

## Product datasheet for **RC400515**

### 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:	M192T
Affected Codon#:	192
Affected NT#:	575
Nucleotide Mutation:	BRCA2 Mutant (M192T), Myc-DDK-tagged ORF clone of Homo sapiens breast Cancer, early onset (BRCA2) as transfection-ready DNA
Effect:	Pancreatic 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:	>RC400515 representing NM_000059 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGATCGCC**

ATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGATT  
TAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC  
AGAAGAATCTGAACATAAAAAACAACAATTACGAACCAACCTATTTAAACTCCACAAAGGAAACCATCT  
TATAATCAGCTGGCTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTC  
CTGTAAGAAGATTAGATAAATTCAAATTAGACTTAGGAAGGAATGTTCCCAATAGTAGACATAAAGTCT  
TCGCACAGTAAAACTAAATGGATCAAGCAGATGATGTTTCTGTCCACTTCTAAATCTTGTCTTAGT  
GAAAGTCTGTTGTTCTACAATGTACACATGTAACACCACAAAGAGATAAGTCAGTGGTATGTGGGAGTT



[View online »](#)

TGTTCATACACCAAAGTTTGTGAAGGGTCGTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGA  
 GGTGGATCCTGATACGTCTTGGTCAAGTCTTTAGCTACACCACCACCCTTAGTTCTACTGTGCTCATA  
 GTCAGAAATGAAGAAGCATCTGAAACTGTATTTCTCATGATACTACTGCTAATGTGAAAAGCTATTTTT  
 CCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGTCTCTGTGACAGACAGTAAAACACAAA  
 TCAAAGAGAAGCTGCAAGTCATGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAA  
 GACCACATTGGAAGTCAATGCCAAATGTCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTG  
 AAGAAGATAGTTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAATCTACAAAAAGTAAAGAACTAGCAA  
 GACTAGGAAAAAATTTTCCATGAAGCAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAAGAA  
 AAATACTCATTTGTATCTGAAGTGAACCAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGA  
 AGCCCTTTGAGAGTGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCA  
 ACTAACCTTTCAGGTCTAAATGGAGCCAGATGGAGAAAAATACCCTATTGCATATTTCTTCATGTGAC  
 CAAAATATTTAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTACTTCAGAGA  
 ATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGTAAATAA  
 GAGAGATGAAGAGCAGCATCTTGAATCTCATACAGACTGCATTCTGCAGTAAAGCAGGCAATATCTGGA  
 ACTTCTCCAGTGGCTTTCATTTCCAGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAG  
 AGACTTCAATGCAAGTTTTTCCAGGTATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGA  
 AAGTGGACTGGAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAAT  
 GGAAGCTGGCCAGCCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTAATATCCACTTTGA  
 AAAAGAAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAATACCGAA  
 AGACCAAAAATCAGAATAATTAAGTGTTCAGCCAGTTTGAAGCAATGCTTTTGAAGCACCCTTACA  
 TTTGCAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTACAGAATGATTCGAAG  
 AACCAATGCTGCTTAACTAGCTCTTTGGGACAATCTGAGGAAATGTTCTAGAAATGAAACATGTTT  
 TAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAAATAAGGAAAAACTACAGTTA  
 TTTATTACCCAGAAGCTGATTCTGTGATGCCTGCAGGAAGGACAGTGTGAAAAATGCTCAAAAAGCA  
 AAAAAGTTTCAGATATAAAGAAGAGGTCTGGCTGCAGCATGTACCCAGTACAACATTCAAAAGTGGAA  
 ATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAATGCCAGCACTCTTATT  
 TTAACTCTACTTCCAAGGATGTTCTGTCAAACCTAGTCATGATTTCTAGAGGCAAGAATCATACAAAA  
 TGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAATATCCCATGGAAAA  
 GAATCAAGATGTATGTGCTTTAAATGAAAATTAAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATG  
 AGAGTAGCATCACCTTCAAGAAAGGTACAATTCACCAAAAACACAATCTAAGAGTAATCAAAAAAATC  
 AAGAAGAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAATTTTCTCAGACATGA  
 GAATAATTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGCTTTAGGAAATACTAAGGAATTCAT  
 GAAACAGACTTGACTTGTGTAACCGAACCCATTTTCAAGAATCTACCATGGTTTTATATGGAGACACAG  
 GTGATAAACAAGCAACCCAAGTGTCAATTAAAAAAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAA  
 TAGTGTAAAGCAGCATATAAAAAAGACTCTAGGTCAAGATTTAAATCGGACATCTCCTTGAATATAGAT  
 AAAATACCAGAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACA  
 GTTTTGGAGGTAGCTTCAAGACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAG  
 CAAAATGTTCTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATGTAATACC  
 TTGGCATTAGATAATCAAAAGAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGA  
 GTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTT  
 TAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAATTTTCTACTATATTAGAAGAA  
 TCAGGAAGTCAGTTTGAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAG  
 TGCCTGAAAACAGATGACTATCTTAAAGACCCTTCTGAGGAATGCAGAGATGCTGATCTTCATGTCAT  
 AATGAATGCCCATCGATTGGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAACGG  
 AAGTTTGTGGCCTGTTGAAAAATGACTGTAACAAAAGTCTTCTGGTTATTTAACAGATGAAAAATGAAG  
 TGGGGTTTAGGGCTTTTATTCTGCTCATGGCACAAAACCTGAATGTTTCTACTGAAGCTCTGCAAAAAGC  
 TGTGAAACTGTTTGTGATATTGAGAATATTAGTGAGGAACTCTGCAGAGGTACATCCAATAAGTTTA  
 TCTTCAAGTAAATGTCATGATTCTGTTGTTCAATGTTTAAAGATGAAAAATCATAATGATAAACTGTAA  
 GTGAAAAAATAATAATGCCAACTGATATTACAAAATAATTTGAAATGACTACTGGCACTTTTGTGGA  
 AGAAATTAAGTAAAAATCAAGAGAAATGAAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAAT  
 TCTCATAACTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTGTTTGTATTATAAAGATGAAA  
 CGGACTTGCTATTTACTGATCAGCACAACATATGTCTTAAATTAATCTGGCCAGTTTATGAAGGAGGGAAA

CACTCAGATTAAGAAGATTTGTCAAGTTAACTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCAT  
 GGTAATACTTCAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAAAGATTTTGAGACTT  
 CTGATACATTTTTTTCAGACTGCAAGTGGGAAAAATATTAGTGTGCGCCAAAGAGTCATTTAATAAAATTTG  
 AAATTTCTTTGATCAGAAACCAGAAGAAATGCATAACTTTTCTTAAATTTCTGAATTACATTCTGACATA  
 AGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTAAACACAAAATCTGAAAGAAA  
 GTGTCCAGTTGGTACTGGAAATCAACTAGTGACCTCCAGGGACAACCCGAACGTGATGAAAAGATCAA  
 AGAACCTACTCTATTGGGTTTTTCATACAGCTAGCGGGAAAAAAGTTAAAATTTGCAAAGGAATCTTTGGAC  
 AAAGTGAAAAACCTTTTTGATGAAAAAGCAAGGTAAGTAAATCACCAGTTTTAGCCATCAATGGG  
 CAAAGACCCTAAAGTACAGAGAGGCTGTAAAGACCTGAATTAGCATGTGAGACCATTGAGATCACAGC  
 TGCCCCAAAGTGTAAAGAAATGCAGAATCTCTCAATAATGATAAAAACTTGTTTCTATTGAGACTGTG  
 GTGCCACCTAAGCTCTAAGTGATAATTTATGTAGACAACTGAAAATCTCAAAACATCAAAAAGTATCT  
 TTTTGAAGTTAAAGTACATGAAAATGTAGAAAAAGAACAGCAAAAAGTCTGCAACTTGTACACAAA  
 TCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAACTTCT  
 GTGAGTCAGACTTCATTACTGGAAGCAAAAAATGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAA  
 GAATAAATACTGCAGATTATGTAGGAAATTTTGTATGAAAATTAATCAAACAGTACTATAGCTGAAAA  
 TGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCC  
 TACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGC  
 CAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAGAGATGC  
 AAATGCATACCCACAACTGTAATGAAGATATTTGCGTTGAGGAACTTGTGACTAGCTCTTACCCTGC  
 AAAAAATAAAATGCAGCCATTAATTTGCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCAT  
 TTAGGATAGCCAGTGGTAAAATCGTTTTGTGTTTCATGAAACAATTAAGAAAGTAAAGACATATTTAC  
 AGACAGTTTCAGTAAAGTAATTAAGGAAAAACAGGAGAATAAATCAAAAAATTTGCCAAACGAAAATATG  
 GCAGTTGTTACGAGGCATTGGATGATTCAGAGGATATCTTCATAACTCTAGATAAGTAAAGTGA  
 GCACGCATTCACATAAGGTTTTTGTGACATTCAGAGTGAAGAATTTTACAACATAACCAAAATATGTC  
 TGGATTGGAGAAAGTTTCTAAAAATACCTTGTGATGTTAGTTTGGAACTTCAGATATATGAAATGT  
 AGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGAA  
 AATCTGTCCAGGTATCAGATGCTTATTACAAAACGCAAGACAAGTGTCTTGAATAGAAAGATAGTAC  
 CAAGCAAGTCTTTTCCAAAGTATTGTTTAAAAGTAACGAACATTCAGACCAGCTCACAAGAGAAGAAAAT  
 ACTGCTATACGTACTCCAGAACATTTAATATCCCAAAAAGGCTTTTATATAATGTGGTAAATTCATCTG  
 CTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTCCATTTTGAAGGTTCTTACACAAAGTTAA  
 GGGAGTGTAGAGGAATTTGATTTAATCAGAAGTGGAGTACTTCACTATTCACCTACGTCTAGACAA  
 AATGTATCAAAAATACCTCCTCGTGTGATAAGAGAAACCCAGAGCACTGTGAAACTCAGAAATGGAAA  
 AAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATATCA  
 CTCTATTAAGGTTTCTCCATATCTCTCAATTTCAACAAGACAAAACAACAGTTGGTATTAGGAACCAAA  
 GTGTCACTTGTGAGAACATTCATGTTTTGGGAAAAAGAACAGGCTTCACTAAAAACGTAATAATGGAAA  
 TTGGTAAAACGAACTTTTTCTGATGTTCTGTGAAAACAAATAGAAAGTTGTTCTACTTACTCCAA  
 AGATTCAGAAAACACTTTTGAACAGAGCAGTAGAAATGCTAAAGCTTTTATGGAAGATGATGAAGT  
 ACAGATCTAAACTGCCAAGTCAAGCCACATTTCTTTTTACATGTCCGAAAATGAGGAAATGGTTT  
 TGTCAAATTCAGAATTTGGAAAAAGAGAGGAGAGCCCTTATCTTAGTGGGAGAACCCCAATCAAAAAG  
 AAACCTTAAATGAATTTGACAGGATAATAGAAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT  
 CCAGATGGCACATAAAAAGATCGAAGATTGTTTATGCATCATGTTTCTTTAGAGCCGATTACCTGTGTAC  
 CCTTTCGCACAACATAAGGAACGTCAAGAGATACAGAAATCCAAATTTTACCACCTGGTCAAGAAATTTCT  
 GTCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCAATTTAGCAGTTTCAGGACAT  
 CCATTTTATCAAGTTTCTGCTACAAGAAATGAAAAATGAGACACTTGATTACTACAGGCAGACCAACCA  
 AAGTCTTTGTTCCACCTTTTAAAACATAATCACATTTTACAGAGTTGAACAGTGTGTTAGGAATATTA  
 CTTGGAGGAAAACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAATAAGATTAAT  
 GACAATGAGATTCATCAGTTTAACAAAAACAACCTCAATCAAGCAGCAGCTGTAACCTTTCACAAAGTGTG  
 AAGAAGAACCTTTAGATTTAATTACAAGTCTTCAAGATGCCAGAGATATACAGGATATGCGAATTAAGAA  
 GAAACAAGGCAACGCGTCTTTCCACAGCCAGGCAAGTCTGTATCTTGAAAAACATCCACTCTGCCTCGA  
 ATCTCTCTGAAAGCAGCAGTAGGAGGCCAAGTTCCCTCTGCGTGTCTCATAAACAGCTGTATACGTATG  
 GCGTTTCTAAACATTGCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTTCAGTTTCACTGAAGATTA  
 TTTTGGTAAGGAAAGTTTATGGACTGAAAAAGGAATACAGTTGGCTGATGGTGGATGGCTCATACCTCC

AATGATGGAAAGGCTGGAAAAGAAGAATTTTATAGGGCTCTGTGTGACACTCCAGGTGTGGATCCAAAGC  
 TTATTTCTAGAATTTGGGTTTATAATCACTATAGATGGATCATATGAAAAGTGGCAGCTATGGAATGTGC  
 CTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCAGAAAGGGTGTCTTCACTAAAATACAGATAT  
 GATACGGAAATGATAGAAGCAGAAGATCGGCTATAAAAAAGATAATGAAAAGGGATGACACAGCTGCAA  
 AAACACTTGTCTCTGTGTTTCTGACATAATTTCACTGAGCGCAAATATATCTGAAAATCTAGCAATAA  
 AACTAGTAGTCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGGTATGCTGTTAAGGCC  
 CAGTTAGATCCTCCCCTTCTAGCTGTCTTAAAGAATGGCAGACTGACAGTTGGTCAGAAGATTATCTTTC  
 ATGGAGCAGAAGTGGTGGGCTCCTGATGCCTGTACACCTCTTGAAGCCCAGAACTCTTATGTTAAA  
 GATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAAGTGGATTCTTCTGACCCTAGACCT  
 TTTCTCTGCCCTTATCATCGCTTTTCACTGATGGAGGAAATGTTGGTTGTGTTGATGTAATTATTCAAA  
 GAGCATACCCTATACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTGCAATGAAAGAGAGGA  
 AGAAAAGGAAGCAGCAAAATATGTGGAGGCCAACAAAAGAGACTAGAAGCCTTATTCCTAAAATTCAG  
 GAGGAATTTGAAGAACATGAAGAAAACACAACAAACCATATTTACCATCACGTGCACTAACAGACAGC  
 AAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCAGCTTACCT  
 TGAGGGTTATTTCACTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAA  
 CAAGCTCAGATCCAGTTGAAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAA  
 GGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAGAAAAGATTCACTTACT  
 GAGTATTTGGCGTCCATCATCAGATTTATTTCTGTAAACAGAAGGAAAGAGATACAGAATTTATCAT  
 CTTGCAACTTCAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAACTC  
 AGTATCAACAACCTACCGTTTCAGATGAAATTTATTTCACTTACCAGCCACGGGAGCCCTTCACTT  
 CAGCAATTTTATAGATCCAGACTTTTCAAGCATCTTGTCTGAGGTGGACCTAATAGGATTTGCTGTTTCT  
 GTTGTGAAAAAACAGGACTTGGCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAA  
 AGTTTTGGATAGACTTAAAGAGCATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAGTG  
 GCGTCCAGAATCCAAATCAGGCCTTCTACTTTATTTGCTGGAGATTTTCTGTGTTTTCTGCTAGTCCA  
 AAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAACTGTTGAGAATATTGACATACTTTGCA  
 ATGAAGCAGAAAAAAGCTTATGCATATACTGCATGCAATGATCCCAAGTGGTCCACCCCAACTAAAGA  
 CTGTACTTCAGGGCCGTACACTGCTCAAATCATCCTGGTACAGGAAACAAGCTTCTGATGTCTTCTCCT  
 AATTGTGAGATATATTATCAAAGTCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTG  
 TCTCAGCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAAGAACTGCAAAA  
 GAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTT  
 TCTCCGGCTGCACAGAAGGCATTTCAAGCCCAAGGAGTTGTGGCACCATAACGAAACCCCATAAAGA  
 AAAAAGAACTGAATTCCTCAGATGACTCCATTTAAAAAATCAATGAAATTTCTTTTGGAAAGTAA  
 TTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAA  
 CAATTTATATCTGTCAGTGAATCCACTAGGACTGCTCCACCAGTTTCAAGAAGATTATCTCAGACTGAAAC  
 GACGTTGACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAA  
 TAAGCAGGACACAATTACAATAAAAAATATATC

AGCGGACCCACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC  
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

**Protein Sequence:**

>RC400515 representing NM\_000059

Red=Cloning site Green=Tags(s)

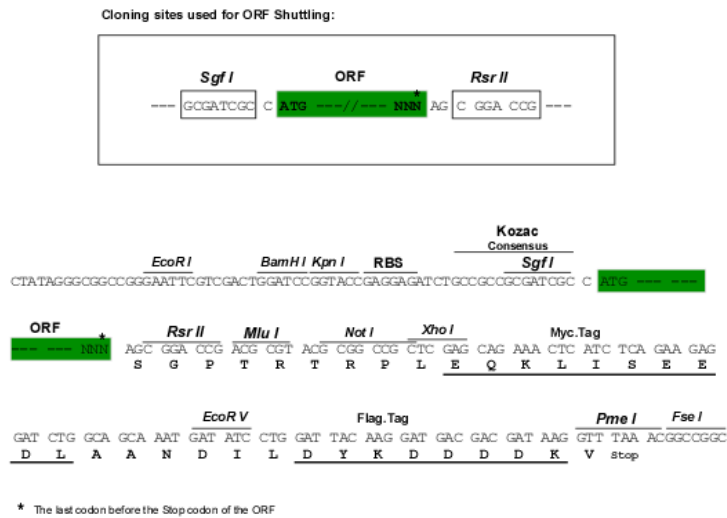
MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSEAPPYNSEPAEESHKNNNYEPNLFKTPQRKPS  
 YNQLASTPIIFKEQGLTLPYQSPVKELDKFKLDLGRNVPNSRHKSLRTVKTMDQADDVSCPLLNLSCLS  
 ESPVVLQCTHVTPQRDKSVVCGSLFHTPKFVKGRQTPKHISESLGAEVDPDTSWSSSLATPPTLSSTVLI  
 VRNEEASETVPFHDTTANVKSIFYSNHDESLKKNDRFIA SVTDSSENTNQREAASHGFGKTSNFSKVNCSK  
 DHIGKSMPNVLEDEVYETVVDTSSEDSFSLCFSKCRTKNLQKVRTSKTRKKIFHEANADECEKSNQVKE  
 KYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVP SLACEWSQLTSLGLNGAQMEKIPLLHISDCD  
 QNISEKDLLDTENKRKDFLTSNSLPRISLSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAIISG  
 TSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDPNFKKETEASESGLEIHTVCSQKEDSLCPNLIDN  
 GSWPATTTQNSVALKNAGLISTLKKTKNFYIAIHDETSYKGGKIPKDQKSELINCSAQFEANAFEAPLT  
 FANADSGLLHSSVKRSCSQNDSEPTLSLTSSFGTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQL

FITPEADSLSCLQEGQCENDPKSKKVSIDIKEEVLAACHPVQHSKVEYSDTDFQSQKSLLYDHENASTLI  
 LTPTSKDVL SNLVMISRKESYKMSDKLKGNNYSDVELTKNIPMEKNQDVCALNENYKNVELLPPEKYM  
 RVASPSRKVQFNQNTNLRVIQKNQEETTSISKITVNPDSEELFSDNENNFVQVANERNLALGNTKELH  
 ETDLTVCNEPIFKNSTMVL YGDTGDKQATQVSIKKDLVYVLAENKNSVKQHIKMTLGQDLKSDISLNDI  
 KIPEKNNDYMNKWAGLLGPI SNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIIEEQYPTSLACVEIVNT  
 LALDNQKLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHLTPSQKAEITELSTILEE  
 SGSQFEFTQFRKPSYILQKSTFEVPENQMTILKTTSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKR  
 KFAGLLKNDCKNSASGYLTDENEVGRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETSAEVHPISL  
 SSSKCHDSVVSVMFKIENHNDKTVSEKNKNCQLILQNNIEMTTGTFVVEITENYKRNTENEDNKYTAASRN  
 SHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKLSGQFMKEGNTQIKEDLSLTFLEVAKAQEACH  
 GNTSNKEQLTATKTEQNIKFETSDTFFQTASGKNISVAKESFNKIVNFFDQKPEELHNFSLNSELHSDI  
 RKNKMDILSYEETDIVKHKILKESVPGTGNQLVTFQGGQPERDEKIKEPTLLGFHTASGKVKIAKESLD  
 KVKNLFDEKEQGTSEITFSHQWAKTLKYREACKDLELACETIEITAAPKCKEMQNSLNNDKNLVSIETV  
 VPPKLLSDNLCRQNTENLKTSSIFLKVKHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCSRKTS  
 VSQTSLLAEAKWLRGIFDQPERINTADYVGNLYENNSNSTIAENDKNHLSEKQD TYLSNSSMSNSYS  
 YHSDEVYNDSGYL SKNKLDSGIEPVLKNVEDQKNTSFSKVISNVKDANAYPQTVNEDICVEELVTSSSPC  
 KNKNAAIKLSISNSNFEVGPFAFRIASGKIVCVSHETIKKVKDIFTDSFSKVIKENNENKSKICQTKIM  
 AGCYEALDDESEDILHNSLDNDECSTHSHKVFADIQSEEILQHNQNMGLEKYSKISPCDVSLETSDICKC  
 SIGKHLKSVSSANTCGIFSTASGKSVQVSDASLQARQVFSEIEDSTKQVFSKVLFKSNEHSDQLTREEN  
 TAIRTPPEHLISQKGFYNVNVSSAFSGFSTASGKQVSILESSLHKVKGVL EEFDLIRTEHSLHYSPTSQ  
 NVSKILPRVDKRNPEHCVNSEMEKTCSEKFLSNLNVEGGSSENNHSIKVSPYLSQFQDKQQLVLGKTK  
 VSLVENIHVLGKEQASPKNVKMEIGKTETFSDVPVKTNIEVCSTYSKDSSENYFETEAVEIAKAFMEDDEL  
 TDSKLP SHATHSLFTCPENEEMVLSNSRIGKRRGEPLILVGEPSIKRNLNDFDRIENQEKSLKASKST  
 PDGTIKDRRLFMHHVSLLEPITCVPFRTTKERQEIQNPNFTAPGQEFLSKSHLYEHLTLEKSSSNLAVSGH  
 PFYQVSA TRNEKMRHLITTRPTKVFVPPFKTKSHFHRVEQCVRNINLEENRQKQNDIGHGSDSKNKIN  
 DNEIHQFNKNSNQAAAVTFTKCEEEPLDLITSLQNARDIQDMRIKKKQRQRFVFPQPSGLYLAKTSTLPR  
 ISLKAAVGGQVPSACSHKQLYTYGVSKHCIKINSKNAESFQFHTEDYFGKESLWTGKGIQLADGGWLIPS  
 NDGKAGKEEFYRALCDTPGVDPKLSRIWVYNHYRWIIWKLAAAMECAFPEFANRCLSPERVLLQLKYRY  
 DTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLSANISETSSNKTSSADTQKVAIIELTDGWYAVKA  
 QLDPPLLAVLKNGRLLTVGQKIILHGAELVGS DACTPLEAPESLMLKISANSTRPARWYTKLGFDPDRP  
 FPLPLSSLFSDGGNVGCVDVIIQRAYPIQWMEKTS SGLYIFRNEREEEEKA AKYVEAQQKRL EALFTKIQ  
 EEFEEHEENTTKPYLPSRALTRQQVRALQDGAELYEAVKNAADPAYLEGYFSEEQLRALNNHRQMLNDKK  
 QAQIQLEIRKAMESAEQKEQGLSRDVTTVWKLRIVSYSKKEKDSVILSIWRPSSDLYSLLTEGKRYRIYH  
 LATSKSKSERANIQLAATKTKYQQLPVSDIILFQIYQPREPLHFSKFLDPDFQPSCSEVDLIGFVVS  
 VVKKTGLAPFVYL SDECYNLLAIKFWIDLNEDIKPHMLIAASNLQWRPESKSGLLTLFAGDFSVFSASP  
 KEGHFQETFNKMKNTVENIDILCNEAENKLMHILHANDPKWSTPTKDC TSGPYTAQIIPGTGNKLLMSSP  
 NCEIYYQSPLSLCMAKRKSVSTPVSAQMTSKSCKGEKEIDDQKNCKRRALDFL SRLPLPPPVPSPICTFV  
 SPAAQKAFQPPRSCGTYETPIKKKELNSPQMTPFKFFNEISLLESNSIADEELALINTQALLSGSTGEK  
 QFISVSESTRAPTSSDYLRLLKRRCTTSLIKEQESSQASTECEKKNQDTITTKKYI

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]