Probable histone H2AXa (OsI_012923), Recombinant Protein

CD BioSciences
Plant Protein

Cat *RP13858*

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)*

Species

Oryza sativa subsp. indica (Rice)

Full Product Name

Recombinant Oryza sativa subsp. indica Probable histone H2AXa (OsI_012923)

Product Gene Name

OsI_012923 recombinant protein

Purity

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

Sequence

MSSSQGGGGR GKAKTTKAVS RSSKAGLQFP VGRIARYLKA GKYAERVGAG APVYLSAVLE YLAAEVLELA GNAARDNKKN RIVPRHIQLA VRNDEELSRL LGTVTIAAGG VLPNIQQVLL PKKGGGKGDI GSASQEF

Sequence Positions

1-137, 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

14,271 Da

Storage

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

Protein Family

Probable histone

NCBI Accession

A2XLI0.1

NCBI GI

158512879

NCBI Official Full Name

Probable histone H2AXa

UniProt Gene Name

OsI_012923

UniProt Protein Name

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UniProt Primary Accession

A2XLI0

UniProt Comments

Variant histone H2A which replaces conventional H2A in a subset of nucleosomes. 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. Required for checkpoint-mediated arrest of cell cycle progression in response to low doses of ionizing radiation and for efficient repair of DNA double strand breaks (DSBs) specifically when modified by C-terminal phosphorylation .