SANTA CRUZ BIOTECHNOLOGY, INC.

Zip1 (yN-16): sc-48716

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

Zip1 is a yeast synaptonemal complex (SC) central region component and is required for normal meiotic recombination and crossover interference. Zip1 plays at least one role in recombination that does not involve SC polymerization along the chromosomes. Perhaps some Zip1 molecules act first in or around the sites of recombinational interactions to influence the recombination process and thence nucleate SC formation. Zip1 is predicted to form an α-helical coiled coil, flanked by globular domains at the amino and carboxy termini. The amino-terminal domain of Zip1 is located in the middle of the central region of the SC, whereas the carboxy-terminal domain is embedded in the lateral elements of the complex. Furthermore, the carboxy terminus, but not the amino terminus, of Zip1 is required for its localization to chromosomes. The zip1 mutant, which exhibits defects in synaptonemal complex formation and meiotic recombination, triggers a checkpoint that causes cells to arrest at the pachytene stage of meiotic prophase.

REFERENCES

1. Storlazzi, A., et al. 1996. Synaptonemal complex (SC) component Zip1 plays a role in meiotic recombination independent of SC polymerization along the chromosomes. Proc. Natl. Acad. Sci. USA 93: 9043-9048.
2. Xu, L., et al. 1997. Meiotic cells monitor the status of the interhomolog recombination complex. Genes Dev. 11: 106-108.
3. Tung, K.S. and Roeder, G.S. 1998. Meiotic chromosome morphology and behavior in Zip1 mutants of *Saccharomyces cerevisiae*. Genetics 149: 817-832.
4. Dong, H. and Roeder, G.S. 2000. Organization of the yeast Zip1 protein within the central region of the synaptonemal complex. J. Cell Biol. 148: 417-426.
5. Bailis, J.M., et al. 2000. Bypass of a meiotic checkpoint by overproduction of meiotic chromosomal proteins. Mol. Cell. Biol. 20: 4838-4848.

SOURCE

Zip1 (yN-16) is an affinity purified goat polyclonal antibody raised against a peptide mapping near the N-terminus of Zip1 of *Saccharomyces cerevisiae* origin.

PRODUCT

Each vial contains 200 µg IgG in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

Blocking peptide available for competition studies, sc-48716 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.

RESEARCH USE

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

APPLICATIONS

Zip1 (yN-16) is recommended for detection of Zip1 of *Saccharomyces cerevisiae* origin by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000), 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).

Molecular Weight of Zip1: 109 kDa.

RECOMMENDED SECONDARY REAGENTS

To ensure optimal results, the following support (secondary) reagents are recommended: 1) Western Blotting: use donkey anti-goat IgG-HRP: sc-2020 (dilution range: 1:2000-1:100,000) or Cruz Marker™ compatible donkey anti-goat IgG-HRP: sc-2033 (dilution range: 1:2000-1:5000), Cruz Marker™ Molecular Weight Standards: sc-2035, TBS Blotto A Blocking Reagent: sc-2333 and Western Blotting Luminol Reagent: sc-2048. 2) Immunofluorescence: use donkey anti-goat IgG-FITC: sc-2024 (dilution range: 1:100-1:400) or donkey anti-goat IgG-TR: sc-2783 (dilution range: 1:100-1:400) with UltraCruz™ Mounting Medium: sc-24941.

SELECT PRODUCT CITATIONS

1. Bardhan, A., et al. 2010. Meiotic cohesin promotes pairing of nonhomologous centromeres in early meiotic prophase. Mol. Biol. Cell 21: 1799-1809.

PROTOCOLS

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