

Product datasheet

Recombinant Human Histone H2A.Z protein (denatured) ab177637

1 Image

Description

Product name	Recombinant Human Histone H2A.Z protein (denatured)	
Purity	> 85 % SDS-PAGE.	
Expression system	Escherichia coli	
Accession	P0C0S5	
Protein length	Full length protein	
Animal free	No	
Nature	Recombinant	
Species	Human	
Sequence	MGSSHHHHHSSGLVPRGSHMGSMAGGKAGKDSGKAK TKAVSRSQRAGLQ FPVGRHRHLKSRRTTSHGRVGATAAVYSAAILEYLTAEVLE LAGNASKDL KVKRITPRHLQLAIRGDEELDSLKATIAGGGVIPHIHKSLLIGK KGQQKT V	
Predicted molecular weight	16 kDa including tags	
Amino acids	1 to 128	
Tags	His tag N-Terminus	
Additional sequence information	NP_002097.	
Description	Recombinant Human Histone H2A.Z protein	

Specifications

Our [Abpromise guarantee](#) covers the use of **ab177637** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications SDS-PAGE

Form Liquid

Preparation and Storage

Stability and Storage

Shipped at 4°C. Store at +4°C short term (1-2 weeks). Upon delivery aliquot. Store at -20°C or -80°C. Avoid freeze / thaw cycle.

pH: 8.00

Constituents: 0.32% Tris-HCl buffer, 2.4% Urea, 10% Glycerol (glycerin, glycerine)

General Info

Function

Variant histone H2A which replaces conventional H2A in a subset of nucleosomes. 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. May be involved in the formation of constitutive heterochromatin. May be required for chromosome segregation during cell division.

Sequence similarities

Belongs to the histone H2A family.

Post-translational modifications

Monoubiquitination of Lys-122 gives a specific tag for epigenetic transcriptional repression. Acetylated on Lys-5, Lys-8 and Lys-12 during interphase. Acetylation disappears at mitosis. Monomethylated on Lys-5 and Lys-8 by SETD6. SETD6 predominantly methylates Lys-8, lys-5 being a possible secondary site. Not phosphorylated.

Cellular localization

Nucleus. Chromosome.

Images



15% SDS-PAGE analysis of ab177637 (3µg).

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