

## Product datasheet for **TL319518V**

### H2AC7 Human shRNA Lentiviral Particle (Locus ID 3013)

#### Product data:

<b>Product Type:</b>	shRNA Lentiviral Particles
<b>Locus ID:</b>	3013
<b>Synonyms:</b>	H2A.3; H2A/g; H2AFG; HIST1H2AD
<b>Vector:</b>	pGFP-C-shLenti (TR30023)
<b>Format:</b>	Lentiviral particles
<b>Components:</b>	HIST1H2AD - Human shRNA lentiviral particles (4 unique 29mer target-specific shRNA, 1 scramble control), 0.5 ml each, $>10^7$ TU/ml.
<b>RefSeq:</b>	<a href="#">NM_021065</a> , <a href="#">NM_021065.1</a> , <a href="#">NM_021065.2</a> , <a href="#">NM_021065.3</a> , <a href="#">BC093807</a> , <a href="#">BC093809</a> , <a href="#">BC128035</a>
<b>UniProt ID:</b>	<a href="#">P20671</a>
<b>Summary:</b>	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped around a nucleosome, an octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene is intronless and encodes a replication-dependent histone that is a member of the histone H2A family. Transcripts from this gene lack polyA tails; instead, they contain a palindromic termination element. This gene is found in the large histone gene cluster on chromosome 6p22-p21.3. [provided by RefSeq, Aug 2015]
<b>shRNA Design:</b>	These shRNA constructs were designed against multiple splice variants at this gene locus. To be certain that your variant of interest is targeted, please contact <a href="mailto:techsupport@origene.com">techsupport@origene.com</a> . If you need a special design or shRNA sequence, please utilize our <a href="#">custom shRNA service</a> .



**Performance Guaranteed:** OriGene guarantees that the sequences in the shRNA expression cassettes are verified to correspond to the target gene with 100% identity. One of the four constructs at minimum are guaranteed to produce 70% or more gene expression knock-down provided a minimum transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly assess knockdown, the gene expression level from the included scramble control vector must be used in comparison with the target-specific shRNA transfected samples.

For non-conforming shRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the shRNA kit. To arrange for a free replacement with newly designed constructs, please contact Technical Services at [techsupport@origene.com](mailto:techsupport@origene.com). Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled shRNA control (Western Blot data preferred).