

Probable histone H2A.2 (Os07g0545400, LOC_Os07g36140), Recombinant Protein

Cat RP14163

Size 0.02 mg (E-Coli)/ 0.1 mg (E-Coli)/ 0.02 mg (Yeast)/ 0.1 mg
(Yeast)/ 0.02 mg (Baculovirus)/ 0.02 mg (Mammalian-Cell)/ 1

mg (E-Coli)/ 0.1 mg (Baculovirus)/ 1 mg (Yeast)/ 0.1 mg
(Mammalian-Cell)/ 1 mg (Baculovirus)/ 0.5 mg (Mammalian-
Cell)
Oryza sativa subsp. japonica (Rice)

Species

Full Product Name

Recombinant Oryza sativa subsp. japonica Probable histone H2A.2 (Os07g0545400, LOC_Os07g36140)

Product Gene Name

Os07g0545400 recombinant protein

Product Synonym Gene Name

Os07g0545400; LOC_Os07g36140

Purity

Greater or equal to 85% purity as determined by SDS-PAGE. (lot specific)

Sequence

MAGRGAIGS GAAKKAMRSR SKAGLQFPVG RIARFLKAGK YAERVGAGAP VYLAADVLEYL AAEVLELAGN
AARDNKKTRI VPRHIQLAVR NDEELSRLLG TVTIASGGVM PNIHNNLLPK KAGGSAKAAA GDDDN

Sequence Positions

1-135, Full length protein

Format

Lyophilized or liquid (Format to be determined during the manufacturing process)

Host

E Coli or Yeast or Baculovirus or Mammalian Cell

Molecular Weight

13,976 Da

Storage

Store at -20°C. For long-term storage, store at -20°C or -80°C. Store working aliquots at 4°C for up to one week.
Repeated freezing and thawing is not recommended.

NCBI Accession

XP_015646584.1

NCBI GI

1002284562

NCBI GenBank Nucleotide

XM_015791098.1

NCBI GenID

4343519

NCBI Official Full Name

FOR RESEARCH OR FURTHER MANUFACTURING USE ONLY

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Cell)
NCBI Official Symbol
LOC4343519

NCBI Official Synonym Symbols

OsJ_023674; OJ1582_D10.26

NCBI Protein Information

probable histone H2A.2

UniProt Gene Name

Os07g0545400

UniProt Protein Name

Probable histone H2A.2

UniProt Primary Accession

Q6ZL42

UniProt Secondary Accession

Q0D5P4

UniProt Related Accession

Q6ZL42

UniProt Comments

Core component of nucleosome. 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.

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