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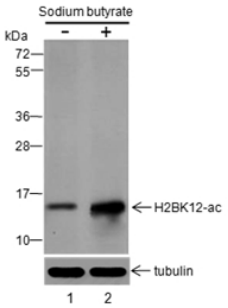
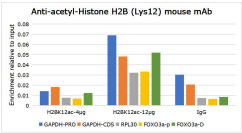
Histone H2B (Acetyl K12) Mouse mAb

Catalog Number:	bsm-60046M
Target Protein:	Histone H2B (Acetyl K12)
Concentration:	1mg/ml
Form:	Liquid
Host:	Mouse
Clonality:	Monoclonal
Clone No.:	H2D4
Isotype:	IgG
Applications:	WB (1:500-2000), IHC-P (1:100-500), IHC-F (1:50-100), IF (1:50-100)
Reactivity:	Human (predicted:Mouse, Rat)
Predicted MW:	14 kDa
Entrez Gene:	3018
Swiss Prot:	P33778
Purification:	affinity purified by Protein G
Storage:	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol. Shipped at 4°C. Store at -20°C for one year. Avoid repeated freeze/thaw cycles.
Background:	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Nucleosomes consist of approximately 146 bp of DNA wrapped around a histone octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene is intronless and encodes a member of the histone H2B family. Transcripts from this gene lack polyA tails; instead, they contain a palindromic termination element. This gene is found in the large histone gene cluster on chromosome 6p22-p21.3. [provided by RefSeq, Jul 2008].

VALIDATION IMAGES



Blocking buffer: 5% NFDM/TBST Primary ab dilution: 1:2000 Primary ab incubation condition: 2 hours at room temperature Secondary ab: Goat Anti-Mouse IgG H&L (HRP) Lysate: (-) HeLa, (+) HeLa+Sodium butyrate (30mM, 4hr) Protein loading quantity: 20 µg Exposure time: 60 s Predicted MW: 14 kDa Observed MW: 14 kDa



Cell type: HeLa + Serum starvation (12 h) + SBA (5 mM, 24 h) Cross-linking conditions: No cross-linking Amount of chromatin per IP: 5×106 cells Amount of Ab per IP: 12 µg Beads type and amount per IP: 50 µL of Protein A/G MagBeads Comment: The ChIP was performed with 1 µg of normal rabbit IgG as a negative control. Real time quantitative PCR was performed on immunoprecipitated DNA using primers specific for the human GAPDH promoter, GAPDH CDS region, RPL30 Exon 3, FOXO3a-promoter and FOXO3a-downstream. Data are presented as enrichment of each sample relative to total amount of input chromatin at each amplicon.