

Set1 (1.4): sc-101858

BACKGROUND

The trithorax gene family functions to maintain specific patterns of gene expression throughout cellular development by activating or repressing transcription. Members of this family contain a highly conserved 130- to 140-amino acid motif designated the SET domain, and include the *Drosophila* and human trithorax and Su(var)3-9 protein homologues. The *Saccharomyces cerevisiae* trithorax homolog Set1, a Histone H3-lysine 4 (H3-K4) methylase, regulates chromatin structure, DNA repair, and telomeric function. It also regulates rDNA silencing, either directly or indirectly, via H3 methylation. Set1 forms a complex with six other nonessential proteins. This complex, designated COMPASS (complex proteins associated with Set1) includes Cps25, Cps30, Cps35, Cps40, Cps50, and Cps60. Phosphorylation of the C-terminal domain (CTD) of Pol II at Serine 5 by the TFIIF-associated kinase mediates the transition between initiation and elongation. Set1 associates with this phosphorylated form of Pol II, and may provide a molecular memory of recent transcriptional activity.

REFERENCES

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- Miller, T., et al. 2001. COMPASS: a complex of proteins associated with a trithorax-related SET domain protein. *Proc. Natl. Acad. Sci. USA* 98: 12902-12907.
- Schramke, V., et al. 2001. The Set1 δ mutation unveils a novel signaling pathway relayed by the Rad53-dependent hyperphosphorylation of replication protein A that leads to transcriptional activation of repair genes. *Genes Dev.* 15: 1845-1858.
- Briggs, S.D., et al. 2001. Histone H3 Lysine 4 methylation is mediated by Set1 and required for cell growth and rDNA silencing in *Saccharomyces cerevisiae*. *Genes Dev.* 15: 3286-3295.
- Bryk, M., et al. 2002. Evidence that Set1, a factor required for methylation of Histone H3, regulates rDNA silencing in *S. cerevisiae* by a Sir2-independent mechanism. *Curr. Biol.* 12: 165-170.
- Nagy, P.L., et al. 2002. A trithorax-group complex purified from *Saccharomyces cerevisiae* is required for methylation of Histone H3. *Proc. Natl. Acad. Sci. USA* 99: 90-94.
- Krogan, N.J., et al. 2002. COMPASS, a Histone H3 (lysine 4) methyltransferase required for telomeric silencing of gene expression. *J. Biol. Chem.* 277: 10753-10755.
- Ng, H.H., et al. 2003. Targeted recruitment of Set1 histone methylase by elongating Pol II provides a localized mark and memory of recent transcriptional activity. *Mol. Cell* 11: 709-719.

SOURCE

Set1 (1.4) is a mouse monoclonal antibody raised against a recombinant protein corresponding to amino acids 470-1080 of Set1 of *Saccharomyces cerevisiae* origin.

PRODUCT

Each vial contains 200 μ g IgG₁ kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

Set1 (1.4) is available conjugated to agarose (sc-101858 AC), 500 μ g/0.25 ml agarose in 1 ml, for IP; to HRP (sc-101858 HRP), 200 μ g/ml, for WB, IHC(P) and ELISA; to either phycoerythrin (sc-101858 PE), fluorescein (sc-101858 FITC), Alexa Fluor® 488 (sc-101858 AF488), Alexa Fluor® 546 (sc-101858 AF546), Alexa Fluor® 594 (sc-101858 AF594) or Alexa Fluor® 647 (sc-101858 AF647), 200 μ g/ml, for WB (RGB), IF, IHC(P) and FCM; and to either Alexa Fluor® 680 (sc-101858 AF680) or Alexa Fluor® 790 (sc-101858 AF790), 200 μ g/ml, for Near-Infrared (NIR) WB, IF and FCM.

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APPLICATIONS

Set1 (1.4) is recommended for detection of Set1 of *Saccharomyces cerevisiae* origin by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000) and immunoprecipitation [1-2 μ g per 100-500 μ g of total protein (1 ml of cell lysate)].

Molecular Weight of Set1: 124 kDa.

RECOMMENDED SUPPORT REAGENTS

To ensure optimal results, the following support reagents are recommended: 1) Western Blotting: use m-IgG κ BP-HRP: sc-516102 or m-IgG κ 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 A/G PLUS-Agarose: sc-2003 (0.5 ml agarose/2.0 ml).

SELECT PRODUCT CITATIONS

- Schibler, A., et al. 2016. Histone H3K4 methylation regulates deactivation of the spindle assembly checkpoint through direct binding of Mad2. *Genes Dev.* 30: 1187-1197.
- Bae, H.J., et al. 2020. The Set1 N-terminal domain and Swd2 interact with RNA polymerase II CTD to recruit COMPASS. *Nat. Commun.* 11: 2181.
- Yu, Q., et al. 2022. Phosphorylation of Jhd2 by the Ras-cAMP-PKA(Tpk2) pathway regulates histone modifications and autophagy. *Nat. Commun.* 13: 5675.

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.