

## Product datasheet for **SC204616**

### **KDM1A (NM\_015013) Human 3' UTR Clone**

#### **Product data:**

**Product Type:** 3' UTR Clones  
**Product Name:** KDM1A (NM\_015013) Human 3' UTR Clone  
**Vector:** pMirTarget (PS100062)  
**Symbol:** KDM1A  
**Synonyms:** AOF2; BHC110; CPRF; KDM1; LSD1  
**ACCN:** NM\_015013  
**Insert Size:** 355 bp  
**Insert Sequence:** >SC204616 3'UTR clone of NM\_015013

The sequence shown below is from the reference sequence of NM\_015013. The complete sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

```
GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
GTTCTGCACAGCAGTCCCCAAGCATGTGAGACAGATGCATTCTAAGGGAAGAGGCCCATGTGCCTGTT
CTGCCATGTAAGGAAGGCTCTTCTAGCAATACTAGATCCCACTGAGAAAATCCACCTGGCATCTGGG
CTCCTGATCAGCTGATGGAGCTCCTGATTGACAAAGGAGCTTGCTCCTTTGAATGACCTAGAGCACA
GGGAGGAACCTTGCCATTAGTTTGAATTGTGTTCTTCGTAAAGACTGAGGCAAGCAAGTGTGTGAAA
TAACATCATCTTAGTCCCTTGGTGTGTGGGTTTTTTGTTTTTTTTTATATTTGAGAATAAAACTCA
TATAAAATTG
ACGCGTAAGCGGCCGCGCATCTAGATTGGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTCGATTCCACCGCCCTTCTATGAAAGG
```

**Restriction Sites:** SgfI-MluI

**OTI Disclaimer:** Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences, e.g., single nucleotide polymorphisms (SNPs).

**Components:** The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

**RefSeq:** [NM\\_015013.4](#)



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**Summary:** This gene encodes a nuclear protein containing a SWIRM domain, a FAD-binding motif, and an amine oxidase domain. This protein is a component of several histone deacetylase complexes, though it silences genes by functioning as a histone demethylase. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2009]

**Locus ID:** 23028

**MW:** 13.2