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YB84025Hu01 100 $\mu$ g

Histone Cluster 1, H2aj (HIST1H2AJ)

Organism: Homo sapiens (Human)

*Instruction manual*

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

7th Edition (Revised in May, 2013)

## [ PROPERTIES ]

**Residues:** Met1~Lys128 (Accession # Q99878), with two N-terminal Tags, His-tag and GST-tag.

**Host:** *E. coli*

**Subcellular Location:** Nucleus. Chromosome.

**Purity:** >95%

**Endotoxin Level:** <1.0EU per 1 $\mu$ g (determined by the LAL method).

**Formulation:** Supplied as lyophilized form in PBS, pH7.4 containing 5% sucrose, 0.01% sarcosyl.

**Predicted isoelectric point:** 9.4

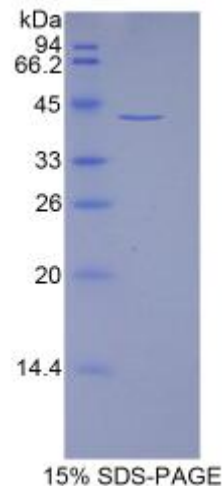
**Predicted Molecular Mass:** 41.0kDa

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

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

## [ USAGE ]

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





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## [ STORAGE AND STABILITY ]

**Storage:** Avoid repeated freeze/thaw cycles.

Store at 2-8°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 GST-tag, its sequence is listed below.

```
MRNKKFELGL EFPNLPYYID GDVKLTSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL
DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD
VVLYDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPKSD
G S T S G S G H H H H H S A G L V P R G S T A 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
L F 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 ARDNKTRII PRHLQLAIRN DEELNKLKLG
VTIAQGGVLP NIQAVLLPKK TESHKTK
```