

## Product datasheet for SC323290

### BRG1 (SMARCA4) (NM\_001128849) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	BRG1 (SMARCA4) (NM_001128849) Human Untagged Clone
Tag:	Tag Free
Symbol:	SMARCA4
Synonyms:	BAF190; BAF190A; BRG1; CSS4; hSNF2b; MRD16; RTPS2; SNF2; SNF2-beta; SNF2L4; SNF2LB; SWI2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC323290 representing NM_001128849. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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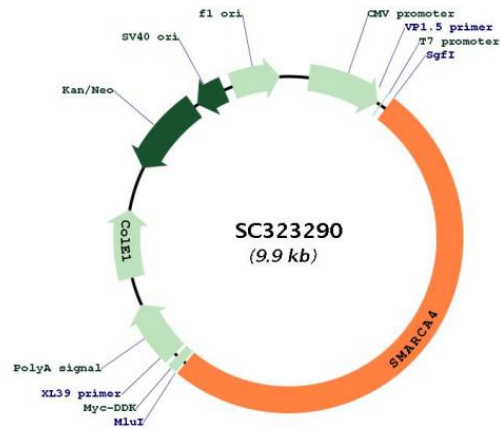
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Restriction Sites:

Sgfl-MluI

Plasmid Map:



ACCN: NM\_001128849

Insert Size: 5040 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](mailto: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:** 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\\_001128849.1](#)

**RefSeq Size:** 5589 bp

**RefSeq ORF:** 5040 bp

**Locus ID:** 6597

**Cytogenetics:** 19p13.2

**Protein Families:** Druggable Genome, Transcription Factors

**MW:** 188.1 kDa

**Gene Summary:** The protein encoded by this gene is a member of the SWI/SNF family of proteins and is similar to the brahma protein of *Drosophila*. Members of this family have helicase and ATPase activities and are thought to regulate transcription of certain genes by altering the chromatin structure around those genes. The encoded protein is part of the large ATP-dependent chromatin remodeling complex SNF/SWI, which is required for transcriptional activation of genes normally repressed by chromatin. In addition, this protein can bind BRCA1, as well as regulate the expression of the tumorigenic protein CD44. Mutations in this gene cause rhabdoid tumor predisposition syndrome type 2. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, May 2012]  
**Transcript Variant:** This variant (1) encodes the longest isoform (A, also known as 2). There are no publicly available full-length transcripts representing the exon combination of this variant; it is based on mRNA annotation on DNA accession AF254822.1, which is derived from data in PMID:11085541. **Sequence Note:** The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.