

Product datasheet for MC227175

Crem (NM_001271506) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
 Product Name: Crem (NM_001271506) Mouse Untagged Clone
 Tag: Tag Free
 Symbol: Crem
 Synonyms: IC; ICER; ICERI
 Vector: pCMV6-Entry (PS100001)
 E. coli Selection: Kanamycin (25 ug/mL)
 Cell Selection: Neomycin
 Fully Sequenced ORF: >MC227175 representing NM_001271506
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCCGCGATCGCC

ATGAGCAAATGTGGCAGGAAAAAGTATATGAGGACAAATGTAAGGCAAATGACCATGGAACAGTTGAAT
 CACAGCAGGATCGAAGTGAACACGTTCTGTGGCAGAGCATAGCTCTGCTCATATGCAGACTGGTCAAAT
 TTCTGTTCTACTCTAGCTCAGTTTCTGTAGCTGGATCAGGCACTGGAAGAGGCTCCCCAGCTGTGACT
 CTAGTACAGTTACCTTCAGGCCAACTGTACAGGTCCAGGGAGTTATTCAGACACCACATCCATCGGTTA
 TTCAATACCACAAATACAACTGTTTCAGGTAGCAACAATTGCAGAGACAGATGATTCTGCAGACTCAGA
 AGTAATTGATTTCGCATAAACGTAGAGAAATTTTTCACGAAGACCCTCATATAGAAAAATACTGAATGAA
 CTTTCTCTGTATGTGCCTGGTATTTCCCAAGATTGAAGAAGAAAAATCAGAGGAAGAAGGGACACCACCTA
 ACATTGCTACCATGGCAGTACCAACTAGCATATATCAGACTAGCACGGGGCAATACATTGCTATAGCTCA
 AGGTGGAACAATCCAGATTTCTAACCCAGGATCTGATGGTGTTCAGGGACTCCAGGCATTAACAATGACA
 AATTCAGGAGCTCCTCCGCCAGGTGCTACAATTGTACAGTATGCAGCACAATCAGCCGATGGTACACAGC
 AGTTCTTTGTCCAGGCAGCCAGTTGTTGTTCAAGCTGCCACAGGTGACATGCCAACTTACCAGATCCG
 AGCTCCTACTACTGCTTTGCCACAAGGTGTGGTATGGCTGCCTACCAGGAAGCCTGCACAGTCCCAG
 CAACTAGCAGAAGAAGCAACTCGCAAGCGGGAGCTGAGGCTGATGAAAAACAGGGAGCTGCCCGGAGT
 GTCGCAGGAAGAAGAAGAAATATGTCAAATGTCTTGAAAAATCGTGTGGCTGTGCTTGAAAAATCAAACAA
 GACCTCATTGAGGAAGTCAAGGCCCTCAAGACCTTTATTGCCATAAAGCAGAGTAA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
 ACCN: NM_001271506



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Insert Size:	1038 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).
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<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:	<u>NM_001271506.1</u> , <u>NP_001258435.1</u>
RefSeq Size:	2723 bp
RefSeq ORF:	1038 bp
Locus ID:	12916
UniProt ID:	<u>P27699</u>
Cytogenetics:	18 A1
Gene Summary:	<p>This gene encodes a basic-leucine zipper domain-containing protein that localizes to gene promoters, where it binds to the cyclic AMP response element (CRE). Different protein isoforms encoded by this gene may function as either activators or repressors of transcription. Activity of this gene is important in multiple developmental processes, including spermatogenesis. Mutation of this gene causes male infertility. Alternative splicing and promoter usage result in multiple transcript variants for this gene. [provided by RefSeq, Oct 2012]</p> <p>Transcript Variant: This variant (15, also known as tau alpha gamma) lacks an alternate in-frame exon and uses an alternate splice site in the 3' coding region, compared to variant 1. The encoded isoform (15) is shorter and has a distinct C-terminus, compared to isoform 1.</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>