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Product datasheet for SC308857

SMARCA2 (NM_003070) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	SMARCA2 (NM_003070) Human Untagged Clone
Tag:	Tag Free
Symbol:	SMARCA2
Synonyms:	BAF190; BIS; BRM; hBRM; hSNF2a; NCBRS; SNF2; SNF2L2; SNF2LA; Sth1p; SWI2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

Fully Sequenced ORF:

>SC308857 representing NM_003070.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGTCCACGCCCACAGACCCTGGTGCGATGCCCCACCCAGGGCCTTCGCCGGGGCCTGGGCCTTCCCCT
GGGCCAATTCTTGGGCCTAGTCCAGGACCAGGACCATCCCCAGGTTCCGTCCACAGCATGATGGGGCCA
AGTCCTGGACCTCCAAGTGTCTCCCATCCTATGCCGACGATGGGGTCCACAGACTTCCCACAGGAAGGC
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TCCATGAAGGGCACTGGTATGCGACCACCTCACCCAGGCATGGGCCCTCCCCAGAGTCCAATGGATCAA
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CAGGCCATGAGCCAGCCCAACAGAGGTCCCTCACCTTTCAGTCCTGTCCAGCTGCATCAGCTTCGAGCT
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CATGCCAACACTGAAAGAGAGCAGAAGAAGGAGACAGAGCGGATTGAAAAGGAGAGAATGCGGCGACTG

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ATGGCTGAAGATGAGGAGGGTTATAGAAAACTGATTGATCAAAAGAAAGACAGGCGTTTAGCTTACCTT
TTGCAGCAGACCGATGAGTATGTAGCCAATCTGACCAATCTGGTTTGGGAGCACAAGCAAGCCCAGGCA
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CCCAAACTGACAAAGCAGATGAACGCTATCATCGATACTGTGATAAACTACAAAGATAGGTGTAACGTG
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TTCATTCAGTTACCTTCAAGGAAAGAATTACCAGAATACTATGAATTAATTAGGAAGCCAGTGGATTTC
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GATGATGAGTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: SgfI-MluI

Plasmid Map:	
ACCN:	NM_003070
Insert Size:	4773 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_003070.4
RefSeq Size:	5892 bp
RefSeq ORF:	4773 bp
Locus ID:	6595
UniProt ID:	P51531
Cytogenetics:	9p24.3
Domains:	SNF2_N, DEAD, BROMO, helicase_C, HSA, BRK
Protein Families:	Druggable Genome
MW:	181.3 kDa

Gene Summary: The protein encoded by this gene is a member of the SWI/SNF family of proteins and is highly 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. Alternatively spliced transcript variants encoding different isoforms have been found for this gene, which contains a trinucleotide repeat (CAG) length polymorphism. [provided by RefSeq, Jan 2014]
Transcript Variant: This variant (1) represents the longest transcript and encodes the longest isoform (a). Variants 1 and 3 encode the same protein (isoform a). 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.