Recombinant Mononucleosomes H3.1 (K18I)

Catalog No: 81260, 81960
Expressed In: *E. coli*

Quantity: 20, 1000 µg
Concentration: 1.04 µg/µl
Source: Human

Buffer Contents: Recombinant Mononucleosomes H3.1 (K18I) (20 µg protein + 20 µg DNA) is supplied in 10 mM Tris-HCl pH 8.0, 1 mM EDTA, 2 mM DTT, 20% glycerol.

Background: *In vivo*, histones are wrapped around by DNA in chromatin. Therefore, nucleosomes are more physiologically relevant substrates than histones and histone-derived peptides for in vitro studies. More importantly, some histone methyltransferases are signifcantly more active, as well as specifc, 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.

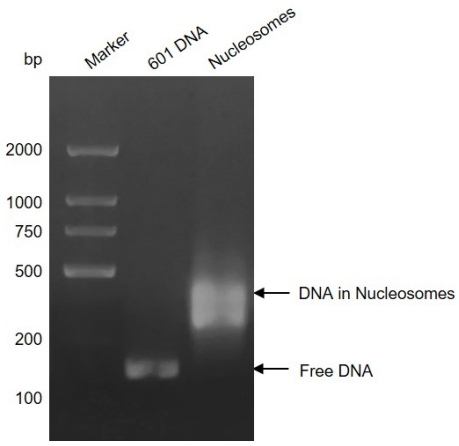
Histones are linked to tumorigenesis primarily through alterations in their PTMs and the enzymes regulating these modifications, suggesting that they might disrupt the reading, writing, and/or erasing of these marks. Mutations in histone H3 occur with high genetic penetrance within rare pediatric gliomas and sarcomas. In H3 variants, the mutation is most often a lysine-to-methionine (K-M) mutation, occasionally glycine mutations (G34R/V/W/L) occur too. More K-to-M/I mutations were observed, raising the possibility that the functional effects associated with known K-to-M/I changes (that is, function in a dominant fashion to block the methylation of corresponding lysines on wild type histones) may extend to additional contexts. Researchers found that mutations in the subset with a TMB ≤ 2 mutations per Mb included H3 (K27M) and H3 (G34W), and other mutations like H3 (E105K/Q), mutations at H3 N-terminal residues at or near PTM sites including R2, R8, K18 and R26, as well as residues in the acidic patch such as H2A residues E56, E64, E9, and E92 and H2B residues E105 and E133, which might act as oncohistones. According to the structural analysis, specifically for the KDM6 family, the hydrophobic mutation - histone H3 K18I- showed a significantly higher affinity towards the KDM6 enzymes.

Protein Details: Recombinant Mononucleosomes H3.1 (K18I) consist of a 167 bp of 601 DNA without tags and two molecules each of histones H2A that includes amino acids 1-130 (end) (accession number NM_003512), H2B that includes amino acids 1-126 (end) (accession number NM_003518), H3.1 that includes amino acids 1-136 (end) (accession number NM_003529) with a point mutation Lys18Ile, and H4 that includes amino acids 1-103 (end) (accession number NM_003548). All of these histones were expressed in *E. coli* cells. The molecular weight of histone octamer is 108 kDa.

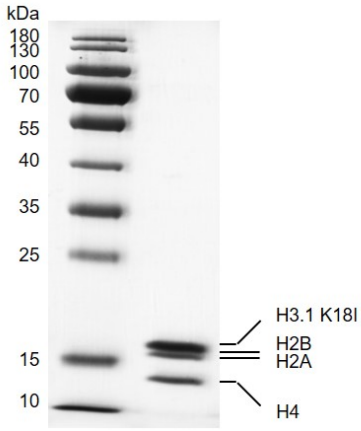
Application Notes: Recombinant Mononucleosomes H3.1 (K18I) is suitable for use as substrate for histone modification enzymes, or to generate chromatin *in vitro*.

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 guaranteed for 6 months from date of receipt.

This product is for research use only and is not for use in diagnostic procedures.



Recombinant Mononucleosomes H3.1 (K18I) DNA gel
Recombinant Mononucleosomes H3.1 (K18I) were run on a 2% agarose gel and stained with ethidium bromide. Lane 1: DNA marker. Lane 2: 601 DNA which was used for assembly of nucleosomes. Lane 3: Intact mononucleosomes H3.1 (K18I). Intact mononucleosomes H3.1 (K18I) migrated much higher than free 601 DNA. The agarose gel shows that almost all of 601 DNA wrapped histone octamers to form nucleosomes.



Recombinant Mononucleosomes H3.1 (K18I)
12.5% SDS-PAGE gel stained with Coomassie Blue
Purity: >95%