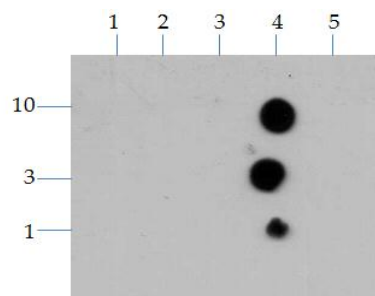
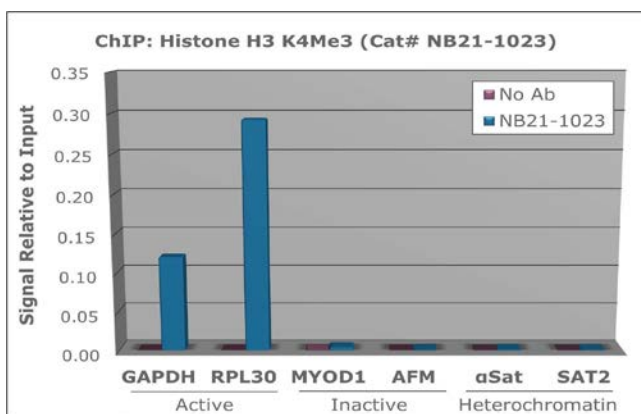


**Description:** Histone H3 trimethyl lysine 4 antibody  
**Species:** Human, mouse, rat, C. elegans  
**Applications:** Westerns, dot blots, CHIP  
**Modification:** K4Me3  
**Immunogen:** Synthetic peptide containing trimethylated lysine 4 of histone H3  
**Gene Symbol:** HIST2H3C Entrez: 126961 (hu), 260423 (mu) Swiss Prot: Q71DI3 (hu), P84228 (mu)

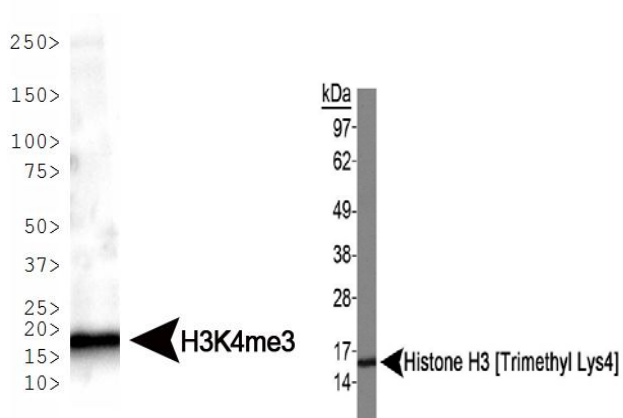
**Cat#:** NB21-1023  
**Gene:** HIST2H3C  
**Ab Type:** Rabbit affinity purified pAb  
**Marker:** H3K4Me3

**Images:**

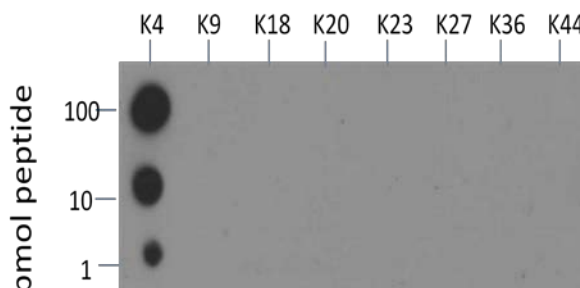


1. K4
2. K4-KMe1
3. K4-KMe2
4. K4-KMe3
5. K23-KMe3

**Western blot - C. elegans embryo lysate (left) and HeLa cell nuclear extract (right)**



NB21-1023 antibody cross-reactivity with H3 or H4 peptides containing KMe3 modifications at specific lysines



**Background:**

The nucleosome is comprised of 146 bp of DNA wrapped around a series of histone proteins arranged as an octamer consisting of 2 copies of histone H2A, H2B, H3 and H4 (1). Within the nucleosome core the histone proteins are covalent

modified at specific residues predominantly within the N-terminal tail including lysine (acetylation, methylation, SUMOylation, and ubiquitylation), arginine methylation and citrullination, serine and threonine phosphorylation, as well as proline isomerization (2,3). The lysine side chains can carry up to three methyl groups (mono-, di- and trimethylated forms) and the arginine side chain can be monomethylated or can be dimethylated as the symmetric or asymmetric forms. The modifications show temporal, disease-specific, and other types of cell-specific regulation and there are specific families of enzymes that regulate the methylation, demethylation, acetylation, deacetylation and other modifications (4-8). Research has indicated that whereas the histone mark H3K4Me3 (tri-methyl lysine 4 of histone H3) localizes to gene promoter regions (it is associated with transcriptional activation) other modifications at H3K4 such as monomethyl is present predominantly at enhancer sequences (5). Specific marks have been shown to be associated with the activation (H3K9Me1, H3K27Me1, and H4K20Me1) or repression (H3K9Me2 and Me3, H3K27Me2 and Me3, and H4K20Me2 and Me3) of genes. Monomethylation of H4 at K20, catalyzed by SET8, is essential to genome replication and stability. Multiple DNA breaks are associated with demethylation at this site, resulting in activation of p53 to avoid mitosis and aberrant chromosomal activity. In mammalian stem cells, Xist expression blocks the formation of H4K20me1, which is one of the first examples of a direct connection between chromatin and stem cell differentiation.

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3. Zee, BM, Levin, RS, DiMaggio, PA and Garcia, BA. Global Turnover of histone post-translational modifications and variants in human cells. *Epigenetics and Chromatin.* [2010] 3:22.
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5. Heintzman ND, Stuart RK, Hon G, Fu Y, Ching CW, Hawkins RD, Barrera LO, Van Calcar S, Qu C, Ching KA, Wang W, Weng Z, Green RD, Crawford GE, Ren B. Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. *Nat Genet.* [2007] 39(3):311–8.
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7. Bernstein BE, Meissner A, Lander ES. The mammalian epigenome. *Cell.* [2007] 128(4):669–81.
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**Dilutions:** WB, DB – 1:1,000 to 1:2,500; ChIP 2-5 micrograms per 10<sup>6</sup> cells.

**Unit Size:** 50 micrograms (0.05mg)

**Storage:** Short term storage at 4°C, long term storage at -20°C. Avoid unnecessary freeze-thaw.

**Buffer:** PBS, pH 7.4 with 30% glycerol

**Preservative:** 0.05% sodium azide

**Limitations:** This product is for research purposes only and is not approved for use in clinical diagnostics or for use in humans.

[Ask a question](#)

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