Product datasheet for SC335351

BARD1 (NM_001282545) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	BARD1 (NM_001282545) Human Untagged Clone
Tag:	Tag Free
Symbol:	BARD1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335351 representing NM_001282545. Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGCCGGATAATCGGCAGCCGAGGAACCGGCAGCCGAGGATCCGCTCCGGGAACGAGCCTCGTTCCGCG
CCCGCCATGGAACCGGATGGTCGCGGTGCCTGGGCCCACAGTCGCGCCGCGCTCGACCGCCTGGAGAAG
CTGCTGCGCTGCTCGCGTTGTACTAACATTCTGAGAGAGCCTGTGTGTTTAGGAGGATGTGAGCACATC
TTCTGTAGTAATATATTTGGTCTGCGGCCTGTCGATTATACAGATGATGAAAGTATGAAATCGCTATTG
CTGCTACCAGAGAAGAATGAATCATCCTCAGCTAGCCACTGCTCAGTAATGAACACTGGGCAGCGTAGG
GATGGACCTCTTGTACTTATAGGCAGTGGGCTGTCTTCAGAACAACAGAAAATGCTCAGTGAGCTTGCA
GTAATTCTTAAGGCTAAAAAATATACTGAGTTTGACAGTACAGTAACTCATGTTGTTGTTCCTGGTGAT
GCAGTTCAAAGTACCTTGAAGTGTATGCTTGGGATTCTCAATGGATGCTGGATTCTAAAATTTGAATGG
GTAAAAGCATGTCTACGAAGAAAAGTATGTGAACAGGAAGAAAAGTATGAAATTCCTGAAGGTCCACGC
AGAAGCAGGCTCAACAGAGAACAGCTGTTGCCAAAGCTGTTTGATGGATGCTACTTCTATTTGTGGGGA
ACCTTCAAACACCATCCAAAGGACAACCTTATTAAGCTCGTCACTGCAGGTGGGGGCCAGATCCTCAGT
AGAAAGCCCAAGCCAGACAGTGACGTGACTCAGACCATCAATACAGTCGCATACCATGCGAGACCCGAT
TCTGATCAGCGCTTCTGCACACAGTATATCATCTATGAAGATTTGTGTAATTATCACCCAGAGAGGGTT
CGGCAGGGCAAAGTCTGGAAGGCTCCTTCGAGCTGGTTTATAGACTGTGTGATGTCCTTTGAGTTGCTT
CCTCTTGACAGCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites:	SgfI-MluI

View online »

Plasmid Map:
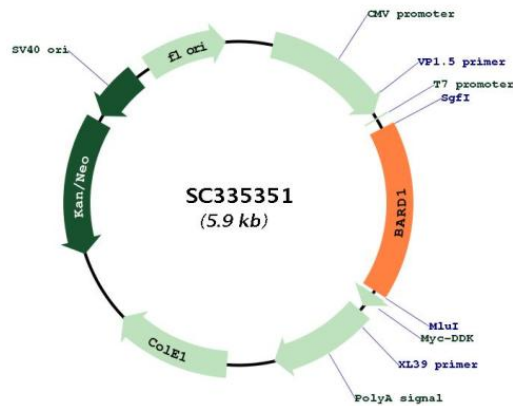
ACCN:	NM_001282545
Insert Size:	981 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
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_001282545.1
RefSeq Size:	4170 bp
RefSeq ORF:	981 bp
Locus ID:	580
Cytogenetics:	2q35

Protein Families:	Druggable Genome
MW:	37.1 kDa
Gene Summary:	This gene encodes a protein which interacts with the N-terminal region of BRCA1. In addition to its ability to bind BRCA1 in vivo and in vitro, it shares homology with the 2 most conserved regions of BRCA1: the N-terminal RING motif and the C-terminal BRCT domain. The RING motif is a cysteine-rich sequence found in a variety of proteins that regulate cell growth, including the products of tumor suppressor genes and dominant protooncogenes. This protein also contains 3 tandem ankyrin repeats. The BARD1/BRCA1 interaction is disrupted by tumorigenic amino acid substitutions in BRCA1, implying that the formation of a stable complex between these proteins may be an essential aspect of BRCA1 tumor suppression. This protein may be the target of oncogenic mutations in breast or ovarian cancer. Multiple alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2013] Transcript Variant: This variant (3) lacks four consecutive exons in the coding region, compared to variant 1. The resulting isoform (3, also known as phi) lacks an internal segment, compared to 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.