

## Product datasheet for **RC400623**

### BRCA2 (NM\_000059) Human Mutant ORF Clone

#### Product data:

Product Type:	Mutant ORF Clones
Product Name:	BRCA2 (NM_000059) Human Mutant ORF Clone
Mutation Description:	I1929v
Affected Codon#:	1929
Affected NT#:	5785
Nucleotide Mutation:	BRCA2 Mutant (I1929v), Myc-DDK-tagged ORF clone of Homo sapiens breast Cancer, early onset (BRCA2) as transfection-ready DNA
Effect:	Breast cancer
Symbol:	BRCA2
Synonyms:	BRCC2; BROVCA2; FACD; FAD; FAD1; FANCD; FANCD1; GLM3; PNCA2; XRCC11
E. coli Selection:	Kanamycin (25 ug/mL)
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
Tag:	Myc-DDK
ACCN:	NM_000059
ORF Size:	10254 bp
Restriction Sites:	Sgfl-RsrII
ORF Nucleotide Sequence:	>RC400623 representing NM_000059 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**GCGATCGCC**

ATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTGAAATTTTAAAGACACGCTGCAACAAAGCAGATT  
TAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC  
AGAAGAATCTGAACATAAAAACAACAATTACGAACCAACCTATTTAAAACCTCCACAAAGGAAACCATCT  
TATAATCAGCTGGCTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTC  
CTGTAAGAATTAGATAAATTCAAATTAGACTTAGGAAGGAATGTTCCCAATAGTAGACATAAAGTCT  
TCGCACAGTAAAACATAAATGGATCAAGCAGATGATGTTTCTGTCCACTTCTAAATCTTGTCTTAGT  
GAAAGTCTGTTGTTCTACAATGTACACATGTAACACCACAAAGAGATAAGTCAGTGGTATGTGGGAGTT



[View online »](#)

TGTTTCATACACCAAAGTTTGTGAAGGGTCGTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGA  
GGTGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACCACCCTTAGTTCTACTGTGCTCATA  
GTCAGAAATGAAGAAGCATCTGAAACTGTATTTCTCATGATACTACTGCTAATGTGAAAAGCTATTTTT  
CCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGTCTCTGTGACAGACAGTGAAAACACAAA  
TCAAAGAGAAGCTGCAAGTCATGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAA  
GACCACATTGGAAGTCAATGCCAAATGTCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTG  
AAGAAGATAGTTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAATCTCAAAAAAGTAAAGAACTAGCAA  
GACTAGGAAAAAATTTTCCATGAAGCAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAAGAA  
AAATACTCATTTGTATCTGAAGTGAACCAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGA  
AGCCCTTTGAGAGTGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCA  
ACTAACCTTTAGGCTCAAATGGAGCCAGATGGAGAAAAATACCCTATTGCATATTTCTTCATGTGAC  
CAAAATATTTAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTACTTCAGAGA  
ATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGAATAAA  
GAGAGATGAAGAGCAGCATCTTGAATCTCATACTGACTGCATTCTTGAGTAAAGCAGGCAATATCTGGA  
ACTTCTCCAGTGGCTTTCATTTAGGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAG  
AGACTTTCAATGCAAGTTTTTCCAGTCAATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGA  
AAGTGGACTGGAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAAT  
GGAAGCTGGCCAGCCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTAATATCCACTTTGA  
AAAAGAAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAATACCGAA  
AGACCAAAAAATCAGAATAATTAAGTGTTCAGCCAGTTTGAAGCAATGCTTTTGAAGCACCATTACA  
TTTGCAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTACAGAATGATTCGAAG  
AACCAATTTGCTTAACTAGCTCTTTGGGACAATCTGAGGAAATGTTCTAGAAATGAAACATGTTT  
TAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTATAAAGGAAAAACTACAGTTA  
TTTATTACCCAGAAGCTGATTCTGTGATGCCTGCAGGAAGGACAGTGTGAAAAATGCTCAAAAAAGCA  
AAAAAGTTTCAGATATAAAGAAGAGGTCTGGCTGCAGCATGTACCCAGTACAACATTCAAAAGTGGAA  
ATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAAATGCCAGCACTCTTATT  
TTAACTCTACTTCCAAGGATGTTCTGTCAAACCTAGTCATGATTTCTAGAGGCAAGAATCATACAAAA  
TGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAAATTTCCCATGGAAAA  
GAATCAAGATGTATGTGCTTTAAATGAAAAATTAAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATG  
AGAGTAGCATCACCTTCAAGAAAGGTACAATTAACCAAAAACACAATCTAAGAGTAATCAAAAAAATC  
AAGAAGAACTACTTCAATTTCAAAAAAATCACTGTCAATCCAGACTCTGAAGAATTTTCTCAGACATGA  
GAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGCTTTAGGAAATACTAAGGAATTCAT  
GAAACAGACTTGACTTGTGTAACGAACCCATTTTCAAGAATCTACCATGGTTTTATATGGAGACACAG  
GTGATAAACAAGCAACCAAGTGTCAATTAAAAAAGATTTGGTTTATGTTCTTGCAAGGAGAACAAAAA  
TAGTGTAAAGCAGCATATAAAAAATGACTCTAGGTCAAGATTTAAATCGGACATCTCCTTGAATATAGAT  
AAAATACCAGAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACA  
GTTTTGGAGGTAGCTTCAAGACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAG  
CAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATGTAATACC  
TTGGCATTAGATAATCAAAAGAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGA  
GTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTT  
TAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAATTTTCTACTATATTAGAAGAA  
TCAGGAAGTCAAGTTGAAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAG  
TGCTGAAAACAGATGACTATCTTAAAGACCCTTCTGAGGAATGCAGAGATGCTGATCTTCATGTGAT  
AATGAATGCCCATCGATTGGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAACGG  
AAGTTTGTGCTGGCTGTTGAAAAATGACTGTAACAAAAGTCTTCTGGTTATTTAACAGATGAAAAATGAAG  
TGGGGTTTAGGGCTTTTATTCTGCTCATGGCACAAAATGAATGTTTCTACTGAAGCTCTGCAAAAAGC  
TGTGAAACTGTTTGTGATATTGAGAATATTAGTGAGGAACTCTGCAGAGGTACATCCAATAAGTTTA  
TCTTCAAGTAAATGTCATGATTCTGTTGTTCAATGTTTAAAGATGAAAAATCATAATGATAAACTGTAA  
GTGAAAAAATAATAATGCCAACTGATATTACAAAATAAATTTGAAATGACTACTGGCACTTTTGTGGA  
AGAAATTAAGTAAAAATCAAGAGAAATGAAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAAT  
TCTCATAACTTAGAATTTGATGGCAGTATTCAAGTAAAAATGATACTGTTTGTATTATAAAGATGAAA  
CGGACTTGCTATTTACTGATCAGCACAACATATGTCTTAAATTAATCTGGCCAGTTTATGAAGGAGGGAAA

CACTCAGATTAAGAAGATTTGTCAAGTTAACTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCAT  
 GGTAATACTTCAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAAGATTTTGAGACTT  
 CTGATACATTTTTTTCAGACTGCAAGTGGGAAAAATATTAGTGTGCGCCAAAGAGTCATTTAATAAAATTGT  
 AAATTTCTTTGATCAGAAACCAGAAGAAATGCATAACTTTTCTTAAATTTCTGAATTACATTCTGACATA  
 AGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTAAACACAAAATCTGAAAGAAA  
 GTGTCCAGTTGGTACTGGAAATCAACTAGTGACCTCCAGGGACAACCCGAACGTGATGAAAAGATCAA  
 AGAACCTACTCTATTGGGTTTTTCATACAGCTAGCGGGAAAAAAGTTAAATTTGCAAAGGAATCTTTGGAC  
 AAAGTGAAAAACCTTTTTGATGAAAAAGCAAGGTAAGTAAATCACCAGTTTTAGCCATCAATGGG  
 CAAAGACCCTAAAGTACAGAGAGGCTGTAAAGACCTGAATTAGCATGTGAGACCATTGAGATCACAGC  
 TGCCCCAAAGTGTAAAGAAATGCAGAATTCTCTCAATAATGATAAAAACTTGTTTCTATTGAGACTGTG  
 GTGCCACCTAAGCTCTAAGTGATAATTTATGTAGACAACTGAAAATCTCAAAACATCAAAAAGTATCT  
 TTTTGAAGTTAAAGTACATGAAAATGTAGAAAAAGAACAGCAAAAAGTCTGCAACTTGTACACAAA  
 TCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAACTTCT  
 GTGAGTCAGACTTCATTACTGGAAGCAAAAAATGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAA  
 GAATAAATACTGCAGATTATGTAGGAAATTTTGTATGAAAATTAATCAAACAGTACTATAGCTGAAA  
 TGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTAAGTAAACAGTAGCATGTCTAACAGCTATTCC  
 TACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGC  
 CAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAGAGATGC  
 AAATGCATACCCACAACTGTAATGAAGATAATTTGCGTTGAGGAACTTGTGACTAGCTCTTACCCTGC  
 AAAAAATAAAATGCAGCCATTAATTTGCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCAT  
 TTAGGATAGCCAGTGGTAAATCGTTTTGTGTTTCATGAAACAATTAAGGAAAGTAAAGACATATTTAC  
 AGACAGTTTCAGTAAAGTAATTAAGGAAAAACAGGAGAATAAATCAAAAAATTTGCCAAACGAAAATATG  
 GCAGTTGTTACGAGGCATTGGATGATTCAGAGGATATCTTCATAACTCTAGATAAGTAAAGTGA  
 GCACGCATTCACATAAGGTTTTTGTGACATTCAGAGTGAAGAAGTTTTACAACATAACCAAAATATGTC  
 TGGATTGGAGAAAGTTTCTAAAAATACCTTGTGATGTTAGTTTGGAACTTCAGATATATGTAATGT  
 AGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATCTTGTGGGATTTTTAGCACAGCAAGTGAA  
 AATCTGTCCAGGTATCAGATGCTTATTACAAAACGCAAGACAAGTGTCTTGAATAGAAAGATAGTAC  
 CAAGCAAGTCTTTTCAAAGTATTGTTTAAAAGTAACGAACATTCAGACCAGCTCACAAGAGAAGAAAAT  
 ACTGCTATACGTACTCCAGAACATTTAATATCCAAAAAGGCTTTTATATAATGTGGTAAATTCATCTG  
 CTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTCCATTTTGAAGGTTCTTACACAAAGTTAA  
 GGGAGTGTAGAGGAATTTGATTTAATCAGAAGTGGAGTACTTCACTATTCACCTACGTCTAGACAA  
 AATGTATCAAAAATACCTCCTCGTGTGATAAGAGAAACCCAGAGCACTGTGAAACTCAGAAATGGAAA  
 AAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTCTTTCAGAAAATATCA  
 CTCTATTAAGTTTCTCCATATCTCTCAATTTCAACAAGACAAAACAACAGTTGGTATTAGGAACCAAA  
 GTGTCACTTGTGAGAACATTCATGTTTTGGGAAAAAGAACAGGCTTCACTAAAAACGTAATAATGGAAA  
 TTGGTAAAACGAACTTTTTCTGATGTTTCTGTGAAAACAAATAGAAAGTTGTTCTACTTACTCCAA  
 AGATTCAGAAAACACTTTTGAACAGAGCAGTAGAAATGCTAAAGCTTTTATGGAAGATGATGAAGT  
 ACAGATCTAACTGCCAAGTCAAGCCACATTTCTTTTTACATGTCCCGAAAATGAGGAAATGGTTT  
 TGTCAAATTCAGAATTTGGAAAAAGAGAGGAGAGCCCTTATCTTAGTGGGAGAACCCCAATCAAAAAG  
 AAACCTTATAAATGAATTTGACAGGATAATAGAAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT  
 CCAGATGGCACATAAAAAGATCGAAGATTGTTTATGCATCATGTTTCTTTAGAGCCGATTACCTGTGTAC  
 CCTTTCGCACAACATAAGGAACGTCAAGAGATACAGAAATCCAAATTTTACCACCTGGTCAAGAAATTTCT  
 GTCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCAATTTAGCAGTTTTCAGGACAT  
 CCATTTTATCAAGTTTCTGCTACAAGAAATGAAAAATGAGACACTTGATTACTACAGGCAGACCAACCA  
 AAGTCTTTGTTCCACCTTTTAAACTAAATCACATTTTACAGAGTTGAACAGTGTGTTAGGAATATTA  
 CTTGGAGGAAAACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAATAAGATTAAT  
 GACAATGAGATTCATCAGTTTAACAAAAACAACCTCAATCAAGCAGCAGCTGTAACCTTTCACAAAGTGTG  
 AAGAAGAACCTTTAGATTTAATTACAAGTCTTCAAGATGCCAGAGATATACAGGATATGCGAATTAAGAA  
 GAAACAAGGCAACGCGTCTTTCCACAGCCAGGAGTCTGTATCTTGAAAAACATCCACTCTGCCTCGA  
 ATCTCTCTGAAAGCAGCAGTAGGAGGCCAAGTTCCCTCTGCGTGTCTCATAAACAGCTGTATACGTATG  
 GCGTTTCTAAACATTGCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTTCAGTTTACACTGAAGATTA  
 TTTTGGTAAGGAAAGTTTATGGACTGGAAAAGGAATACAGTTGGCTGATGGTGGATGGCTCATACCTCC

```

AATGATGGAAAGGCTGGAAAAGAAGAATTTTATAGGGCTCTGTGTGACACTCCAGGTGTGGATCCAAAGC
TTATTTCTAGAATTTGGGTTTATAATCACTATAGATGGATCATATGAAAAGTGGCAGCTATGGAATGTGC
CTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCCAGAAAGGGTGTCTTCAACTAAAATACAGATAT
GATACGGAAATTTGATAGAAGCAGAAGATCGGCTATAAAAAAGATAATGAAAAGGGATGACACAGCTGCAA
AAACACTTGTCTCTGTGTTTCTGACATAATTTTATTGAGCGCAAAATATATCTGAAACTTCTAGCAATAA
AACTAGTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGGTATGCTGTAAAGGCC
CAGTTAGATCCTCCCCTTCTAGCTGTCTTAAAGAATGGCAGACTGACAGTTGGTCAGAAGATTATCTTTC
ATGGAGCAGAAGTGGTGGGCTCCTGATGCCTGTACACCTCTTGAAGCCCAGAAATCTTTATGTTAAA
GATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAAGTGGATTCTTCTGACCCTAGACCT
TTTCTCTGCCCTTATCATCGCTTTTTCAGTGTGGAGGAAATGTTGGTGTGTTGATGTAATTATTCAAA
GAGCATACCCTATACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTGCAATGAAAGAGAGGA
AGAAAAGGAAGCAGCAAAATATGTGGAGGCCAACAAAAGAGACTAGAAGCCTTATTCCTAAAATTCAG
GAGGAATTTGAAGAACATGAAGAAAACACAACAAAACCATATTTACCATCACGTGCACTAACAGACAGC
AAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCAGCTTACCT
TGAGGGTTATTTTTCAGTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAA
CAAGCTCAGATCCAGTTGAAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAA
GGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAGAAAAGATTTCAGTTATACT
GAGTATTTGGCGTCCATCATCAGATTTATTTCTGTAAACAGAAGGAAAGAGATACAGAATTTATCAT
CTTGCAACTTCAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAAACTC
AGTATCAACAACCTACCGTTCAGATGAAATTTTATTTTTCAGATTTACCAGCCACGGGAGCCCTTCACTT
CAGCAATTTTATAGATCCAGACTTTTTCAGCCATCTTGTCTGAGGTGGACCTAATAGGATTTGTCGTTTCT
GTTGTGAAAAAAGCAGGACTTGGCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAA
AGTTTGGATAGACTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAGTG
GCGTCCAGAATCCAAATCAGGCCTTCTTACTTTATTTGCTGGAGATTTTCTGTGTTTTCTGCTAGTCCA
AAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAACTGTTGAGAATATTGACATACTTTGCA
ATGAAGCAGAAAAAAGCTTATGCATATACTGCATGCAATGATCCCAAGTGGTCCACCCCAACTAAAGA
CTGTACTTCAGGGCCGTACACTGCTCAAATCATTCTGGTACAGGAAACAAGCTTCTGATGTCTTCTCCT
AATTGTGAGATATATTATCAAAGTCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTG
TCTCAGCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAAGAACTGCAAAAA
GAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTT
TCTCCGGCTGCACAGAAGGCATTTACAGCCCAAGGAGTTGTGGCACCATAACGAAACCCCATAAAGA
AAAAAGAACTGAATTCCTCAGATGACTCCATTTAAAAAATCAATGAAATTTCTTTTGGAAAGTAA
TTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAA
CAATTTATATCTGTCAAGTCCACTAGGACTGCTCCACCAGTTTCAAGAAGATTATCTCAGACTGAAAC
GACGTTGACTACATCTGTATCAAAGAACAGGAGAGTTCCAGGCCAGTACGGAAGAATGTGAGAAAAA
TAAGCAGGACACAATTACAATAAAAAATATATC

```

```

AGCGGACCCACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC
TGGATTACAAGGATGACGACGA TAAGGTTTAA

```

**Protein Sequence:**

>RC400623 representing NM\_000059

Red=Cloning site Green=Tags(s)

```

MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSSEAPPYNSEPAEESHKNNNYEPNLFKTPQRKPS
YNQLASTPIIFKEQGLTLPLYQSPVKELDKFKLDLGRNVPNSRHKSLRTVKTMDQADDVSCPLLNLSCLS
ESPVVLQCTHVTPQRDKSVVCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLI
VRNEEASETVFPHDTTANVKSIFYSNHDESLKKNDRFIA SVTDSSENTNQREAAASHGFGKTSNGNSFKVNSCK
DHIGKSMPNVLEDEVYETVVDTSSEDSFSLCF SKCRTKNLQKVRTSKTRKKIFHEANADECEKSNQVKE
KYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVP SLACEWSQLTSLGLNGAQMEKIPLLHISDCD
QNISEKDLLDTENKRKKDFLTSNSLPRISL PKSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAIISG
TSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDPNFKKETEASESGLEIHTVCSQKEDSLCPNLIDN
GSPATTTQNSVALKNAGLISTLKKTKNF IYAIHDETSYKGGKIPKDQKSELINCSAQFEANAFEAPLT
FANADSGLLHSSVKRSCSQNDSEPTLSLTSSFGTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQL

```

FITPEADSL SCLQEGQCENDPKSKKVS DIKEEVLAAACHPVQHSKVEYSDTDFQSQSLLYDHENASTLI  
 LTPTSKDVL SNLVMISRKESYKMSDKLKGNNYSDVELTKNIPMEKNQDVCALNENYKNVELLPPEKYM  
 RVASPSRKVQFNQNTNLRVIQKNQEETTSISKITVNPDSEELFSDNENNFVFQVANERNLALGNTKELH  
 ETDLTCVNEPIFKNSTMVL YGDTGDKQATQVSIKKDLVYVLAENKNSVKQHIKMTLGQDLKSDISLNDI  
 KIPEKNNDYMNKWAGLLGPI SNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIIEEQYPTSLACVEIVNT  
 LALDNQKLLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHLTPSQKAEITELSTILEE  
 SGSQFEFTQFRKPSYILQKSTFEVPENQMTILKTTSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKR  
 KFAGLLKNDCKNSASGYLTDENEVGRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETSAEVHPISL  
 SSSKCHDSVVSVMFKIENHNDKTVSEKNKNCQLILQNNIEMTTGTFVVEITENYKRNTENEDNKYTAASRN  
 SHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKL SGQFMKEGNTQIKEDLSDLTFLEVAKAQEACH  
 GNTSNKEQLTATKTEQNIKFETSDTFFQTASGKNISVAKESFNKIVNFFDQKPEELHNFSLNSELHSDI  
 RKNKMDILSYEETDIVKHKILKESVPGTGNQLVTFQGGQPERDEKIKEPTLLGFHTASGKVKIAKESLD  
 KVKNFLFDEKEQGTSEITFSHQWAKTLKYREACKDLELACETIEITAAPKCKEMQNSLNNDKNLVSIETV  
 VPPKLLSDNLCRQNTENLKTSSIFLKVKHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCSRKTS  
 VSQTSLL EAKKWLREGIFDQPERINTADYVGNLYENNSNSTIAENDKNHLSEKQD TYLSNSSMSNSYS  
 YHSDEVYNDSGYL SKNKLDSGIEPVLKNVEDQKNTSFSKVISNVKDANAYPQTVNEDICVEELVTSSSPC  
 KNKNAAIKLSISNSNFEVGPFAFRIASGKIVCVSHETIKKVKDIFTDSFSKVIKENNENKSKICQTKIM  
 AGCYEALDDESEDILHNSLDNDECSTHSHKVFADIQSEEVLQHNQNMGLEKYSKISPCDVSLETSDICKC  
 SIGKHLKSVSSANTCGIFSTASGKSVQVSDASLQARQVFSEIEDSTKQVFSKVLFKSNEHSDQLTREEN  
 TAIRTPPEHLISQKGFYNVNVSSAFSGFSTASGKQVSILESSLHKVKGVL EEFDLIRTEHSLHYSPTS RQ  
 NVSKILPRVDKRNPEHCVNSEMEKTCSEKFKLSNNLNVEGGSSENNHSIKVSPYL SQFQDKQQLVLGTK  
 VSLVENIHVLGKEQASPKNVKMEIGKTETTFSDVPVKTNIEVCSTYSKDSENYFETEAVEIAKAFMEDDEL  
 TDSKLP SHATHSLFTCPENEEMVLSNSRIGKRRGEPLILVGEPSIKRNLNNEFDRIIENQEKSLKASKST  
 PDGTIKDRRLFMHHVSL EPI TCVPFRITKERQEIQNPNFTAPGQEF LSKSHLYEHLTLEKSSSNLAVSGH  
 PFYQVSA TRNEKMRHLITTRPTKVFVPPFKTKSHFHRVEQCVRNINLEENRQKQNDIGHGSDSKNKIN  
 DNEIHQFNKNSNQAAAVTFTKCEEEPLDLITSLQNARDIQDMRIKKKQRQRVFPQPSGLYLAKTSTLPR  
 ISLKA AVGGQVPSACSHKQLYTYGVSKHCIKINSKNAESFQFHTEDYFGKESLWTGKGIQLADGGWLIPS  
 NDGKAGKEEFYRALCDTPGVDPKLSRIWVYNHYRWIIWKLAA MECAFPKEFANRCLSPERVLLQLKYRY  
 DTEIDRSRRSAIKKIMERDDTAAKTLVLCVSDIISLSANISETSSNKTSSADTQKVAIIELTDGWYAVKA  
 QLDPPLLAVLKNGR LTVGQKIILHGAELVGS DACTPLEAPESLMLKISANSTRPARWYTKLGFDPDRP  
 FPLPLSSLFSDGGNVGCVDVIIQRAYPIQWMEKTS SGLYIFRNEREEKEAAKYVEAQQKRL EALFTKIQ  
 EEFEEHEENTTKPYLPSRALTRQQVRALQDGAELYEAVKNAADPAYLEGYFSEEQLRALNNHRQMLNDKK  
 QAQIQLEIRKAMESAEQKEQGLSRDVTTVWKLRIVSYSKKEKDSVILSIWRPSSDLYSLLTEGKRYRIYH  
 LATSKSKSERANIQLAATKKTQYQQLPVSD EILFQIYQPREPLHFSKFLDPDFQPSCSEVDLIGFVVS  
 VVKKTGLAPFVYL SDECYNLLAIKFWIDLNEDI IKPHMLIAASNLQWRPESKSGLLTLFAGDFSVFSASP  
 KEGHFQETFNKMKNTVENIDILCNEAENKLMHILHANDPKWSTPTKDC TSGPYTAQIIPGTGNKLLMSSP  
 NCEIYYQSPLSLCMAKRKSVSTPVSAQMTSKSCKGEKEID DQKNCKRRALDFL SRLPLPPPVPSPICTFV  
 SPAAQKAFQPPRSCGTYETPIKKKELNSPQMTPFKFFNEISLLESNSIADEELALINTQALLSGSTGEK  
 QFISVSESTRTAPTSS ELYRLKRRCTTSLIKEQESSQASTE ECEKNKQDTITTKKYI

SGPTRRRLEQKLI SEEDLAANDILDYKDDDDKV

**Restriction Sites:**

Sgfl-RsrII

**Cloning Scheme:**

**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.

**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).

**RefSeq:**

[NP\\_000050](#)

**RefSeq Size:**

10254 bp

**RefSeq ORF:**

10257 bp

**Locus ID:**

675

**Cytogenetics:**

13q13.1

**Protein Families:**

Druggable Genome

**Protein Pathways:** Homologous recombination, Pancreatic cancer, Pathways in cancer

**MW:** 376 kDa

**Gene Summary:** Inherited mutations in BRCA1 and this gene, BRCA2, confer increased lifetime risk of developing breast or ovarian cancer. Both BRCA1 and BRCA2 are involved in maintenance of genome stability, specifically the homologous recombination pathway for double-strand DNA repair. The largest exon in both genes is exon 11, which harbors the most important and frequent mutations in breast cancer patients. The BRCA2 gene was found on chromosome 13q12.3 in human. The BRCA2 protein contains several copies of a 70 aa motif called the BRC motif, and these motifs mediate binding to the RAD51 recombinase which functions in DNA repair. BRCA2 is considered a tumor suppressor gene, as tumors with BRCA2 mutations generally exhibit loss of heterozygosity (LOH) of the wild-type allele. [provided by RefSeq, May 2020]