

## Product datasheet for **MC208007**

### Creb1 (NM\_009952) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Creb1 (NM\_009952) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Creb1  
**Synonyms:** 2310001E10Rik; 3526402H21Rik; AV083133; Creb; Creb-1  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Cell Selection:** Neomycin  
**Fully Sequenced ORF:** >MC208007 representing NM\_009952  
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGGATCGCC**

ATGACCATGGAATCTGGAGCAGACAACCAGCAGAGTGGAGATGCTGCTGTAAACAGAAGCTGAAAATCAAC  
AAATGACAGTTCAAGCCCAGCCACAGATTGCCACATTAGCCCAGGTATCCATGCCAGCAGCTCATGCAAC  
ATCATCTGCTCCCACTGTAACCTTAGTGCAGCTGCCCAATGGGCAGACAGTCCAGGTCCATGGCGTTATC  
CAGGGCGCCAGCCATCAGTTATCCAGTCTCCACAAGTCCAAACAGTTCAGTCTTCTGTAAGGACTTAA  
AAAGACTTTTCTCCGGAACCTCAGATTTCAACTATTGCAGAAAGTGAAGATTACACAGGAGTCTGTGGATAG  
TGTAACCTGATTCCAAAAACGAAGGGAAATCCTTTCAAGGAGGCCTTCTACAGGAAAAATTTGAATGAC  
TTATCTTCTGATGCACCAGGGGTGCCAAGGATTGAAGAAGAAAAGTCAGAAGAGGAGACTTCAGCCCTG  
CCATCACCAGTGTAAACAGTGCCAACCCCATTTACCAAACCTAGCAGTGGCAGTACATTGCCATTACCCA  
GGGAGGAGCAATACAGCTGGCTAACAATGGTACGGATGGGTACAGGGCTGCAGACATTAACCATGACC  
AATGCAGCTGCCACTCAGCCGGTACTACCATTCTACAGTATGCACAGACCACTGATGGACAGCAGATT  
TAGTGCCAGCAACCAAGTTGTTGTTCAAGCTGCCTCAGGCGATGTACAAACATACCAGATCCGCACAGC  
ACCCACGAGCACCATTGCCCTGGAGTTGTTATGGCGTCTCCAGCACTTCTACACAGCCTGTGAA  
GAAGCAGCACGGAAGAGAGAGGTCCGTCTAATGAAGAACAGGAGGCAGCAAGAGAAATGTCGTAGAAAGA  
AGAAAGAATATGTGAAATGTTTAGAGAACAGAGTGGCAGTGCTTGAAAACCAAAACAAACATTGATTGA  
GGAGCTAAAAGCACTTAAGGACCTTACTGCCACAATCAGATTAA

**ACGGT**ACGGCGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** SgfI-MluI  
**ACCN:** NM\_009952



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<b>Insert Size:</b>	1026 bp
<b>OTI Disclaimer:</b>	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).
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>RefSeq:</b>	<u><a href="#">NM_009952.2</a></u> , <u><a href="#">NP_034082.1</a></u>
<b>RefSeq Size:</b>	8431 bp
<b>RefSeq ORF:</b>	1026 bp
<b>Locus ID:</b>	12912
<b>UniProt ID:</b>	<u><a href="#">Q01147</a></u>
<b>Cytogenetics:</b>	1 32.74 cM
<b>Gene Summary:</b>	<p>Phosphorylation-dependent transcription factor that stimulates transcription upon binding to the DNA cAMP response element (CRE), a sequence present in many viral and cellular promoters. Transcription activation is enhanced by the TORC coactivators which act independently of Ser-133 phosphorylation. Involved in different cellular processes including the synchronization of circadian rhythmicity and the differentiation of adipose cells. [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (B) includes an alternate in-frame exon in the 5' coding region, compared to variant A, resulting in a longer protein (isoform B), compared to isoform A.</p> <p>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.</p>