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Product datasheet for SC316293

SLIT2 (NM_004787) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	SLIT2 (NM_004787) Human Untagged Clone
Tag:	Tag Free
Symbol:	SLIT2
Synonyms:	SLIL3; Slit-2
Mammalian Cell Selection:	None
Vector:	pCMV6-XL5
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF:

>OriGene sequence for NM_004787 edited
CAGACACTGCGCGGTTCCCTCGGAGCAGCAAGCTAAAGAAAGCCCCCAGTGCCGGCGAGG
AAGGAGGCGGCGGGGAAAGATGCGCGGCGTTGGCTGGCAGATGCTGTCCCTGTCGCTGGG
GTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGCAGGCGTGCCCGGCGCAGTGCTCTTG
CTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCGCAGCGTGCCCAGGAATATCCC
CCGCAACACCGAGAGACTGGATTTAAATGGAAATAACATCACAAGAATTACGAAGACAGA
TTTTGCTGGTCTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCAT
TGAAAGAGGAGCATTCCAGGATCTTAAAGAACTAGAGAGACTGCGTTTAAACAGAAATCA
CCTTCAGCTGTTTCCTGAGTTGCTGTTTCTTGGGACTGCGAAGCTATACAGGCTTGATCT
CAGTGAAAACCAAATTCAGGCAATCCCAAGGAAAGCTTTCCGTGGGGCAGTTGACATAAA
AAATTTGCAACTGGATTACAACCAGATCAGCTGTATTGAAGATGGGGCATTCAGGGCTCT
CCGGGACCTGGAAGTGCTCACTCTCAACAATAACAACATTACTAGACTTTCTGTGGCAAG
TTTCAACCATATGCCTAAACTTAGGACTTTTCGACTGCATTCAAACAACCTGTATTGTGA
CTGCCACCTGGCCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACAC
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TGTCCTCTATGGAAATAAAATCACAGAACTCCCCAAAAGTTTATTTGAAGGACTGTTTTC
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TGGTGCCCGTTGCACCAGCCCCCGCCGCCTGGCAAACAAAAGAATTGGACAGATCAAAAG
CAAGAAATTCCGTTGTTCAGCTAAAGAACAGTATTTCATTCCAGGTACAGAAGATTATCG

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ATCAAAATTAAGTGGAGACTGCTTTGCGGATCTGGCTTGCCCTGAAAAGTGTCGCTGTGA
AGGAACCACAGTAGATTGCTCTAATCAAAAGCTCAACAAAATCCCGGAGCACATTCCCCA
GTACACTGCAGAGTTGCGTCTCAATAATAATGAATTTACCGTGTTGGAAGCCACAGGAAT
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TCGAGGGGAAAGGATAAGAGATTATTACCAAAAGCAGCAGGGCTATGCTGCTTGCCAAAC
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ACCGCTGAGGAGCAAGCGGCGGAAATACTCTTTCGAATGCACTGACGGCTCCTCCTTTGT
GGACGAGGTTGAGAAAGTGGTGAAGTGCGGCTGTACGAGGTGTGTGTCCTAAACACACTC

CCGGCAGCTCTGTCTTT

5' Read Nucleotide Sequence:

>OriGene 5' read for NM_004787 unedited
GTACCCTCTGTATACGACTCCTATAGGGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
CGCCCTTCAGACACTGCGCGGTTCCCTCGGAGCAGCAAGCTAAAGAAAGCCCCCAGTGCC
GGCGAGGAAGGAGGCGGCGGGGAAAGATGCGCGGCGTTGGCTGGCAGATGCTGTCCCTGT
CGCTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGCAGGCGTGCCCGGCGCAGT
GCTCTTGCTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCGCAGCGTGCCCAGGA
ATATCCCCCGCAACACCGAGAGACTGGATTTAAATGGAAATAACATCACAAGAATTACGA
AGACAGATTTTGCTGGTCTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTA
GCACCATTGAAAGAGGAGCATTCCAGGATCTTAAAGAACTAGAGAGACTGCGTTTAAACA
GAAATCACCTTCAGCTGTTTCCTGAGTTGCTGTTTCTTGGGACTGCGAAGCTATACAGGC
TTGATCTCAGTGAAAACCAAATTCAGGCAATCCCAAGGAAAGCTTTCCGTGGGGCAGTTG
ACATAAAAAATTTGCAACTGGATTACAACCAGATCAGCTGTATTGAAGATGGGGCATTCA
GGGCTCTCCGGGACCTGGAAGTGCTCACTCTCAACAATAACAACATTACTAGACTTTCTG
TGGCAAGTTTCAACCATATGCCTAAACTTAGACTTTTCGACTGCATTCAAACAACCTGTA
TTGTGACTGCCACCTGGCCCTGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCT
GTACACTCAGTGTATGGGCCCCTCCCACCTGAGAGCCATAATGTAGCCGAGTTCAAAAAC
GAGAATTTGTTCTGCAGTGGTCACCAGTCATTTATGGCT

Restriction Sites: Please inquire

ACCN: NM_004787

Insert Size: 4700 bp

OTI Disclaimer: Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info

OTI Annotation: The ORF of this clone has been fully sequenced and found to be a perfect match to NM_004787.1.

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:
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.

RefSeq:	NM_004787.1, NP_004778.1
RefSeq Size:	4950 bp
RefSeq ORF:	4590 bp
Locus ID:	9353
UniProt ID:	O94813
Cytogenetics:	4p15.31
Domains:	LRRNT, LRRCT, LRR, LamG, EGF_CA, LRR_TYP, CT, EGF, EGF, LRR_PS
Protein Families:	Druggable Genome, Secreted Protein
Protein Pathways:	Axon guidance
Gene Summary:	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] Transcript Variant: This variant (1) represents the longest transcript and encodes the longest 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.