the mesoderm. Dev. Biol. 166: 465-476.
2. Sauvageau, G., et al. 1997. Overexpression of HOXB3 in hematopoietic cells causes defective lymphoid development and progressive myeloproliferation. Immunity 6: 13-22.

CHROMOSOMAL LOCATION

Genetic locus: HOXB6 (human) mapping to 17q21.32; Hoxb6 (mouse) mapping to 11 D.

SOURCE

HoxB6 (S-20) is an affinity purified goat polyclonal antibody raised against a peptide mapping within an internal region of HoxB6 of human origin.

PRODUCT

Each vial contains 200 µg IgG in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin. Also available as TransCruz reagent for Gel Supershift and ChIP applications, sc-17171 X, 200 µg/0.1 ml.

Blocking peptide available for competition studies, sc-17171 P, (100 µg peptide in 0.5 ml PBS containing < 0.1% sodium azide and 0.2% BSA).

STORAGE

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

PROTOCOLS

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

APPLICATIONS

HoxB6 (S-20) is recommended for detection of HoxB6 of mouse, rat and human origin by Western Blotting (starting dilution 1:200, 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) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

HoxB6 (S-20) is also recommended for detection of HoxB6 in additional species, including equine, canine, bovine and porcine.

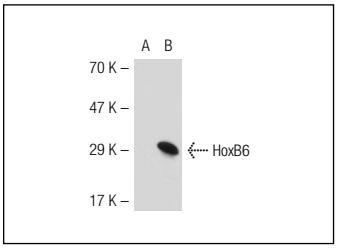
Suitable for use as control antibody for HoxB6 siRNA (h): sc-38694, HoxB6 siRNA (m): sc-38695, HoxB6 shRNA Plasmid (h): sc-38694-SH, HoxB6 shRNA Plasmid (m): sc-38695-SH, HoxB6 shRNA (h) Lentiviral Particles: sc-38694-V and HoxB6 shRNA (m) Lentiviral Particles: sc-38695-V.

HoxB6 (S-20) X TransCruz antibody is recommended for Gel Supershift and ChIP applications.

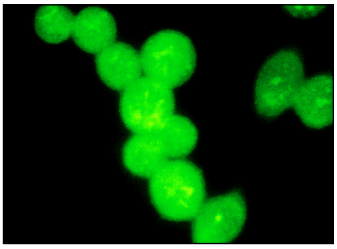
Molecular Weight of HoxB6 isoform 1/2: 25/15 kDa.

Positive Controls: HoxB6 (m): 293T Lysate: sc-125468.

DATA



HoxB6 (S-20): sc-17171. Western blot analysis of HoxB6 expression in non-transfected: sc-117752 (**A**) and mouse HoxB6 transfected: sc-125468 (**B**) 293T whole cell lysates.



HoxB6 (S-20): sc-17171. Immunofluorescence staining of methanol-fixed SW480 cells showing nuclear localization.

SELECT PRODUCT CITATIONS

1. Shen, W., et al. 2004. HOXB6 protein is bound to CREB-binding protein and represses globin expression in a DNA binding-dependent, PBX interaction-independent process. J. Biol. Chem. 279: 39895-39904.
2. Yamashita, R., et al. 2011. Genome-wide characterization of transcriptional start sites in humans by integrative transcriptome analysis. Genome Res. 21: 775-789.

RESEARCH USE

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