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Product datasheet for MC217512

Kat7 (NM_177619) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Kat7 (NM_177619) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Kat7
Synonyms:	Hbo1; Hboa; Myst2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

Fully Sequenced ORF:	>NCBI ORF sequence for NM_177619, the custom clone sequence may differ by one or more nucleotides ATGCCGCGAAGGAAGAGAAATGCAGGCAGTAGTTCAGATGGAACCGAAGATTCCGATTTTTCTACAGATC TCGAGCATACAGACAGTTCAGAGAGTGATGGCACCTCGCGCCGATCTGCCCGAGTCACCCGCTCCTCAGC CAGGCTAAGCCAGAGTTCCCAAGAAACTAAAAATACAGCTGATCATGATGAGTCACCACCTCGAACTCCA ACCGGAAATGCACCTTCTTCTGAGTCTGACATAGACATCTCCAGCCCCAACGTGTCTCATGATGAGAGCA TTGCCAAGGACATGTCCCTGAAGGACTCAGGCAGTGATCTCTCTCACCGTCCCAAGCGACGTCGATTTCA CGAAAGCTACAATTTCAACATGAAGTGTCCTACGCCGGGCTGCAACTCTCTAGGACATCTTACAGGAAAG CACGAGAGACATTTCTCCATCTCAGGATGCCCGCTGTATCATAACCTCTCAGCTGACGAATGCAAGGCAC CAACAGAGAGACAGCTGCGGTATAAGGAAAAGGTGGCTGAACTCAGGAAGAAAAGAAATTCTGGACTGAG CAAAGAGCAGAAGGAGAAATACATGGAACACAGACAGACCTATGGGAACACTCGGGAGCCTCTCTTGGAA AACCTGACAAGTGAATATGACTTAGATCTTTTCCGAAGAGCACAAGCCCGGGCTTCTGAGGATTTGGAGA AGTTAAGGCTTCAAGGCCAAATCACAGAGGGAAGCAACATGATTAAAACAATTGCTTTTGGCCGCTATGA ACTGGACACTTGGTACCACTCTCCCTATCCTGAGGAATATGCGAGGCTGGGACGTCTCTACATGTGTGAA TTCTGCTTAAAGTACATGAAGAGCCAGACAATCCTCCGCCGACACATGGCCAAGTGTGTGTGGAAACACC CCCCTGGTGATGAGATTTATCGCAAAGGCTCCATCTCTGTGTTTGAAGTAGACGGCAAGAAGAACAAGAT CTACTGCCAAAACCTCTGCCTTTTGGCAAAGCTTTTTCTGGACCATAAGACGCTATACTATGATGTAGAA CCTTTCCTGTTCTACGTTATGACAGAAGCGGACAATACTGGCTGTCATCTGATTGGATATTTTTCTAAGG AGAAGAATTCATTTCTCAACTATAATGTCTCGTGCATCCTCACCATGCCTCAGTACATGCGACAGGGCTA CGGGAAGATGCTGATCGATTTCAGTTATTTACTTTCCAAAGTAGAAGAGAAAGTCGGCTCTCCAGAGCGC CCACTGTCAGACCTGGGGCTCATAAGCTACCGCAGCTACTGGAAGGAGGTACTGCTCCGATACCTGCACA ACTTCCAGGGCAAGGAGATCTCCATCAAAGAAATTAGCCAGGAAACAGCTGTGAATCCCGTGGACATTGT CAGCACTCTGCAAGCCCTTCAGATGCTCAAGTATTGGAAAGGCAAGCACCTAGTTTTAAAGAGACAGGAC CTGATAGATGAGTGGATAGCCAAAGAGGCCAAAAGGTCCAACTCCAACAAAACCATGGATCCAAGCTGCT TAAAATGGACCCCTCCCAAGGGCACTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_177619
Insert Size:	1569 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:	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:	BC048904, AAH48904

RefSeq Size:	3262 bp
RefSeq ORF:	1569 bp
Locus ID:	217127
UniProt ID:	Q5SVQ0
Cytogenetics:	11 D
Gene Summary:	Component of the HBO1 complex which has a histone H4-specific acetyltransferase activity, a reduced activity toward histone H3 and is responsible for the bulk of histone H4 acetylation in vivo. Involved in H3K14 (histone H3 lysine 14) acetylation and cell proliferation (PubMed:23319590). Through chromatin acetylation it may regulate DNA replication and act as a coactivator of TP53-dependent transcription. Acts as a coactivator of the licensing factor CDT1. Specifically represses AR-mediated transcription.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) lacks two in-frame exons in the coding region, compared to variant 1. This results in a shorter protein (isoform 3), compared to isoform 1. Sequence Note: This RefSeq record was created from 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.