

## Product datasheet for RC201434L3V

## OriGene Technologies, Inc.

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## Histone H2A.X (H2AFX) (NM\_002105) Human Tagged ORF Clone Lentiviral Particle

## **Product data:**

**Product Type:** Lentiviral Particles

**Product Name:** Histone H2A.X (H2AFX) (NM\_002105) Human Tagged ORF Clone Lentiviral Particle

Symbol: Histone H2A.X

**Synonyms:** H2A.X; H2A/X; H2AFX

Mammalian Cell

Selection:

Puromycin

**Vector:** pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK
ACCN: NM 002105

ORF Size: 429 bp

**ORF Nucleotide** 

OTI Disclaimer:

The ORF insert of this clone is exactly the same as(RC201434).

Sequence:

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing

variants is recommended prior to use. More info

**OTI Annotation:** This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

**RefSeg:** NM 002105.1

 RefSeq Size:
 1651 bp

 RefSeq ORF:
 432 bp

 Locus ID:
 3014

 UniProt ID:
 P16104

 Cytogenetics:
 11q23.3

**Domains:** H2A, histone

**Protein Families:** Druggable Genome





**Protein Pathways:** Systemic lupus erythematosus

MW: 15.1 kDa

**Gene Summary:** Histones are basic nuclear proteins that are responsible for the nucleosome structure of the

chromosomal fiber in eukaryotes. Two molecules of each of the four core histones (H2A, H2B, H3, and H4) form an octamer, around which approximately 146 bp of DNA is wrapped in repeating units, called nucleosomes. The linker histone, H1, interacts with linker DNA between nucleosomes and functions in the compaction of chromatin into higher order structures. This gene encodes a replication-independent histone that is a member of the histone H2A family, and generates two transcripts through the use of the conserved stemloop termination motif, and the polyA addition motif. [provided by RefSeq, Oct 2015]