



Histone cluster 1 H2BC siRNA (h): sc-105473

BACKGROUND

Eukaryotic histones are basic and water soluble nuclear proteins that form hetero-octameric nucleosome particles by wrapping 146 base pairs of DNA in a left-handed super-helical turn sequentially to form chromosomal fiber. Two molecules of each of the four core Histones (H2A, H2B, H3, and H4) form the octamer; formed of two H2A-H2B dimers and two H3-H4 dimers, forming two nearly symmetrical halves by tertiary structure. Over 80% of nucleosomes contain the linker Histone H1, derived from an intronless gene, that interacts with linker DNA between nucleosomes and mediates compaction into higher order chromatin. Histones are subject to posttranslational modification by enzymes primarily on their N-terminal tails, but also in their globular domains. Such modifications include methylation, citrullination, acetylation, phosphorylation, sumoylation, ubiquitination and ADP-ribosylation. The Histone cluster 1 H2BC gene is intronless and maps to a small histone gene cluster on human chromosome 6p22.2.

REFERENCES

1. Rupp, R.A., et al. 2005. Gene regulation by Histone H1: new links to DNA methylation. *Cell* 123: 1178-1179.
2. Martin, C., et al. 2005. The diverse functions of histone lysine methylation. *Nat. Rev. Mol. Cell Biol.* 6: 838-849.
3. Gunjan, A., et al. 2005. Regulation of histone synthesis and nucleosome assembly. *Biochimie* 87: 625-635.
4. Bode, A.M., et al. 2005. Inducible covalent posttranslational modification of Histone H3. *Sci. STKE* 2005: re4.
5. Bustin, M., et al. 2005. The dynamics of Histone H1 function in chromatin. *Mol. Cell* 17: 617-620.
6. de la Cruz, X., et al. 2005. Do protein motifs read the histone code? *Bioessays* 27: 164-175.
7. Hake, S.B., et al. 2006. Histone H3 variants and their potential role in indexing mammalian genomes: the "H3 barcode hypothesis". *Proc. Natl. Acad. Sci. USA* 103: 6428-6435.
8. Nightingale, K.P., et al. 2006. Histone modifications: signalling receptors and potential elements of a heritable epigenetic code. *Curr. Opin. Genet. Dev.* 16: 125-136.
9. Wurtele, H., et al. 2006. Histone post-translational modifications and the response to DNA double-strand breaks. *Curr. Opin. Cell Biol* 18: 137-144.

CHROMOSOMAL LOCATION

Genetic locus: HIST1H2BC (human) mapping to 6p22.2.

PRESEARCH 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.

RODUCT

Histone cluster 1 H2BC siRNA (h) is a pool of 2 target-specific 19-25 nt siRNAs designed to knock down gene expression. Each vial contains 3.3 nmol of lyophilized siRNA, sufficient for a 10 μ M solution once resuspended using protocol below. Suitable for 50-100 transfections. Also see Histone cluster 1 H2BC shRNA Plasmid (h): sc-105473-SH and Histone cluster 1 H2BC shRNA (h) Lentiviral Particles: sc-105473-V as alternate gene silencing products.

For independent verification of Histone cluster 1 H2BC (h) gene silencing results, we also provide the individual siRNA duplex components. Each is available as 3.3 nmol of lyophilized siRNA. These include: sc-105473A and sc-105473B.

STORAGE AND RESUSPENSION

Store lyophilized siRNA duplex at -20° C with desiccant. Stable for at least one year from the date of shipment. Once resuspended, store at -20° C, avoid contact with RNAses and repeated freeze thaw cycles.

Resuspend lyophilized siRNA duplex in 330 μ l of the RNase-free water provided. Resuspension of the siRNA duplex in 330 μ l of RNase-free water makes a 10 μ M solution in a 10 μ M Tris-HCl, pH 8.0, 20 mM NaCl, 1 mM EDTA buffered solution.

APPLICATIONS

Histone cluster 1 H2BC siRNA (h) is recommended for the inhibition of Histone cluster 1 H2BC expression in human cells.

SUPPORT REAGENTS

For optimal siRNA transfection efficiency, Santa Cruz Biotechnology's siRNA Transfection Reagent: sc-29528 (0.3 ml), siRNA Transfection Medium: sc-36868 (20 ml) and siRNA Dilution Buffer: sc-29527 (1.5 ml) are recommended. Control siRNAs or Fluorescein Conjugated Control siRNAs are available as 10 μ M in 66 μ l. Each contain a scrambled sequence that will not lead to the specific degradation of any known cellular mRNA. Fluorescein Conjugated Control siRNAs include: sc-36869, sc-44239, sc-44240 and sc-44241. Control siRNAs include: sc-37007, sc-44230, sc-44231, sc-44232, sc-44233, sc-44234, sc-44235, sc-44236, sc-44237 and sc-44238.