Recombinant Mononucleosomes (H2A.Z)

Catalog No: 81072
Lot No: 35617001
Expressed In: *E. coli*

Quantity: 50 µg
Concentration: 0.58 µg/µl
Source: Human

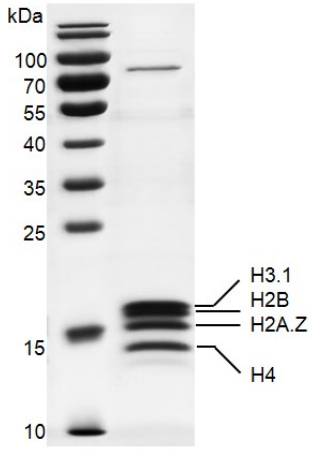
Buffer Contents: Recombinant Mononucleosomes (H2A.Z) (50 µg protein + 50 µg DNA) are supplied in 10 mM Tris-HCl pH 8.0, 1 mM EDTA, 2 mM DTT and 20% glycerol.

Background: *In vivo*, nucleosome is the basic structural unit of chromatin. It is consisted of about 146 bp of DNA wrapped around a core of eight histones of four different types: H2A, H2B, H3 and H4. Histones are subject to posttranslational modifications, such as methylation, acetylation, phosphorylation, mono-ubiquitination, tec. Histone modifications influence multiple chromatin templated processes such as gene transcription, DNA repair and recombination. Besides the “major“ histones, there are some histone variants in specific regions of chromatin or in specific cell types. Histone variants were involved in multiple biology processes including chromosome segregation, DNA repair, transcriptional regulation and mRNA processing.
H2A.Z (also known as H2AFZ, Histone Family Member Z) is a histone H2A family member. It is highly conserved from yeast to human, with 90% of its primary sequence preserved among different species, showing only 60% homology with canonical histone H2A. H2A.Z is found in approximately 10% of mammalian nucleosomes. H2A.Z has been one of the most studied H2A variants in recent years. It plays an important role in different biological processes such as DNA replication, DNA repair, transcription regulation, cell cycle, spermatogenesis, chromosome segregation, centromere structure and maintenance of heterochromatic/euchromatic status. However, different studies reported diverse conclusions in the nucleosome stability and transcriptional regulation. The contradictory roles of H2A.Z *in vivo* might be explained by different combinations of H2A.Z with other epigenetic regulators, PTMs on H2A.Z and interaction with chromatin binding proteins. Nucleosomes are more physiologically relevant substrates than histones and histone-derived peptides for *in vitro* studies. More importantly, some histone methyltransferases are significantly more active, as well as specific, when using nucleosomal substrates in HMT assays, such as DOT1L and NSD family enzymes. Nucleosomes are also widely used in histone methyltransferase screening assays to identify small molecular inhibitors for drug discovery.

Protein Details: Recombinant Mononucleosomes (H2A.Z) consist of 167 bp of 601 DNA and two molecules each of histones H2A.Z that includes amino acids 1-128 (end) (accession number NP_002097.1), H2B that includes amino acids 1-126 (end) (accession number NP_003509.1), H3 that includes amino acids 1-136 (end) (accession number NP_003520.1), and H4 that includes amino acids 1-103 (end) (accession number NP_003539.1). All of these histones were expressed in *E. coli* cells. The molecular weight of histone octamer is ~108.3 kDa.

Application Notes: Recombinant Mononucleosomes (H2A.Z) are suitable for use as substrates in the study of enzyme kinetics, inhibitor screening, and selectivity profiling.

Storage and Guarantee: Recombinant proteins in solution are temperature sensitive and must be stored at -80°C to prevent degradation. Avoid repeated freeze/thaw cycles and keep on ice when not in storage. This product is for research use only and is not for use in diagnostic procedures. This product is guaranteed for 6 months from date of arrival.

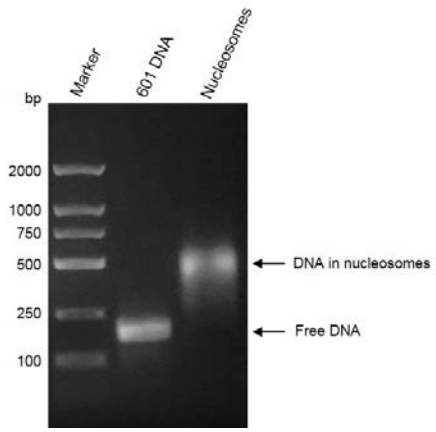


Recombinant Mononucleosomes (H2A.Z)

13% SDS-PAGE Coomassie staining

MW: 108.3 kDa

Purity: ≥ 85%



Recombinant Mononucleosomes (H2A.Z) DNA gel
Mononucleosomes (H2A.Z) were run on a 2% agarose gel and stained with ethidium bromide. Lane 1: DNA marker. Lane 2: free 601 DNA. Lane 3: Intact mononucleosomes. Intact mononucleosomes migrate much higher than free 601 DNA. The agarose gel result shows that almost all of 601 DNA wraps histone octamers to form mononucleosomes