

Histone H2B (7E2) Mouse mAb
Catalog # AP53518**Specification**

Histone H2B (7E2) Mouse mAb - Product Information

Application	WB, IHC
Primary Accession	P33778
Reactivity	Rat
Host	Mouse
Clonality	Monoclonal Antibody
Calculated MW	13950

Histone H2B (7E2) Mouse mAb - Additional Information**Gene ID** 3018**Other Names**

H2B GL105, H2B.1, Histone H2B type 1B, HIST1H2BB

Dilution

WB~~1:100000

IHC~~1:100~500

Histone H2B (7E2) Mouse mAb - Protein Information**Name** H2BC3 ([HGNC:4751](#))**Function**

Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling.

Cellular Location

Nucleus. Chromosome.

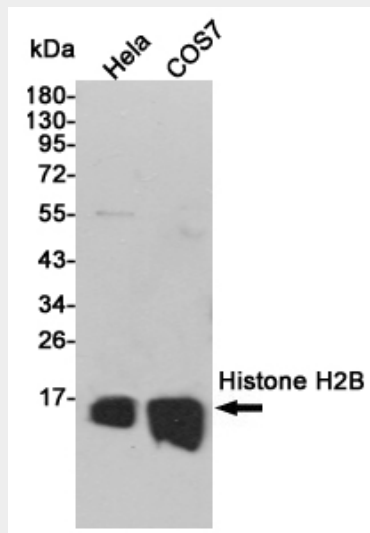
Histone H2B (7E2) Mouse mAb - Protocols

Provided below are standard protocols that you may find useful for product applications.

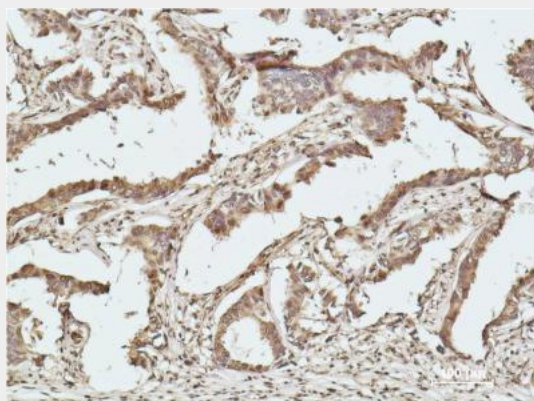
- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)

- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

Histone H2B (7E2) Mouse mAb - Images



Western blot detection of Histone H2B in HeLa and COS7 cell lysates using Histone H2B mouse mAb (1:100000 diluted). Predicted band size: 14kDa. Observed band size: 14kDa.



Immunohistochemical analysis of paraffin-embedded human breast carcinoma using Histone H2B mouse mAb diluted at 1:500.

Histone H2B (7E2) Mouse mAb - Background

Swiss-Prot Acc.P33778. Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling.