

Product datasheet for **SC318000**

HDAC2 (NM_001527) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	HDAC2 (NM_001527) Human Untagged Clone
Tag:	Tag Free
Symbol:	HDAC2
Synonyms:	HD2; KDAC2; RPD3; YAF1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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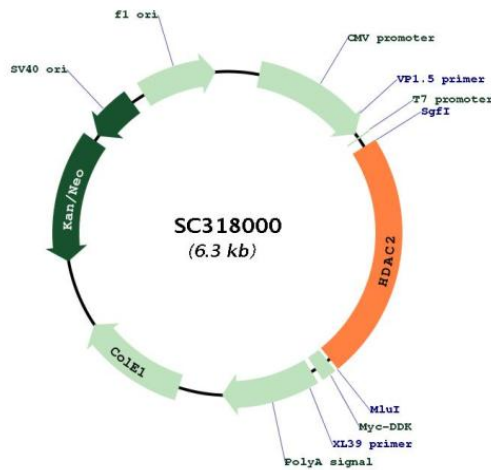
Fully Sequenced ORF: >SC318000 representing NM_001527.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGCGTACAGTCAAGGAGGCGGCAAAAAAAAAAGTCTGCTACTACTACGACGGTGATATTGGAAATTAT
TATTATGGACAGGGTCATCCCATGAAGCCTCATAGAATCCGCATGACCCATAACTTGCTGTAAATTAT
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CAGCTCAGCAACCCCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
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Restriction Sites: SgfI-MluI

Plasmid Map:



ACCN: NM_001527

Insert Size:	1467 bp
OTI Disclaimer:	<p>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 custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.</p> <p>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</p>
OTI Annotation:	<p>This clone may be unstable or toxic at high copy number in common E. coli strain. We recommend using a lower copy number E. coli strain, such as CopyCutter strain (http://www.epibio.com/item.asp?ID=435) for transformation and plasmid preparation. Please be aware that the DNA yield could be low. Additional aliquots of this clone can be ordered from OriGene.</p>
Components:	<p>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).</p>
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_001527.3
RefSeq Size:	6656 bp
RefSeq ORF:	1467 bp
Locus ID:	3066
UniProt ID:	Q92769
Cytogenetics:	6q21
Domains:	Hist_deacetyl
Protein Families:	Druggable Genome, Stem cell - Pluripotency, Transcription Factors
Protein Pathways:	Cell cycle, Chronic myeloid leukemia, Huntington's disease, Notch signaling pathway, Pathways in cancer
MW:	55.4 kDa

Gene Summary:

This gene product belongs to the histone deacetylase family. Histone deacetylases act via the formation of large multiprotein complexes, and are responsible for the deacetylation of lysine residues at the N-terminal regions of core histones (H2A, H2B, H3 and H4). This protein forms transcriptional repressor complexes by associating with many different proteins, including YY1, a mammalian zinc-finger transcription factor. Thus, it plays an important role in transcriptional regulation, cell cycle progression and developmental events. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2010]

Transcript Variant: This variant (1) 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.