

## Product datasheet for **SC335479**

### **RAD52 (NM\_001297421) Human Untagged Clone**

#### Product data:

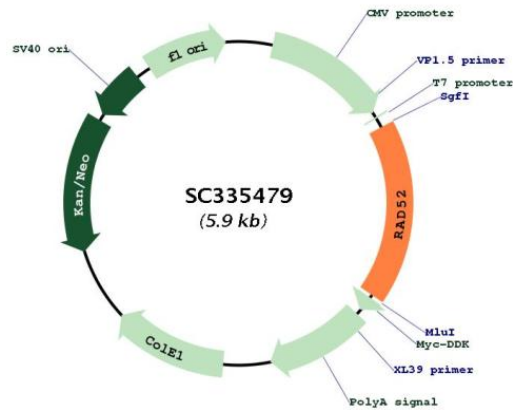
Product Type:	Expression Plasmids
Product Name:	RAD52 (NM_001297421) Human Untagged Clone
Tag:	Tag Free
Symbol:	RAD52
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335479 representing NM_001297421. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGTTGGTTACAATGGCTGGGCACACTCCATCACGCAGCAGAATGTGGATTTTGTGACCTCAACAAT
GGCAAGTTCTACGTGGGAGTCTGTGCATTTGTGAGGGTCCAGCTGAAGGATGGTTCATATCATGAAGAT
GTTGGTTATGGTGTAGTGAGGGCCTCAAGTCCAAGGCTTTATCTTTGGAGAAGGCAAGGAAGGAGGCG
GTGACAGACGGGCTGAAGCGAGCCCTCAGGAGTTTGGGAATGCACTTGGAACTGTATTCTGGACAAA
GACTACCTGAGATCACTAAATAAGCTTCCACGCCAGTTGCCTCTTGAAGTGGATTTAACTAAAGCGAAG
AGACAAGATCTTGAACCGTCTGTGGAGGAGGCAAGATACAACAGCTGCCGACCGAACATGGCCCTGGGA
CACCCACAGCTGCAGCAGGTGACCTCCCTTCCAGACCCAGCCATGCTGTGATACCGGCGACCAAGGAC
TGCAGCTCCCGAAGCCTGAGCTCATCCGCCGTGGAGAGCGAGGCCACGCACCAGCGGAAGCTCCGGCAG
AAGCAGCTGCAGCAGCAGTTCCGGGAGCGGATGGAGAAGCAGCAGGTTGAGTCTCCACGCCGTCAGCT
GAGAAGAGTGAGGCAGCGCCTCCGGCCCTCCTGTGACGCACAGCACTCCTGTAAGTGTCTCAGAACCA
CTCCTGGAGAAAGACTTCTTGCAGGAGTGACTCAAGAATTAATCAAGACTCTTGAAGACAACCTCTGAA
AAGTGGGCTGTGACTCCCGATGCAGGGGATGGTGTGGTCAAGCCCTCGTCTAGAGCAGACCCAGCCAG
ACCTCTGACACATTAGCCTTGAACAACCCAGATGGTGACCCAGAACAGGACTCCACACAGCGTTTGCCAC
CAGAAACCACAAGCAAAATCTGGATCTTGGACCTCCAACTTATAGCGCTGACCAACGCACAACAGGA
AACTGGGAATCTCATAGGAAGAGCCAGGACATGAAGAAAAGGAAATATGATCCATCTTAA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTAAACGGCCGGC
```

Restriction Sites: SgfI-MluI



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**Plasmid Map:**


**ACCN:** NM\_001297421

**Insert Size:** 1026 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\\_001297421.1](#)

**RefSeq Size:** 2847 bp

**RefSeq ORF:** 1026 bp

**Locus ID:** 5893

**Cytogenetics:** 12p13.33

**Protein Families:** Druggable Genome

**Protein Pathways:** Homologous recombination

**MW:** 38 kDa

**Gene Summary:** The protein encoded by this gene shares similarity with *Saccharomyces cerevisiae* Rad52, a protein important for DNA double-strand break repair and homologous recombination. This gene product was shown to bind single-stranded DNA ends, and mediate the DNA-DNA interaction necessary for the annealing of complementary DNA strands. It was also found to interact with DNA recombination protein RAD51, which suggested its role in RAD51 related DNA recombination and repair. A pseudogene of this gene is present on chromosome 2. Alternative splicing results in multiple transcript variants. Additional alternatively spliced transcript variants of this gene have been described, but their full-length nature is not known. [provided by RefSeq, Jul 2014]

Transcript Variant: This variant (4) differs in the 5' UTR, lacks a portion of the 5' coding region, and uses a downstream start codon compared to variant 1. The encoded isoform (c) has a shorter N-terminus compared to 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.