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YB86773Hu01 100µg Histone Cluster 1, H2ah (HIST1H2AH) Organism: Homo sapiens (Human) Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

kDa [PROPERTIES] 94 66.2 45 **Residues:** Metl[~]Lys128 (Accession # Q96KK5), with two N-33 terminal Tags, His-tag and GST-tag. 26 Host: E. coli Subcellular Location: Nucleus. Chromosome. 20 **Purity:** >95% 14.4 Endotoxin Level: <1.0EU per $1 \mu g$ (determined by the LAL method). 15% SDS-PAGE **Formulation:** Supplied as lyophilized form in PBS, pH7.4, containing 5% sucrose, 0.01% sarcosyl. Predicted isoelectric point: 9.4 Predicted Molecular Mass: 41.0kDa

Applications: SDS-PAGE; WB; ELISA; IP.

(May be suitable for use in other assays to be determined by the end user.)

[<u>USAGE</u>]

Reconstitute in sterile PBS, pH7.2-pH7.4.

7th Edition (Revised in May, 2013)



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[STORAGE AND STABILITY]

Storage: Avoid repeated freeze/thaw cycles.

Store at $2-8^{\circ}C$ for one month.

Aliquot and store at -80° C for 12 months.

Stability Test: The thermal stability is described by the loss rate of the target protein. The loss rate was determined by accelerated thermal degradation test, that is, incubate the protein at 37° C for 48h, and no obvious degradation and precipitation were observed. (Referring from China Biological Products Standard, which was calculated by the Arrhenius equation.) The loss of this protein is less than 5% within the expiration date under appropriate storage condition.

[SEQUENCES]

The target protein is fused with two N-terminal Tags, His-tag and GSTtag, its sequence is listed below. MRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD G S T S G S G H H H H H H S A G LV P R G S TA I G M K E T A A A K F E R Q H M D S P D L G T L E V LF Q G P L G S E F – M S G R G K Q G G K A R A K A K T R S S R A G L Q F P V G R V H R L L R K G N Y AERVGAGAPV YLAAVLEYLT AEILELAGNA ARDNKKTRII PRHLQLAIRN DEELNKLLGK VTIAQGGVLP NIQAVLLPKK TESHHKAK