

## Product datasheet for **MC227241**

### Sftpb (NM\_001282071) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Sftpb (NM\_001282071) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Sftpb  
**Synonyms:** AI562151; SF-B; Sftp-3; Sftp3; SP-B  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Cell Selection:** Neomycin  
**Fully Sequenced ORF:** >MC227241 representing NM\_001282071  
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**GCGATCGCC**

ATGGCCAAGTCGCACCTACTGCAGTGGCTACTGCTGCTTCTACCTCTGCTGCCAGGTGCAGCTATCA  
 CGTCGGCCTCATCCCTGGAGTGTGCACAAGGCCCTCAATTCTGGTGCCAAAGCCTGGAGCATGCAGTGA  
 GTGCAGAGCCCTGGGGCACTGCCTGCAGGAAGTCTGGGGCATGCAGGAGCTAATGACCTGTGCCAAGAG  
 TGTGAGGATATTGTCCACCTCCTCACAAGATGACCAAGGAAGATGCTTCCAGGAAGCAATCCGGAAGT  
 TCCTGGAACAAGAATGTGATATCCTTCCCTTGAAGCTGCTTGTGCCCCGGTGTGCGCAAGTGCTTGATGT  
 CTACCTGCCCTGGTTATTGACTACTTCCAGAGCCAGATTAACCCCAAAGCCATCTGCAATCATGTGGGC  
 CTGTGCCACGTGGGCAGGCTAAGCCAGAACAAGATCCAGGGATGCCGGATGCCGTTCCAAACCCTCTGC  
 TGGACAAGCTGGTCCCTGTGCTGCCAGGAGCCCTCTGGCAAGGCCTGGCCCTCACACTCAGGACTT  
 CTCTGAGCAACAGCTCCCCATCCCTGCCCTTCTGCTGGCTTTCAGAACTCTGATCAAGCGGGTTCAA  
 GCCGTGATCCCCAAGTGCCTGGCTGAGCGCTACACAGTTCTCTGCTAGACGCACTGCTGGGCCGTGTGG  
 TGCCCCAGCTAGTCTGTGGCCTTGTCTCCGATGTTCCACTGAGGATGCCATGGGCCCTGCCCTCCCTGC  
 TGTGGAGCCTCTGATAGAAGAATGGCCACTACAGGACACTGAGTGCCATTTCTGCAAGTCTGTGATCAAC  
 CAGGCCTGGAACACCAAGTGAACAGGCTATGCCACAGGCAATGCACCAGGCCTGCCTTCGTTCTGGCTAG  
 ACAGGCCAAAAGTGTGAACAGTTTGTGGAACAGCACATGCCCCAGCTGCTGGCCCTGGTGCCTAGGAGCCA  
 GGATGCCACATCACCTGCCAGGCCCTTGGCGTATGTGAGGCCCGGCTAGCCCTCTGCAGTGCTTCCAA  
 ACCCCACACCT**TGA**

**ACGCGT**ACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** SgfI-MluI  
**ACCN:** NM\_001282071



[View online »](#)

<b>Insert Size:</b>	1065 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>OTI Annotation:</b>	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
<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_001282071.2</a></u> , <u><a href="#">NP_001269000.1</a></u>
<b>RefSeq Size:</b>	1492 bp
<b>RefSeq ORF:</b>	1065 bp
<b>Locus ID:</b>	20388
<b>Cytogenetics:</b>	6 32.27 cM
<b>Gene Summary:</b>	<p>Pulmonary surfactant-associated proteins promote alveolar stability by lowering the surface tension at the air-liquid interface in the peripheral air spaces. SP-B increases the collapse pressure of palmitic acid to nearly 70 millinewtons per meter.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) uses an alternate in-frame splice site in the coding region and an alternate splice site in the 3' UTR, compared to variant 1. This results in a shorter protein (isoform 2), compared to isoform 1. 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>