

Product datasheet for MC227129

Pbx1 (NM_001291509) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Pbx1 (NM_001291509) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Pbx1
Synonyms:	2310056B04Rik; D230003C07Rik; Pbx; Pbx-; Pbx-1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC227129 representing NM_001291509 Red=Cloning site Blue=ORF Orange=Stop codon

TTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGC**C

ATGGACGAGCAGCCGAGGCTGATGCATTCACGCTGGGGTGGGATGGCCGGACACCCCGCCTGTCCC
 AGCACTTGCAGGATGGGGCCGAGGGACCGAGGGGAGGGCGGGAGGAAGCAGGACATCGGGACATTTT
 ACAGCAAATTATGACCATCACAGACCAGAGTTTGGATGAAGCGCAGGCCAGAAAACATGCTTTAACTGC
 CACAGAATGAAGCCTGCCTTGTTAATGTGTGTGTAATCAAAGAAAAACAGTTTGTAGTATTCGGG
 GAGCCCAAGAAGAGGAGCCACAGACCCCGAGCTCATGCGACTGGACAACATGCTGCTAGCAGAAGGGT
 GCGGGGGCCTGAGAAGGGCGGAGGCTCGGCAGCGCGCGCGGCAGCGCAGCTTCTGGGGGTGCAGGT
 TCAGACAACCTCAGTGGAGCATTCCGACTACAGAGCCAACTCTCACAGATCAGACAAATCTACCACACAG
 AGCTGGAGAAGTATGAGCAGGCATGCAATGAATTCACCACCCACGTGATGAACCTCCTTCGAGAGCAAAG
 CCGGACCAGGCCCATCTCTCCGAAGGAGATCGAGCGGATGGTGAGCATCATCCACCGCAAGTTCAGCTCC
 ATCCAGATGCAGCTGAAACAGAGCAGTGCAGGCGGTCATGATCCTGCGCTCCCGGTTCTGGATGCGA
 GGCGGAAGAGACGAATTTCAACAAGCAAGCCACAGAAATCTGAATGAATTTCTATTTCCCATCTCAG
 CAACCTTACCCAGTGAGGAAGCCAAAGAGGAGTTAGCCAAGAAGTGCGGCATCACAGTCTCCAGGTG
 GATACCTTCGCCATGTTATCAGCCAGACAGGAGGATACAGTGACGGAATCGCAGCCAGTCAGATGTACA
 GTCCGACGGGCATCAGTGCTAATGGAGGTTGGCAGGATGCTACTACCCCTTCATCAGTGACCTCCCTAC
 AGAAGGCCCTGGCAGTGTTCACTCTGATACCTCCAAC**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI



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ACCN:	NM_001291509
Insert Size:	1020 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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	<u>NM_001291509.1, NP_001278438.1</u>
RefSeq Size:	6890 bp
RefSeq ORF:	1020 bp
Locus ID:	18514
Cytogenetics:	1 75.95 cM
Gene Summary:	<p>This gene encodes a homeobox protein that belongs to the three-amino-acid loop extension/Pre-B cell leukemia transcription factor (TALE/PBX) family of proteins. The encoded protein is involved in several biological processes during embryogenesis including steroidogenesis, sexual development and the maintenance of hematopoietic stem cells. This protein functions in the development of several organ systems and plays a role in skeletal patterning and programming. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2014]</p> <p>Transcript Variant: This variant (d) lacks two alternate in-frame exons in the 3' coding region compared to variant a. The encoded isoform (d) is shorter than isoform a. 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>