

## Product datasheet for **SC338064**

### SLIT2 (NM\_001289136) Human Untagged Clone

#### Product data:

|                           |  |
|---------------------------|--|
| Product Type:             | Expression Plasmids  |
| Product Name:             | SLIT2 (NM_001289136) Human Untagged Clone  |
| Tag:                      | Tag Free   |
| Symbol:                   | SLIT2  |
| Synonyms:                 | SLIL3; Slit-2  |
| Mammalian Cell Selection: | Neomycin   |
| Vector:                   | pCMV6-Entry (PS100001)   |
| E. coli Selection:        | Kanamycin (25 ug/mL)   |
| Fully Sequenced ORF:      | >NCBI ORF sequence for NM_001289136, the custom clone sequence may differ by one or more nucleotides |

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ATGCGCGGCGTTGGCTGGCAGATGCTGTCCCTGTCGCTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGG
CACC CGCAGGCGTGCCCGGCGCAGTGCTCTTGCTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGTGCG
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TACCGTGTGGAAGCCACAGGAATCTTTAAGAACTTCCTCAATTACGTAAAATAAACTTTAGCAACAAT  
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ACTCTTTCGAATGCACTGACGGCTCCTCTTTGTGGACGAGGTTGAGAAAGTGGTGAAGTGGGCTGTAC  
GAGGTGTGTGCTTAA

**Restriction Sites:**

Sgfl-MluI

**ACCN:**

NM\_001289136

**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).

|                               |   |
|-------------------------------|---|
| <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>                | <a href="#">NM_001289136.2</a> , <a href="#">NP_001276065.1</a>   |
| <b>RefSeq Size:</b>           | 8033 bp   |
| <b>RefSeq ORF:</b>            | 4566 bp   |
| <b>Locus ID:</b>              | 9353  |
| <b>UniProt ID:</b>            | <a href="#">O94813</a>  |
| <b>Cytogenetics:</b>          | 4p15.31   |
| <b>Protein Families:</b>      | Druggable Genome, Secreted Protein  |
| <b>Protein Pathways:</b>      | Axon guidance   |
| <b>Gene Summary:</b>          | <p>This gene encodes a member of the slit family of secreted glycoproteins, which are ligands for the Robo family of immunoglobulin receptors. Slit proteins play highly conserved roles in axon guidance and neuronal migration and may also have functions during other cell migration processes including leukocyte migration. Members of the slit family are characterized by an N-terminal signal peptide, four leucine-rich repeats, nine epidermal growth factor repeats, and a C-terminal cysteine knot. Proteolytic processing of this protein gives rise to an N-terminal fragment that contains the four leucine-rich repeats and five epidermal growth factor repeats and a C-terminal fragment that contains four epidermal growth factor repeats and the cysteine knot. Both full length and cleaved proteins are secreted extracellularly and can function in axon repulsion as well as other specific processes. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2015]</p> <p>Transcript Variant: This variant (3) lacks an alternate in-frame exon in the 5' coding region, compared to variant 1. It encodes isoform 3, which is shorter than 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> |