

## Product datasheet for **SC326514**

### ROBO1 (NM\_001145845) Human Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** ROBO1 (NM\_001145845) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** ROBO1  
**Synonyms:** DUTT1; SAX3  
**Vector:** pCMV6 series  
**Fully Sequenced ORF:** >NCBI ORF sequence for NM\_001145845, the custom clone sequence may differ by one or more nucleotides

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ATGATTGCGGAGCCCGCTCACTTTTACCTGTTTGGATTAATATGTCTCTGTTTCAGGCTCC
CGTCTTCGTCAGGAAGATTTTCCACCTCGCATTGTTGAACACCCTTCAGACCTGATTGTC
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GAAACATCTGCCATTAAGGACTCAAACCTAATGCAATTTACCTTTTCCTTGTGAGGGCA  
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CGGCAAATGCAGGATGCTGCTGGCCGTCGACATTTTATGCGTCTCAGTGCCCTAGGCC  
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AATGTAGGTGCAAGAAATATTGCAGAAATGCAGGTAAGTGGAGGATATGAAAGAGGAGAA  
GATAATAATGAAGAATTAGAGGAAACTGAAAGC

**Restriction Sites:**

Please inquire

**ACCN:**

NM\_001145845

<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>	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
<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_001145845.1</a></u> , <u><a href="#">NP_001139317.1</a></u>
<b>RefSeq Size:</b>	7385 bp
<b>RefSeq ORF:</b>	4656 bp
<b>Locus ID:</b>	6091
<b>UniProt ID:</b>	<u><a href="#">Q9Y6N7</a></u>
<b>Cytogenetics:</b>	3p12.3
<b>Protein Families:</b>	Druggable Genome
<b>Protein Pathways:</b>	Axon guidance

**Gene Summary:**

Bilateral symmetric nervous systems have special midline structures that establish a partition between the two mirror image halves. Some axons project toward and across the midline in response to long-range chemoattractants emanating from the midline. The product of this gene is a member of the immunoglobulin gene superfamily and encodes an integral membrane protein that functions in axon guidance and neuronal precursor cell migration. This receptor is activated by SLIT-family proteins, resulting in a repulsive effect on glioma cell guidance in the developing brain. A related gene is located at an adjacent region on chromosome 3. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Mar 2009]

Transcript Variant: This variant (4) represents use of an alternate promoter and 5' UTR, uses a distinct translation start site, includes an alternate in-frame exon in the 5' coding region, lacks an alternate in-frame exon in the central coding region, and uses an alternate splice site in the central coding region, compared to variant 1. The resulting isoform (d) has a shorter and distinct N-terminus and differs at three internal regions, compared to isoform a. The 5' UTR of this variant contains a 55 aa uORF with a strong Kozak signal that may inhibit translation of this protein. 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.