

## Product datasheet for SC213169

### SHIP (INPP5D) (NM\_005541) Human 3' UTR Clone

#### Product data:

|                           |  |
|---------------------------|--|
| Product Type:             | 3' UTR Clones  |
| Product Name:             | SHIP (INPP5D) (NM_005541) Human 3' UTR Clone   |
| Symbol:                   | SHIP   |
| Synonyms:                 | hp51CN; p150Ship; SHIP; SHIP-1; SHIP1; SIP-145   |
| Mammalian Cell Selection: | Neomycin   |
| Vector:                   | pMirTarget (PS100062)  |
| ACCN:                     | NM_005541  |
| Insert Size:              | 1225 bp  |
| Insert Sequence:          | >SC213169 3'UTR clone of NM_005541<br>The sequence shown below is from the reference sequence of NM_005541. The complete sequence of this clone may contain minor differences, such as SNPs.<br><b>Blue</b> =Stop Codon <b>Red</b> =Cloning site |

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GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAACGATCGCC
GGGCTCTAGGCAGGACTGCCATGCAGTGAAGCCCTCAGTGAGCTGCCACTGAGTCGGGAGCCAGAGG
AACGGCGTGAAGCCACTGGACCCTCTCCGGGACCTCCTGCTGGCTCCTCTGCCAGCTTCTATGCA
AGGCTTTGTGTTTTAGGAAAGGGCCTAGCTTCTGTGTGGCCACAGAGTTCAGTGCCTGTGAGACTTA
GCACCAAGTGCTGAGGCTGGAAGAAAAACGCACACCAGACGGGCAACAAACAGTCTGGGTCGCCAGCTC
GCTCTTGGTACTTGGGACCCAGTGCCTCGTTGAGGGCGCCATTCTGAAGAAAGGAACTGCAGCGCCGA
TTTGAGGGTGGAGATATAGATAATAATAATATTAATAATAATAATGGCCACATGGATCGAACACTCATG
ATGTGCCAAGTGCTGTGCTAAGTGCTTTACGAACATTCGTCATATCAGGATGACCTCGAGAGCTGAGGC
TCTAGCCACCTAAAACCACGTGCCCAAACCCACAGTTTAAAACGGTGTGTGTTCCGGAGGGGTGAAAGC
ATTAAGAAGCCCAGTGCCTCCTGGAGTGAGACAAGGGCTCGGCCTTAAGGAGCTGAAGAGTCTGGGTA
GCTTGTAGGGTACAAGAAGCCTGTTCTGTCCAGCTTCACTGACACAAGCTGCTTTAGCTAAAGTCCC
GCGGTTCCGGCATGGCTAGGCTGAGAGCAGGGATCTACCTGGCTTCTCAGTTCTTTGGTTGGAAGGAG
CAGGAAATCAGCTCCTATTCTCCAGTGGAGAGATCTGGCCTCAGCTTAGAGATGCCAAGGCCTG
TGCCAGGTTCCCTGTGCCCTCCTCGAGGTGGGACGCCATCACCAGCCACAGTTAAGCCAAGCCCCCAA
CATGTATTCCATCGTGTGGTAGAAGAGCTTTGCTGTTGCTCCCGAAAGCCGTGCTCTCCAGCCTGGC
TGCCAGGGAGGGTGGCCTCTTGTTCCAGGCTCTTGAATAGTGCAGCCTTTTCTCTATCTCTGTG
GCTTTCAGCTCTGCTTCTTGGTTATTAGGAGAATAGATGGGTGATGTCTTCTTATGTTGCTTTTTTC
AACATAGCAGAATTAATGTAGGGAGCTAAATCCAGTGGTGTGTGAATGCAGAAGGGAATGCACCCCA
CATTCCCATGATGGAAGTCTGCGTAACCAATAAATTTGTCCTTTTCTCACTCA
ACGCGTAAGCGGCCGCGCATCTAGATTGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTCGATTCCACCGCCCTTCTATGAAAGG

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|---------------------------|---|
| <b>Restriction Sites:</b> | Sgfl-Mlul   |
| <b>OTI Disclaimer:</b>    | Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).  |
| <b>Components:</b>        | The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.  |
| <b>RefSeq:</b>            | <a href="#">NM_005541.5</a>   |
| <b>Summary:</b>           | <p>This gene is a member of the inositol polyphosphate-5-phosphatase (INPP5) family and encodes a protein with an N-terminal SH2 domain, an inositol phosphatase domain, and two C-terminal protein interaction domains. Expression of this protein is restricted to hematopoietic cells where its movement from the cytosol to the plasma membrane is mediated by tyrosine phosphorylation. At the plasma membrane, the protein hydrolyzes the 5' phosphate from phosphatidylinositol (3,4,5)-trisphosphate and inositol-1,3,4,5-tetrakisphosphate, thereby affecting multiple signaling pathways. The protein is also partly localized to the nucleus, where it may be involved in nuclear inositol phosphate signaling processes. Overall, the protein functions as a negative regulator of myeloid cell proliferation and survival. Mutations in this gene are associated with defects and cancers of the immune system. Deficiencies in the encoded protein, SHIP1, have been associated with Inflammatory Bowel Disease types such as Crohn's Disease and Ulcerative Colitis. Alternative splicing of this gene results in multiple transcript variants. [provided by RefSeq, Jul 2020]</p> |
| <b>Locus ID:</b>          | 3635  |
| <b>MW:</b>                | 44.5  |