

Product datasheet for SC124291

H2AZ2 (NM_138635) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	H2AZ2 (NM_138635) Human Untagged Clone
Tag:	Tag Free
Symbol:	H2AZ2
Synonyms:	H2A.Z-2; H2AFV; H2AV
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC124291 sequence for NM_138635 edited (data generated by NextGen Sequencing)

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ATGGCTGGAGGCAAAGCTGGAAAGGACAGTGGGAAGCCAAGGCTAAGGCAGTATCTCGC
TCACAGAGAGCTGGGCTACAGTTTCCTGTGGGCCGCATCCACAGACACTTGAAGACTCGC
ACCACAAGCCATGGAAGGGTGGGTGCCACTGCTGCCGTGTACAGTGTGCGATTCTGGAG
TACCTCACTGCAGAGGTGCTGGAGCTGGCAGGTAATGCTTCTAAGGATCTCAAAGTAAAG
CGTATCACTCCGCGTCACTTGCAGCTTGAATCCGTGGTGTGAAGAGTTGGATTCTCTT
ATCAAGGCTACCATAGCTGGGGTGAGAAGAGAAGGTGTTCTTAG
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Clone variation with respect to NM_138635.3

5' Read Nucleotide Sequence:	>OriGene 5' read for NM_138635 unedited GTAAGTCAAATTTTGTAAACGACTCACTATAGGGCGCCGCAATTCGCACGAGGGCGGG TCGGCAGCGGGAGGGCGCGCGCCGAGCGGAGGCGGAGTTCGGCGCCGAGAACATGGCTGG AGGCAAAGCTGGAAGGACAGTGGGAAGCCAAGGCTAAGGCAGTATCTCGCTCACAGAG AGCTGGGCTACAGTTTCCTGTGGGCCGCATCCACAGACACTTGAAGACTCGCACCACAAG CCATGGAAGGGTGGGTGCCACTGCTGCCGTGTACAGTGTGCGATTCTGGAGTACCTCAC TGCAGAGGTGCTGGAGCTGGCAGGTAATGCTTCTAAGGATCTCAAAGTAAAGCGTATCAC TCCGCGTCACTTGCAGCTTGAATCCGTGGTGTGAAGAGTTGGATTCTTATCAAGGC TACCATAGCTGGGGTGAGAAGAGAAGGTGTTCTTAGATCAGAAGATGCCATTGTATTAG GTGACGGCAAGGTTTTGCTGATTTAGTGAACAAGATTCTACTGGGATGTGTGCTGAGCT GAACCAAGGAAGTCCCGAATGTGCTGAACAAGGACATTTGCTTCTCAGATACGTGAATT CAATTTTAAGCAAGATCTTGATCTGCTTCCAGAGCAGCTTTGATTTAAAGTAATTTTCA GCATTTTCCCTTGCATGAGTAATTTTCTGAATGTATAAAATATTCTATTTATGCTGACC TTTTGGATAAACTGTGTTGCTGCAGTGTGGTCCACACTACCATCCTAAGTGAAGACTTA GTAAGTCTGAGGATCTCCAGGCACTGGAAGAGTGCAGACCTGGCACTGAAATGGTATAG CTAGTGGTCATTCTTCGGTTTTCCGCTCATACGGAGTCCTGACGG
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Restriction Sites:	NotI-NotI
ACCN:	NM_138635
Insert Size:	4500 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_138635.2 , NP_619541.1
RefSeq Size:	825 bp
RefSeq ORF:	345 bp
Locus ID:	94239
UniProt ID:	Q71UI9
Cytogenetics:	7p13
Domains:	histone
Protein Families:	Druggable Genome
Protein Pathways:	Systemic lupus erythematosus
Gene Summary:	<p>Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Nucleosomes consist of approximately 146 bp of DNA wrapped around a histone 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 encodes a replication-independent histone that is a member of the histone H2A family. Several transcript variants encoding different isoforms, have been identified for this gene. [provided by RefSeq, Oct 2015]</p> <p>Transcript Variant: This variant (2) utilizes an alternate exon in the 3' coding region and 3' UTR, compared to variant 1. It encodes a shorter protein (isoform 2) compared to that encoded by variant 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no quality transcript was available for the full length of the gene. The extent of this transcript is supported by transcript alignments.</p>