

Product datasheet for MC216497

Suv39h2 (NM_022724) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Suv39h2 (NM_022724) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Suv39h2
Synonyms:	4930507K23Rik; AA536750; D030054H19Rik; D2Ertd544e; KMT1B
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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	39h2 (NM_022724) Mouse Untagged Clone – MC216497
Fully Sequenced ORF:	>MC216497 representing NM_022724 Red=Cloning site Blue=ORF Orange=Stop codon
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGC</mark> C
	ATGGCCGGCCAGGGCCAAGGCCAGGGGCAGTGAGGCAGGAGGCGCGGGTGTCACCGGGCTCCAGGTCCGC CCCCGAGGCCCAAGGCCAGGCGGCGCGGC
	ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	Sgfl-Mlul
ACCN:	NM_022724
Insert Size:	1434 bp
OTI Disclaimer:	Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at <u>custsupport@origene.com</u> or by calling 301.340.3188 option 3 for pricing and delivery.
	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

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variants is recommended prior to use. More info

ORIGENE Suv39h2 (NM_022724) Mouse Untagged Clone – MC216497		
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. 	
RefSeq:	<u>NM 022724.4, NP 073561.2</u>	
RefSeq Size:	4282 bp	
RefSeq ORF:	1434 bp	
Locus ID:	64707	
UniProt ID:	<u>Q9EQQ0</u>	
Cytogenetics:	2 1.95 cM	
Gene Summary:	Histone methyltransferase that specifically trimethylates 'Lys-9' of histone H3 using 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 histores. Mainly functions in betaresbromatic regions, thereby playing a control	

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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 cell cycle regulation, transcriptional repression and regulation of telomere length. May participate in regulation of higher-order chromatin organization during spermatogenesis. Recruited by the large 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 (1) represents the longer transcript and encodes the functional protein. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.

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