

Product datasheet for **RC229365L3V**

BRCA1 (NM_007298) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	BRCA1 (NM_007298) Human Tagged ORF Clone Lentiviral Particle
Symbol:	BRCA1
Synonyms:	BRCA1; BRCC1; BROVCA1; FANCS; IRIS; PNCA4; PPP1R53; PSCP; RNF53
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_007298
ORF Size:	2277 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC229365).
OTI Disclaimer:	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 clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	NM_007298.3 , NP_009229.2
RefSeq ORF:	2280 bp
Locus ID:	672
UniProt ID:	P38398
Cytogenetics:	17q21.31
Protein Families:	Druggable Genome, Transcription Factors
Protein Pathways:	Ubiquitin mediated proteolysis
MW:	84.8 kDa



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Gene Summary:

This gene encodes a 190 kD nuclear phosphoprotein that plays a role in maintaining genomic stability, and it also acts as a tumor suppressor. The BRCA1 gene contains 22 exons spanning about 110 kb of DNA. The encoded protein combines with other tumor suppressors, DNA damage sensors, and signal transducers to form a large multi-subunit protein complex known as the BRCA1-associated genome surveillance complex (BASC). This gene product associates with RNA polymerase II, and through the C-terminal domain, also interacts with histone deacetylase complexes. This protein thus plays a role in transcription, DNA repair of double-stranded breaks, and recombination. Mutations in this gene are responsible for approximately 40% of inherited breast cancers and more than 80% of inherited breast and ovarian cancers. Alternative splicing plays a role in modulating the subcellular localization and physiological function of this gene. Many alternatively spliced transcript variants, some of which are disease-associated mutations, have been described for this gene, but the full-length nature of only some of these variants has been described. A related pseudogene, which is also located on chromosome 17, has been identified. [provided by RefSeq, May 2020]