

## Product datasheet for **RC400555**

### 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:     | Q713L   |
| Affected Codon#:          | 713   |
| Affected NT#:             | 2138  |
| Nucleotide Mutation:      | BRCA2 Mutant (Q713L), 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:  | >RC400555 representing NM_000059<br>Red=Cloning site Blue=ORF Green=Tags(s)   |

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**GCGATCGCC**

ATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGATT  
TAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC  
AGAAGAATCTGAACATAAAAAACAACAATTACGAACCAACCTATTTAAACTCCACAAAGGAAACCATCT  
TATAATCAGCTGGCTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTC  
CTGTAAGAATTAGATAAATCAAATTAGACTTAGGAAGGAATGTTCCCAATAGTAGACATAAAGTCT  
TCGCACAGTAAAACTAAATGGATCAAGCAGATGATGTTTCTGTCCACTTCTAAATCTTGTCTTAGT  
GAAAGTCTGTTGTTCTACAATGTACACATGTAACACCACAAAGAGATAAGTCAGTGGTATGTGGGAGTT



[View online »](#)

TGTTCATACACCAAAGTTTGTGAAGGGTCGTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGA  
 GGTGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACCACCCTTAGTTCTACTGTGCTCATA  
 GTCAGAAATGAAGAAGCATCTGAAACTGTATTTCTCATGATACTACTGCTAATGTGAAAAGCTATTTTT  
 CCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGTCTCTGTGACAGACAGTGAAAACACAAA  
 TCAAAGAGAAGCTGCAAGTCATGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAA  
 GACCACATTGGAAGTCAATGCCAAATGTCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTG  
 AAGAAGATAGTTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAATCTCAAAAAAGTAAAGAACTAGCAA  
 GACTAGGAAAAAATTTTCCATGAAGCAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAAGAA  
 AAATACTCATTTGTATCTGAAGTGAACCAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGA  
 AGCCCTTTGAGAGTGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCA  
 ACTAACCTTTTCAAGTCTAAATGGAGCCAGATGGAGAAAAATACCCTATTGCATATTTCTTTCATGTGAC  
 CAAAATATTTAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTACTTCAGAGA  
 ATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGAATAAA  
 GAGAGATGAAGAGCAGCATCTTGAATCTCATACTGACTGCATTCTTGCAGTAAAGCAGGCAATATCTGGA  
 ACTTCTCCAGTGGCTTTCATTTCAGGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAG  
 AGACTTCAATGCAAGTTTTTCAAGTGCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGA  
 AAGTGGACTGGAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAAT  
 GGAAGCTGGCCAGCCACCACCACAGAAATCTGTAGCTTTGAAGAATGCAGGTTAATATCCACTTTTGA  
 AAAAGAAAAACAAATAAGTTTATTTATGTATACATGATGAAACATCTTATAAAGGAAAAAATACCGAA  
 AGACCAAAAAATCAGAATAATTAAGTGTTCAGCCAGTTTGAAGCAATGCTTTTGAAGCACCATTACA  
 TTTGCAAAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTACAGAAATGATTCGAAG  
 AACCAATGCTGCTTAACTAGCTCTTTGGGACAATCTGAGGAAATGTTCTAGAAATGAAACATGTTT  
 TAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTATAAAGGAAAAATCAGTTA  
 TTTATTACCCAGAAGCTGATTCTGTGATGCCTGCTGGAAGGACAGTGTGAAAAATGCTCAAAAAAGCA  
 AAAAAGTTTTCAGATATAAAGAAGAGGTCTGGCTGCAGCATGTACCCAGTACAACATTCAAAAGTGGAA  
 ATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAAATGCCAGCACTCTTATT  
 TTAACTCTACTTCCAAGGATGTTCTGTCAAACCTAGTCATGATTTCTAGAGGCAAGAATCATACAAAA  
 TGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAAATTTCCCATGGAAAA  
 GAATCAAGATGTATGTGCTTTAAATGAAAATTAAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATG  
 AGAGTAGCATCACCTTCAAGAAAGGTACAATTCACCAAAAACACAATCTAAGAGTAATCAAAAAAATC  
 AAGAAGAACTACTTCAATTTCAAAAAAATCACTGTCAATCCAGACTCTGAAGAATTTTCTCAGACATGA  
 GAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGTCTTAGGAAATACTAAGGAATTCAT  
 GAAACAGACTTGACTTGTGTAACCGAACCCATTTTCAAGAATCTACCATGGTTTTATATGGAGACACAG  
 GTGATAAACAAGCAACCAAGTGTCAATTAAAAAAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAA  
 TAGTGTAAAGCAGCATATAAAAAATGACTCTAGGTCAAGATTTAAATCGGACATCTCCTTGAATATAGAT  
 AAAATACCAGAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACA  
 GTTTTGGAGGTAGCTTCAAGACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAG  
 CAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATGTAATACC  
 TTGGCATTAGATAATCAAAAGAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGA  
 GTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTT  
 TAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAATTTTCTACTATATTAGAAGAA  
 TCAGGAAGTCAAGTTTGAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAG  
 TGCCTGAAAACAGATGACTATCTTAAAGACCCTTCTGAGGAATGCAGAGATGCTGATCTTCATGTCAT  
 AATGAATGCCCATCGATTGGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAACGG  
 AAGTTTGTGGCCTGTTGAAAAATGACTGTAACAAAAGTCTTCTGGTTATTTAACAGATGAAAAATGAAG  
 TGGGGTTTAGGGCTTTTATTCTGCTCATGGCACAAAATGAATGTTTCTACTGAAGCTCTGCAAAAAGC  
 TGTGAAACTGTTTGTGATATTGAGAATATTAGTGAGGAACTCTGCAGAGGTACATCCAATAAGTTTA  
 TCTTCAAGTAAATGTCATGATTCTGTTGTTCAATGTTTAAAGATGAAAAATCATAATGATAAACTGTAA  
 GTGAAAAAATAATAATGCCAACTGATATTACAAAATAAATTTGAAATGACTACTGGCACTTTTGTGGA  
 AGAAATTAAGTAAAAATCAAGAGAAATGAAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAAT  
 TCTCATAACTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTGTTTGTATTATAAAGATGAAA  
 CGGACTTGCTATTTACTGATCAGCACAACATATGTCTTAAATTTCTGGCCAGTTTATGAAGGAGGGAAA

CACTCAGATTAAGAAGATTTGTCAAGTTAACTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCAT  
 GGTAATACTTCAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAAAGATTTTGAGACTT  
 CTGATACATTTTTTTCAGACTGCAAGTGGGAAAAATATTAGTGTGCGCCAAAGAGTCATTTAATAAAATTTG  
 AAATTTCTTTGATCAGAAACCAGAAGAAATGCATAACTTTTCTTAAATTTCTGAATTACATTCTGACATA  
 AGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTAAACACAAAATCTGAAAGAAA  
 GTGTCCAGTTGGTACTGGAAATCAACTAGTGACCTCCAGGGACAACCCGAACGTGATGAAAAGATCAA  
 AGAACCTACTCTATTGGGTTTTTCATACAGCTAGCGGGAAAAAAGTTAAAATTTGCAAAGGAATCTTTGGAC  
 AAAGTGAAAAACCTTTTTGATGAAAAAGCAAGGTAAGTAAATCACCAGTTTTAGCCATCAATGGG  
 CAAAGACCCTAAAGTACAGAGAGGCTGTAAAGACCTGAATTAGCATGTGAGACCATTGAGATCACAGC  
 TGCCCCAAAGTGTAAAGAAATGCAGAATTCTCTCAATAATGATAAAAACTTGTTTCTATTGAGACTGTG  
 GTGCCACCTAAGCTCTAAGTGATAATTTATGTAGACAACTGAAAATCTCAAAACATCAAAAAGTATCT  
 TTTTGAAGTTAAAGTACATGAAAATGTAGAAAAAGAACAGCAAAAAGTCTGCAACTTGTACACAAA  
 TCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAACTTCT  
 GTGAGTCAGACTTCATTACTGGAAGCAAAAAATGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAA  
 GAATAAATACTGCAGATTATGTAGGAAATTTTGTATGAAAATAATTCAAACAGTACTATAGCTGAAA  
 TGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCC  
 TACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGC  
 CAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAGAGATGC  
 AAATGCATACCCACAACTGTAATGAAGATATTTGCGTTGAGGAACTTGTGACTAGCTCTTACCCTGC  
 AAAAAATAAAATGCAGCCATTAATTTGCCATATCTAATAGTAATAATTTTGGAGTAGGGCCACCTGCAT  
 TTAGGATAGCCAGTGGTAAAATCGTTTTGTGTTTCATGAAACAATTAAGGAAAGTAAAGACATATTTAC  
 AGACAGTTTCAGTAAAGTAATTAAGGAAAAACAGGAGAATAAATCAAAAAATTTGCCAAACGAAAATATG  
 GCAGTTGTTACGAGGCATTGGATGATTCAGAGGATTTCTTCATAACTCTAGATAAGTAAAGTGA  
 GCACGCATTCACATAAGGTTTTTGTGACATTCAGAGTGAAGAATTTTACAACATAACCAAAATATGTC  
 TGGATTGGAGAAAGTTTCTAAAAATACCTTGTGATGTTAGTTTGGAACTTCAGATATATGAAATGT  
 AGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGAA  
 AATCTGTCCAGGTATCAGATGCTTATTACAAAACGCAAGACAAGTGTCTTGAATAGAAAGATAGTAC  
 CAAGCAAGTCTTTTCAAAGTATTGTTTAAAAGTAACGAACATTCAGACCAGCTCACAAGAGAAGAAAAT  
 ACTGCTATACGTACTCCAGAACATTTAATATCCAAAAAGGCTTTTATATAATGTGGTAAATTCATCTG  
 CTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTCCATTTTGAAGGTTCTTACACAAAGTTAA  
 GGGAGTGTAGAGGAATTTGATTTAATCAGAAGTGGAGTACTTCACTATTCACCTACGTCTAGACAA  
 AATGTATCAAAAAATCTCCTCGTGTGATAAGAGAAACCCAGAGCACTGTGAAACTCAGAAATGGAAA  
 AAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATATCA  
 CTCTATTAAGGTTTCTCCATATCTCTCAATTTCAACAAGACAAAACAACAGTTGGTATTAGGAACCAAA  
 GTGTCACTTGTGAGAACATTCATGTTTTGGGAAAAAGAACAGGCTTCACTAAAAACGTAATAATGGAAA  
 TTGGTAAAACGAACTTTTTCTGATGTTCTGTGAAAACAAATAGAAAGTTTGTCTACTTACTCCAA  
 AGATTCAGAAAACACTTTGAAACAGAAGCAGTAGAAATGCTAAAGCTTTTATGGAAGATGATGAAGT  
 ACAGATCTAAACTGCCAAGTCATGCCACATTTCTTTTTACATGTCCGAAAATGAGGAAATGGTTT  
 TGTCAAATTCAGAATTTGGAAAAAGAGAGGAGAGCCCTTATCTTAGTGGGAGAACCCCAATCAAAAAG  
 AAACCTTATAAATGAATTTGACAGGATAATAGAAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT  
 CCAGATGGCACATAAAAAGATCGAAGATTGTTTATGCATCATGTTTCTTTAGAGCCGATTACCTGTGTAC  
 CCTTTCGCACAACATAAGGAACGTCAAGAGATACAGAAATCCAAATTTTACCACCTGGTCAAGAATTTCT  
 GTCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCAATTTAGCAGTTTCAGGACAT  
 CCATTTTATCAAGTTTCTGCTACAAGAAATGAAAAATGAGACACTTGATTACTACAGGCAGACCAACCA  
 AAGTCTTTGTTCCACCTTTTAAAACATAATCACATTTTACAGAGTTGAACAGTGTGTTAGGAATATTA  
 CTTGGAGGAAAACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAATAAGATTAAT  
 GACAATGAGATTCATCAGTTTAAACAAAACAACCTCAATCAAGCAGCAGCTGTAACCTTTCACAAAGTGTG  
 AAGAAGAACCTTTAGATTTAATTACAAGTCTTCAAGATGCCAGAGATATACAGGATATGCGAATTAAGAA  
 GAAACAAGGCAACGCGTCTTTCCACAGCCAGGAGTCTGTATCTTGAAAAACATCCACTCTGCCTCGA  
 ATCTCTCTGAAAGCAGCAGTAGGAGGCCAAGTTCCCTCTGCGTGTCTCATAAACAGCTGTATACGTATG  
 GCGTTTCTAAACATTGCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTTCAGTTTACACTGAAGATTA  
 TTTTGGTAAGGAAAGTTTATGGACTGGAAAAGGAATACAGTTGGCTGATGGTGGATGGCTCATACCTCC

AATGATGGAAAGGCTGGAAAAGAAGAATTTTATAGGGCTCTGTGTGACACTCCAGGTGTGGATCCAAAGC  
 TTATTTCTAGAATTTGGGTTTATAATCACTATAGATGGATCATATGAAAAGTGGCAGCTATGGAATGTGC  
 CTTTCTAAGGAATTTGCTAATAGATGCCTAAGCCAGAAAGGGTGTCTTCAACTAAAATACAGATAT  
 GATACGGAAATGATAGAAGCAGAAGATCGGCTATAAAAAAGATAATGAAAAGGGATGACACAGCTGCAA  
 AAACACTTGTCTCTGTGTTTCTGACATAATTTATTGAGCGCAAATATATCTGAAACTTCTAGCAATAA  
 AACTAGTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGGTATGCTGTAAAGGCC  
 CAGTTAGATCCTCCCCTTAGCTGTCTTAAAGAATGGCAGACTGACAGTTGGTCAGAAGATTATCTTTC  
 ATGGAGCAGAAGTGGTGGGCTCCTGATGCCTGTACACCTCTTGAAGCCCAGAACTCTTATGTTAAA  
 GATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAAGTGGATTCTTCTGACCCTAGACCT  
 TTTCTCTGCCCTTATCATCGCTTTTTCAGTGTGGAGGAAATGTTGGTGTGTTGATGTAATTATTCAAA  
 GAGCATACCCTATACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTGCAATGAAAGAGAGGA  
 AGAAAAGGAAGCAGCAAAATATGTGGAGGCCAACAAAAGAGACTAGAAGCCTTATTCCTAAAATTCAG  
 GAGGAATTTGAAGAACATGAAGAAAACACAACAAACCATATTTACCATCACGTGCACTAACAGACAGC  
 AAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCAGCTTACCT  
 TGAGGGTTATTTTCAGTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAA  
 CAAGCTCAGATCCAGTTGAAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAA  
 GGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAGAAAAGATTTCAGTTATACT  
 GAGTATTTGGCGTCCATCATCAGATTTATTTCTGTAAACAGAAGGAAAGAGATACAGAATTTATCAT  
 CTTGCAACTTCAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAACTC  
 AGTATCAACAACCTACCGTTTCAGATGAAATTTATTTTCAGATTTACCAGCCACGGGAGCCCTTCACTT  
 CAGCAATTTTATAGATCCAGACTTTTCAGCCATCTTGTCTGAGGTGGACCTAATAGGATTTGTCGTTTCT  
 GTTGTGAAAAAAGCAGGACTTGGCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAA  
 AGTTTGGATAGACTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAGTG  
 GCGTCCAGAATCCAAATCAGGCCTTCTTACTTTATTTGCTGGAGATTTTCTGTGTTTTCTGCTAGTCCA  
 AAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAATACTGTTGAGAATATTGACATACTTTGCA  
 ATGAAGCAGAAAAAAGCTTATGCATATACTGCATGCAATGATCCCAAGTGGTCCACCCCAACTAAAGA  
 CTGTACTTCAGGGCCGTACACTGCTCAAATCATTCTGGTACAGGAAACAAGCTTCTGATGTCTTCTCCT  
 AATTGTGAGATATATTATCAAAGTCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTG  
 TCTCAGCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAAGAACTGCAAAA  
 GAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTT  
 TCTCCGGCTGCACAGAAGGCATTTACGCCCAAGGAGTTGTGGCACCATAACGAAACCCCATAAAGA  
 AAAAAGAACTGAATTCCTCAGATGACTCCATTTAAAAAATCAATGAAATTTCTTTTGGAAAGTAA  
 TTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAA  
 CAATTTATATCTGTCAAGTCCACTAGGACTGCTCCACCAGTTTACAGAAGATTATCTCAGACTGAAAC  
 GACGTTGACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAA  
 TAAGCAGGACACAATTACAATAAAAAATATATC

AGCGGACCCACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC  
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

**Protein Sequence:**

>RC400555 representing NM\_000059

Red=Cloning site Green=Tags(s)

MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSSEAPPYNSEPAEESHKNNNYEPNLFKTPQRKPS  
 YNQLASTPIIFKEQGLTLPLQSPVKELDKFKLDLGRNVPNSRHKSLRTVKTMDQADDVSCPLLNLSCLS  
 ESPVVLQCTHVTPQRDKSVVCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSVLI  
 VRNEEASETVFPHDTTANVKSIFYSNHDESLKKNDRFIA SVTDSSENTNQREAASHGFGKTSNGNSFKVNSCK  
 DHIGKSMPNVLEDEVYETVVDTSEEDSFLCFSKCRTKNLQKVRTSKTRKKIFHEANADECEKSNQVKE  
 KYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVP SLACEWSQLTSLGLNGAQMEKIPLLHISDCD  
 QNISEKDLLDTENKRKDFLTSNSLPRISLSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAIISG  
 TSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDPNFKKETEASESGLEIHTVCSQKEDSLCPNLIDN  
 GSWPATTTQNSVALKNAGLITLKKTKNFYIAIHDETSYKGGKIPKDQKSELINCSAQFEANAFEAPLT  
 FANADSGLLHSSVKRSCSQNDSEPTLSLTSSFGTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQL

FITPEADSL SCLLEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQKSLLYDHENASTLI  
 LTPTSKDVL SNLVMISRKESYKMSDKLKGNNYSDVELTKNIPMEKNQDVCALNENYKNVELLPPEKYM  
 RVASPSRKVQFNQNTNLRVIQKNQEETTSISKITVNPDSEELFSDNENNFVFQVANERNLALGNTKELH  
 ETDLTCVNEPIFKNSTMVL YGDTGDKQATQVSIKKDLVYVLAENKNSVKQHIKMTLGQDLKSDISLNDI  
 KIPEKNNDYMNKWAGLLGPI SNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIIEEQYPTSLACVEIVNT  
 LALDNQKLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHLTPSQKAEITELSTILEE  
 SGSQFEFTQFRKPSYILQKSTFEVPENQMTILKTTSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKR  
 KFAGLLKNDCKNSASGYLTDENEVGRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETSAEVHPISL  
 SSSKCHDSVVSVMFKIENHNDKTVSEKNKQCQLILQNNIEMTTGTFVVEITENYKRNTENEDNKYTAASRN  
 SHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKLSGQFMKEGNTQIKEDLSLTFLEVAKAQEACH  
 GNTSNKEQLTATKTEQNIKFETSDTFFQTASGKNISVAKESFNKIVNFFDQKPEELHNFSLNSELHSDI  
 RKNKMDILSYEETDIVKHKILKESVPGTGNQLVTFQGGQPERDEKIKEPTLLGFHTASGKVKIAKESLD  
 KVKNLFDEKEQGTSEITSFHQWAKTLKYREACKDLELACETIEITAAPKCKEMQNSLNNDKNLVSIETV  
 VPPKLLSDNLCRQNTENLKTSSIFLKVKHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCRKTS  
 VSQTSLLAEAKWLRREGIFDQPERINTADYVGNLYENNSNSTIAENDKNHLSEKQD TYLSNSSMSNSYS  
 YHSDEVYNDSGYL SKNKLDSGIEPVLKNVEDQKNTSF SKVISNVKDANAYPQTVNEDICVEELVTSSSPC  
 KNKNAAIKLSISNSNFEVGPFAFRIASGKIVCVSHETIKKVKDIFTDSFSKVIKENNENKSKICQTKIM  
 AGCYEALDDESEDILHNSLDNDECSTHSHKVFADIQSEEILQHNQNMGLEKYSKISPCDVSLETSDICKC  
 SIGKHLKSVSSANTCGIFSTASGKSVQVSDASLQNAQVVFSEIEDSTKQVFSKVLFKSNEHSDQLTREEN  
 TAIRTPPEHLISQKGFYNVNVSSAFSGFSTASGKQVSILESSLHKVKGVLEEFDLIRTEHSLHYSPTSQ  
 NVSKILPRVDKRNPEHCVNSEMEKTCSEKFLSNLNVEGGSSENNHSIKVSPYLSQFQDKQQLVLGKTK  
 VSLVENIHVLGKEQASPKNVKMEIGKTETFSDVPVKTNIEVCSTYSKDSSENYFETEAVEIAKAFMEDDEL  
 TD SKLPSHATHSLFTCPENEEMVLSNSRIGKRRGEPLILVGEPSIKRNLNDFDRIENQEKSLKASKST  
 PDGTIKDRRLFMHHVSLLEPITCVPFRTTKERQEIQNPNFTAPGQEFLSKSHLYEHLTLEKSSSNLAVSGH  
 PFYQVSA TRNEKMRHLITTRPTKVFVPPFKTKSHFHRVEQCVRNINLEENRQKQNDIGHGSDSKNKIN  
 DNEIHQFNKNSNQAAAVTFTKCEEEPLDLITSLQNARDIQDMRIKKKQRQRVFPQPSGLYLAKTSTLPR  
 ISLKAAVGGQVPSACSHKQLYTYGVSKHCIKINSKNAESFQFHTEDYFGKESLWTGKGIQLADGGWLIPS  
 NDGKAGKEEFYRALCDTPGVDPKLSRIWVYNHYRWIIWKLAAAMECAFPEFANRCLSPERVLLQLKYRY  
 DTEIDRSRRSAIKKIMERDDTAAKTLVLCVSDIISLSANISETSSNKTSSADTQKVAIIELTDGWYAVKA  
 QLDPPLLAVLKNGRITVGQKIIILHGAELVGS DACTPLEAPESMLKISANSTRPARWYTKLGFDPDRP  
 FPLPLSSLFSDGGNVGCVDVIIQRAYPIQWMEKTS SGLYIFRNEREEEEKA AKYVEAQQKRLREALFTKIQ  
 EEFEEHEENTTKPYLPSRALTRQQVRLQDGAELYEAVKNAADPAYLEGYFSEEQLRALNNHRQMLNDKK  
 QAQIQLEIRKAMESAEQKEQGLSRDVTTVWKLRIVSYSKKEKDSVILSIWRPSSDLYSLLTEGKRYRIYH  
 LATSKSKSERANIQLAATKKTQYQQLPVSDIILFQIYQPREPLHFSKFLDPDFQPSCSEVDLIGFVVS  
 VVKKTGLAPFVYL SDECYNLLAIKFWIDLNEDIKPHMLIAASNQWRPESKSGLLTLFAGDFSVFSASP  
 KEGHFQETFNKMKNTVENIDILCNEAENKLMHILHANDPKWSTPTKDC TSGPYTAQIIPGTGNKLLMSSP  
 NCEIYYQSPLSLCMAKRKSVSTPVSAQMTSKSCKGEKEIDDQKNCKRRALDFLSRLPLPPPVPSPICTFV  
 SPAAQKAFQPPRSCGTYETPIKKKELNSPQMTPFKFFNEISLLESNSIADEELALINTQALLSGSTGEK  
 QFISVSESTRTAPTSSDYLRKRRCTTSLIKEQESSQASTECEKKNKQDTITTKKYI

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]