

## Product datasheet for **SC326604**

### **SORBS2 (NM\_001145672) Human Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	SORBS2 (NM_001145672) Human Untagged Clone
Tag:	Tag Free
Symbol:	SORBS2
Synonyms:	ARGBP2; PRO0618
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

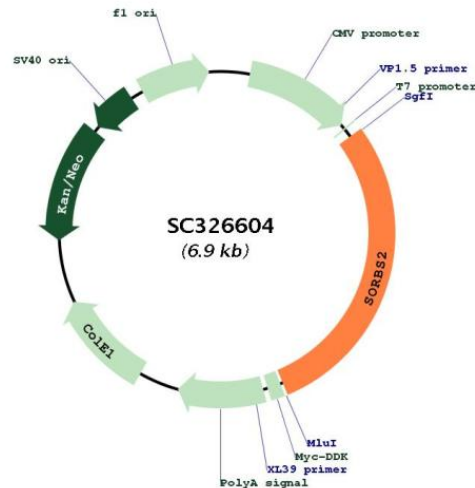


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Fully Sequenced ORF: >SC326604 representing NM\_001145672.  
Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGAACACAGGGCGTGATTCTCAGTCAACAGACTCAGCTTGGAGATCTTACAATGATGGCAATCAGGAG
ACACTGAACGGAGATGCTACATATTCCTCTCTTGACAGCAAAGGTTTTAGAAGCGTTCGACCAAACCTA
CAAGATAAAAGATCACCAACTCAGAGCCAGATAACAGTGAATGGAACTCAGGAGGTGCCGTGAGTCCC
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GTCATGCAGCACGGCACATCCCTCGATTCCACAGACACATATCCCCAGCATGCGCAGTCTCTGGATGGC
ACCACCAGCAGCTCTATCCCCTGTACCGATCCTCAGAGGAAGAGAAGAGAGTGACAGTCATCAAAGCC
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TCCTATGTGGAGTTCGTAAGAAGAACACAAAAGGTGCTGAGGACTACCCTGACCCTCCAATACCCAC
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AGAAGAACCAAAATCTTTGGTACTTTCCCGGAAACTACGTCAAGAGGCTGTGA
ACCGGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
```

Restriction Sites: SgfI-MluI

**Plasmid Map:**


**ACCN:** NM\_001145672

**Insert Size:** 1986 bp

**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).

**OTI Annotation:** 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.

**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\\_001145672.1](#)

**RefSeq Size:** 4356 bp

**RefSeq ORF:** 1986 bp

**Locus ID:** 8470

**UniProt ID:** [O94875](#)

**Cytogenetics:** 4q35.1

**MW:** 73.9 kDa

**Gene Summary:** Arg and c-Abl represent the mammalian members of the Abelson family of non-receptor protein-tyrosine kinases. They interact with the Arg/Abl binding proteins via the SH3 domains present in the carboxy end of the latter group of proteins. This gene encodes the sorbin and SH3 domain containing 2 protein. It has three C-terminal SH3 domains and an N-terminal sorbin homology (SoHo) domain that interacts with lipid raft proteins. The subcellular localization of this protein in epithelial and cardiac muscle cells suggests that it functions as an adapter protein to assemble signaling complexes in stress fibers, and that it is a potential link between Abl family kinases and the actin cytoskeleton. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2008]  
Transcript Variant: This variant (5) originates from an alternate promoter and has a different 5'UTR and first coding exon and includes alternate in-frame exons compared to variant 1. The resulting protein isoform (5) has a distinct N-terminus and 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.