

Product datasheet for MC227563

Suv39h1 (NM_001290716) Mouse Untagged Clone

Product data:

OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	Suv39h1 (NM_001290716) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Suv39h1
Synonyms:	Al852103; AL022883; DXHXS7466e; H3-K9-HMTase 1; KMT1A; mlS6
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC227563 representing NM_001290716 Red=Cloning site Blue=ORF Orange=Stop codon
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGC</mark> C
	ATGGGGGAGCCGGCGACTCTAGGTTGCAGTGTGTGTGTGT

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA

CCGTATTGAATGCAAATGTGGGACAACGGCTTGCCGAAAATACCTCTTCTAG



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Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001290716
Insert Size:	1242 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).
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	 Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	<u>NM 001290716.1, NP 001277645.1</u>
RefSeq Size:	3097 bp
RefSeq ORF:	1242 bp
Locus ID:	20937
UniProt ID:	<u>054864</u>
Cytogenetics:	X 3.64 cM

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Histone methyltransferase that specifically trimethylates 'Lys-9' of histone H3 using Gene Summary: monomethylated H3 'Lys-9' as substrate. H3 'Lys-9' trimethylation represents a specific tag for epigenetic transcriptional repression by recruiting HP1 (CBX1, CBX3 and/or CBX5) proteins to methylated histones. Mainly functions in heterochromatin regions, thereby playing a central role in the establishment of constitutive heterochromatin at pericentric and telomere regions. H3 'Lys-9' trimethylation is also required to direct DNA methylation at pericentric repeats. SUV39H1 is targeted to histone H3 via its interaction with RB1 and is involved in many processes, such as repression of MYOD1-stimulated differentiation, regulation of the control switch for exiting the cell cycle and entering differentiation, repression by the PML-RARA fusion protein, BMP-induced repression, repression of switch recombination to IgA and regulation of telomere length. Component of the eNoSC (energy-dependent nucleolar silencing) complex, a complex that mediates silencing of rDNA in response to intracellular energy status and acts by recruiting histone-modifying enzymes. The eNoSC complex is able to sense the energy status of cell: upon glucose starvation, elevation of NAD(+)/NADP(+) ratio activates SIRT1, leading to histone H3 deacetylation followed by dimethylation of H3 at 'Lys-9' (H3K9me2) by SUV39H1 and the formation of silent chromatin in the rDNA locus. Recruited by the PER complex to the E-box elements of the circadian target genes such as PER2 itself or PER1, contributes to the conversion of local chromatin to a heterochromatin-like repressive state through H3 'Lys-9' trimethylation.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) differs in the 5' UTR, lacks a portion of the 5' coding region, and initiates translation at an alternate start codon, compared to variant 1. The encoded isoform (2) has a distinct N-terminus and is longer than isoform 1.

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