

Product datasheet for SC116621

53BP1 (TP53BP1) (NM_005657) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	53BP1 (TP53BP1) (NM_005657) Human Untagged Clone
Tag:	Tag Free
Symbol:	53BP1
Synonyms:	53BP1; p53BP1; p202; TDRD30
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL4</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC116621 sequence for NM_005657 edited (data generated by NextGen Sequencing)

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Clone variation with respect to NM_005657.2
 1059 c=>g;1234 g=>a;2487 t=>c;3406 a=>c

**5' Read Nucleotide
 Sequence:**

>OriGene 5' read for NM_005657 unedited
 CGTCAAAATTTGTATACGATTCACTATAGGCGGCCGCGATTCCGGCACGAGGGAGTTCGG
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 CCCAATAAGGATGTACATGNTGTAAAAGAGCAATAACN

Locus ID:	7158
UniProt ID:	Q12888
Cytogenetics:	15q15.3
Domains:	BRCT
Protein Families:	Druggable Genome, Transcription Factors
Gene Summary:	<p>This gene encodes a protein that functions in the DNA double-strand break repair pathway choice, promoting non-homologous end joining (NHEJ) pathways, and limiting homologous recombination. This protein plays multiple roles in the DNA damage response, including promoting checkpoint signaling following DNA damage, acting as a scaffold for recruitment of DNA damage response proteins to damaged chromatin, and promoting NHEJ pathways by limiting end resection following a double-strand break. These roles are also important during V(D)J recombination, class switch recombination and at unprotected telomeres. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Aug 2017]</p> <p>Transcript Variant: This variant (3) differs in the 5' UTR and coding sequence compared to variant 1. The resulting isoform (3) is shorter at the N-terminus compared to isoform 1.</p> <p>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.</p>