SANTA CRUZ BIOTECHNOLOGY, INC.

CstF-64 (C-20): sc-16473

BACKGROUND

Polyadenylation of mRNA precursors is a two-step reaction that requires multiple protein factors. The first step, endonucleolytic cleavage of polyadeny lation substrates, requires CstF (cleavage stimulation factor), a heterotrimer that is composed of three distinct subunits. CstF-64 contains an RNA binding domain and is responsible for the RNA binding activity of CstF. CstF-64 is expressed in all somatic cells and in pre- and postmeiotic, but not meiotic, germ cells. However, a large variant of CstF-64, called t CstF-64, is abundantly expressed in meiotic and postmeiotic cells in the testis and to a lesser extent in the brain, and promotes the germ cell pattern of polyadenylation. The gene encoding CstF-64 (designated CSTF2) maps to the X chromosome, whereas τ CstF-64 is encoded by an autosomal gene. The increase in CstF-64 concentration during B cell activation switches IgM heavy chain mRNA expression from membrane-bound to secreted forms, suggesting that CstF-64 plays a key role in regulating IgM heavy chain expression during B cell differentiation.

CHROMOSOMAL LOCATION

Genetic locus: CSTF2 (human) mapping to Xq22.1, CSTF2T (human) mapping to 10q21.1; Cstf2 (mouse) mapping to X E3, Cstf2t (mouse) mapping to 19 C1.

SOURCE

CstF-64 (C-20) is an affinity purified goat polyclonal antibody raised against a peptide mapping near the C-terminus of CstF-64 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.

Blocking peptide available for competition studies, sc-16473 P, (100 µg peptide in 0.5 ml PBS containing < 0.1% sodium azide and 0.2% BSA).

RESEARCH USE

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

PROTOCOLS

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

APPLICATIONS

CstF-64 (C-20) is recommended for detection of CstF-64 and CstF-64T 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).

CstF-64 (C-20) is also recommended for detection of CstF-64 and CstF-64T in additional species, including equine, canine, bovine, porcine and avian.

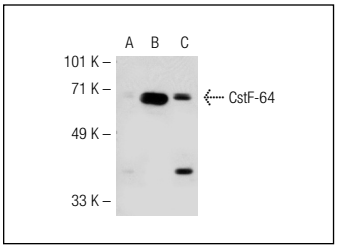
Molecular Weight of CstF-64: 64 kDa.

Positive Controls: CstF-64 (h): 293T Lysate: sc-113457, CstF-64T (m): 293T Lysate: sc-119490 or HeLa whole cell lysate: sc-2200.

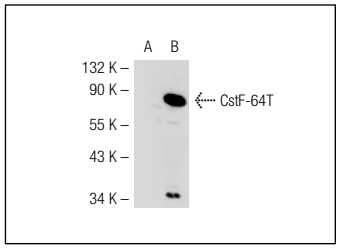
STORAGE

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

DATA



CstF-64 (C-20): sc-16473. Western blot analysis of CstF-64 expression in non-transfected 293T: sc-117752 (**A**), human CstF-64 transfected 293T: sc-113457 (**B**) and HeLa (**C**) whole cell lysates.



CstF-64 (C-20): sc-16473. Western blot analysis of CstF-64T expression in non-transfected: sc-117752 (**A**) and mouse CstF-64T transfected: sc-119490 (**B**) 293T whole cell lysates.

SELECT PRODUCT CITATIONS

1. Uguen, P., et al. 2003. The 3' ends of human pre-snRNAs are produced by RNA polymerase II CTD-dependent RNA processing. EMBO J. 22: 4544-4554.
2. Li, L., et al. 2006. Dynamic nature of cleavage bodies and their spatial relationship to DDX1 bodies, Cajal bodies, and gems. Mol. Biol. Cell 17: 1126-1140.
3. Bruce, A.W., et al. 2006. The transcriptional repressor REST is a critical regulator of the neurosecretory phenotype. J. Neurochem. 98: 1828-1840.
4. Uhlmann, T., et al. 2007. The VP16 activation domain establishes an active mediator lacking Cdk8 *in vivo*. J. Biol. Chem. 282: 2163-2173.
5. Nag, A., et al. 2007. The poly(A)-dependent transcriptional pause is mediated by CPSF acting on the body of the polymerase. Nat. Struct. Mol. Biol. 14: 662-669.
6. Yung, T.M., et al. 2009. Cellular dynamics of the negative transcription elongation factor NELF. Exp. Cell Res. 315: 1693-1705.
7. Bruce, A.W., et al. 2009. Functional diversity for REST (NRSF) is defined by *in vivo* binding affinity hierarchies at the DNA sequence level. Genome Res. 19: 994-1005.
8. Martin, G., et al. 2012. Genome-wide analysis of pre-mRNA 30 end processing reveals a decisive role of human cleavage factor I in the regulation of 30 UTR length. Cell Rep. 1: 753-763.