

Product datasheet for **RC400766**

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:	T3401M
Affected Codon#:	3401
Affected NT#:	10202
Nucleotide Mutation:	BRCA2 Mutant (T3401M), 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:	>RC400766 representing NM_000059 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTTGAATTTTTAAGACACGCTGCAACAAAGCAGATT
TAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC
AGAAGAATCTGAACATAAAAAACAACAATTACGAACCAACCTATTTAAACTCCACAAAGGAAACCATCT
TATAATCAGCTGGCTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTC
CTGTAAGAAGATTAGATAAATTTCAAATTTAGACTTAGGAAGGAATGTTCCCAATAGTAGACATAAAGTCT
TCGCACAGTGAAGAACTAAATGGATCAAGCAGATGATGTTTCTGTCCACTTCTAAATTTCTGTCTTAGT
GAAAGTCTGTTGTTCTACAATGTACACATGTAACACCACAAAGAGATAAGTCAGTGGTATGTGGGAGTT



[View online »](#)

TGTTCATACACCAAAGTTTGTGAAGGGTCGTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGA
 GGTGGATCCTGATATGTCTTGGTCAAGTCTTTAGCTACACCACCACCCTTAGTTCTACTGTGCTCATA
 GTCAGAAATGAAGAAGCATCTGAAACTGTATTTCTCATGATACTACTGCTAATGTGAAAAGCTATTTTT
 CCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGTCTCTGTGACAGACAGTGA AACACAAA
 TCAAAGAGAAGCTGCAAGTCATGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAA
 GACCACATTGGAAAGTCAATGCCAAATGTCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTG
 AAGAAGATAGTTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAATCTACAAAAAGTGAAGAAAGCA
 GACTAGGAAAAAATTTTCCATGAAGCAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAGAA
 AAATACTCATTTGTATCTGAAGTGAACCAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGA
 AGCCCTTTGAGAGTGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCA
 ACTAACCTTTCAGGTCTAAATGGAGCCAGATGGAGAAAAATACCCTATTGCATATTTCTTCATGTGAC
 CAAAATATTTAGAAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTACTTCAGAGA
 ATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGTAAATA
 GAGAGATGAAGAGCAGCATCTTGAATCTCATACTGACTGCATTCTTGCAGTAAAGCAGGCAATATCTGGA
 ACTTCTCCAGTGGCTTTCATTTCAGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAG
 AGACTTCAATGCAAGTTTTTTCAGGTATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGA
 AAGTGGACTGGAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAAT
 GGAAGCTGGCCAGCCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTAATATCCACTTTGA
 AAAAGAAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAATACCGAA
 AGACCAAAAAATCAGAATAATTAAGTGTTCAGCCAGTTTGAAGCAATGCTTTTGAAGCACCATTACA
 TTTGCAAAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTACAGAATGATTCGAAG
 AACCAATTTGCTTAACTAGCTCTTTGGGACAATCTGAGGAAATGTTCTAGAAATGAAACATGTTT
 TAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAAATAAGGAAAAACTACAGTTA
 TTTATTACCCAGAAGCTGATTCTGTGATGCCTGCAGGAAGGACAGTGTGAAAAATGCTCAAAAAAGCA
 AAAAAGTTTCAGATATAAAGAAGAGGTCTGGCTGCAGCATGTACCCAGTACAACATTCAAAAGTGA
 ATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAAATGCCAGCACTCTTATT
 TTAACTCTACTTCCAAGGATGTTCTGTCAAACCTAGTCATGATTTCTAGAGGCAAGAATCATACAAAA
 TGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAAATTTCCCATGGAAAA
 GAATCAAGATGTATGTGCTTTAAATGAAAATTAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATG
 AGAGTAGCATCACCTTCAAGAAAGGTACAATTAACCAAAAACACAATCTAAGAGTAATCAAAAAAATC
 AAGAAGAACTACTTCAATTTCAAAAATAACTGTCAATCCAGACTCTGAAGAATTTTCTCAGACATGA
 GAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGCTTTAGGAAATACTAAGGAATTCAT
 GAAACAGACTTGACTTGTGTAACCGAACCCATTTTCAAGAACTCTACCATGGTTTTATATGGAGACACAG
 GTGATAAAACAAGCAACCCAAGTGTCAATTAAAAAAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAA
 TAGTGTAAAGCAGCATATAAAAAAGACTCTAGGTCAAGATTTAAATCGGACATCTCCTTGAATATAGAT
 AAAATACCAGAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACA
 GTTTTGGAGGTAGCTTCAAGACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAG
 CAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATGTAATACC
 TTGGCATTAGATAATCAAAAGAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGA
 GTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTT
 TAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAATTTTCTACTATATTAGAAGAA
 TCAGGAAGTCAAGTTGAAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAG
 TGCCTGAAAACAGATGACTATCTTAAAGACCCTTCTGAGGAATGCAGAGATGCTGATCTTCATGTCAT
 AATGAATGCCCATCGATTGGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAACGG
 AAGTTTGTGGCCTGTTGAAAAATGACTGTAACAAAAGTCTTCTGGTTATTTAACAGATGAAAAATGAAG
 TGGGGTTTAGGGCTTTTATTCTGCTCATGGCACAAAAGTGAATGTTTCTACTGAAGCTCTGCAAAAAGC
 TGTGAAACTGTTTGTGATATTGAGAATATTAGTGAGGAACTCTGCAGAGGTACATCCAATAAGTTTA
 TCTTCAAGTAAATGTCATGATTCTGTTGTTCAATGTTTAAAGATGAAAAATCATAATGATAAACTGTAA
 GTGAAAAAATAATAATGCCAACTGATATTACAAAATAATTTGAAATGACTACTGGCACTTTTGTGGA
 AGAAATTAAGTAAAAATCAAGAGAAATGAAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAAT
 TCTCATAACTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTGTTTGTATTATAAAGATGAAA
 CGGACTTGCTATTTACTGATCAGCACACATATGTCTTAAATTTCTGGCCAGTTTATGAAGGAGGGAAA

CACTCAGATTAAGAAGATTTGTCAAGTTAACTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCAT
 GGTAATACTTCAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAAGATTTTGAGACTT
 CTGATACATTTTTTTCAGACTGCAAGTGGGAAAAATATTAGTGTGCGCCAAAGAGTCATTTAATAAAATTTG
 AAATTTCTTTGATCAGAAACCAGAAGAAATGCATAACTTTTCTTAAATTTCTGAATTACATTCTGACATA
 AGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTAAACACAAAATCTGAAAGAAA
 GTGTCCAGTTGGTACTGGAATCAACTAGTGACCTCCAGGGACAACCCGAACGTGATGAAAAGATCAA
 AGAACCCTACTCTATTGGGTTTTTCATACAGCTAGCGGGAAAAAAGTTAAATTTGCAAAGGAATCTTTGGAC
 AAAGTGAAAAACCTTTTTGATGAAAAAGCAAGGTAAGTAAATCACCAGTTTTAGCCATCAATGGG
 CAAAGACCCTAAAGTACAGAGAGGCTGTAAAGACCTGAATTAGCATGTGAGACCATTGAGATCACAGC
 TGCCCCAAAGTGTAAAGAAATGCAGAATCTCTCAATAATGATAAAAACTTGTTTCTATTGAGACTGTG
 GTGCCACCTAAGCTCTAAGTGATAATTTATGTAGACAACTGAAAATCTCAAAACATCAAAAAGTATCT
 TTTTGAAGTTAAAGTACATGAAAATGTAGAAAAAGAACAGCAAAAAGTCTGCAACTTGTACACAAA
 TCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAACTTCT
 GTGAGTCAGACTTCATTACTGGAAGCAAAAAATGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAA
 GAATAAATACTGCAGATTATGTAGGAAATTTTGTATGAAAATTAATCAAACAGTACTATAGCTGAAA
 TGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCC
 TACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAATCTGATTCTGGTATTGAGC
 CAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAGAGATGC
 AAATGCATACCCACAACTGTAATGAAGATATTTGCGTTGAGGAACTTGTGACTAGCTCTTACCCTGC
 AAAAAATAAAATGCAGCCATTAATTTGCCATATCTAATAGTAATAATTTTGGAGTAGGGCCACCTGCAT
 TTAGGATAGCCAGTGGTAAATCGTTTTGTGTTTCATGAAACAATTAAGAAAGTAAAGACATATTTAC
 AGACAGTTTCAGTAAAGTAATTAAGGAAAAACAGGAGAATAAATCAAAAAATTTGCCAAACGAAAATATG
 GCAGTTGTTACGAGGCATTGGATGATTCAGAGGATTTCTTCATAACTCTAGATAAGTAAAGTGA
 GCACGCATTCACATAAGGTTTTTGTGACATTCAGAGTGAAGAATTTTACAACATAACCAAAATATGTC
 TGGATTGGAGAAAGTTTCTAAAAATACCTTGTGATGTTAGTTTGGAACTTCAGATATATGAAATGT
 AGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATCTTGTGGGATTTTTAGCACAGCAAGTGAA
 AATCTGTCCAGGTATCAGATGCTTATTACAAAACGCAAGACAAGTGTCTTGAATAGAAAGATAGTAC
 CAAGCAAGTCTTTTCCAAAGTATTGTTTAAAAGTAACGAACATTCAGACCAGCTCACAAGAGAAGAAAAT
 ACTGCTATACGTACTCCAGAACATTTAATATCCAAAAAGGCTTTTATATAATGTGGTAAATTCATCTG
 CTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTCCATTTTGAAGTTCTTACACAAAGTTAA
 GGGAGTGTAGAGGAATTTGATTTAATCAGAAGTGGAGTACTTCACTATTCACCTACGTCTAGACAA
 AATGTATCAAAAAATCTCCTCGTGTGATAAGAGAAACCCAGAGCACTGTGAAACTCAGAAATGGAAA
 AAACCTGCAGTAAAGAATTTAAATATCAAATAACTTAAATGTTGAAGGTGGTCTTTCAGAAAATATCA
 CTCTATTAAGTTTCTCCATATCTCTCAATTTCAACAAGACAAAACAACAGTTGGTATTAGGAACCAAA
 GTGTCACTTGTGAGAACATTCATGTTTTGGGAAAAAGAACAGGCTTCACTAAAAACGTAATAATGGAAA
 TTGGTAAAACTGAACTTTTTCTGATGTTCTGTGAAAACAAATAGAAAGTTGTTCTACTTACTCCAA
 AGATTCAGAAAACACTTTTGAACAGAGCAGTAGAAATGCTAAAGCTTTTATGGAAGATGATGAAGT
 ACAGATCTAAACTGCCAAGTCAAGCCACATTTCTTTTTACATGTCCCGAAAATGAGGAAATGGTTT
 TGTCAAATCAAGAATTGGAAAAAGAGAGGAGAGCCCTTATCTTAGTGGGAGAACCCCAATCAAAAAG
 AAACCTTAAATGAATTTGACAGGATAATAGAAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT
 CCAGATGGCACATAAAAAGATCGAAGATTGTTTATGCATCATGTTTCTTTAGAGCCGATTACCTGTGTAC
 CCTTTCGCACAACATAAGGAACGTCAAGAGATACAGAAATCCAAATTTTACCACCTGGTCAAGAAATTTCT
 GTCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCAATTTAGCAGTTTTCAGGACAT
 CCATTTTATCAAGTTTCTGCTACAAGAAATGAAAAATGAGACACTTGATTACTACAGGCAGACCAACCA
 AAGTCTTTGTTCCACCTTTTAAACTAAATCACATTTTACAGAGTTGAACAGTGTGTTAGGAATATTA
 CTTGGAGGAAAACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAATAAGATTAAT
 GACAATGAGATTCATCAGTTTAACAAAAACAACCTCAATCAAGCAGCAGCTGTAACCTTTCACAAAGTGTG
 AAGAAGAACCTTTAGATTTAATTACAAGTCTTCAAGATGCCAGAGATATACAGGATATGCGAATTAAGAA
 GAAACAAGGCAACGCGTCTTTCCACAGCCAGGAGTCTGTATCTTGAAAAACATCCACTCTGCCTCGA
 ATCTCTCTGAAAGCAGCAGTAGGAGGCCAAGTTCCCTCTGCGTGTCTCATAAACAGCTGTATACGTATG
 GCGTTTCTAAACATTGCATAAAAAATTAACAGCAAAAAATGCAGAGTCTTTTTCAGTTTACACTGAAGATTA
 TTTTGGTAAGGAAAGTTTATGGACTGAAAAAGGAATACAGTTGGCTGATGGTGGATGGCTCATACCCTCC

AATGATGGAAAGGCTGGAAAAGAAGAATTTTATAGGGCTCTGTGTGACACTCCAGGTGTGGATCCAAAGC
 TTATTTCTAGAATTTGGGTTTATAATCACTATAGATGGATCATATGAAACTGGCAGCTATGGAATGTGC
 CTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCCAGAAAGGGTGTCTTCACTAAAATACAGATAT
 GATACGGAAATGATAGAAGCAGAAGATCGGCTATAAAAAAGATAATGAAAGGGATGACACAGCTGCAA
 AAACACTTGTCTCTGTGTTTCTGACATAATTTCACTGAGCGCAAATATATCTGAAACTTCTAGCAATAA
 AACTAGTAGTCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGGTATGCTGTAAAGGCC
 CAGTTAGATCCTCCCCTTCTAGCTGTCTTAAAGAATGGCAGACTGACAGTTGGTCAGAAGATTATCTTTC
 ATGGAGCAGAACTGGTGGGCTCTCCTGATGCCTGTACACTCTTGAAGCCCAGAACTCTTATGTTAAA
 GATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAACCTGGATTCTTCTGACCCTAGACCT
 TTTCTCTGCCCTTATCATCGCTTTTCACTGATGGAGGAAATGTTGGTTGTGTTGATGTAATTATTCAAA
 GAGCATACCCTATACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTGCAATGAAAGAGAGGA
 AGAAAAGGAAGCAGCAAAATATGTGGAGGCCAACAAAAGAGACTAGAAGCCTTATTCCTAAAATTCAG
 GAGGAATTTGAAGAACATGAAGAAAACACAACAAACCATATTTACCATCACGTGCACTAACAGACAGC
 AAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCAGCTTACCT
 TGAGGGTTATTTCACTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAA
 CAAGCTCAGATCCAGTTGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAA
 GGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAGAAAAGATTCACTTACT
 GAGTATTTGGCGTCCATCATCAGATTTATTTCTGTAAACAGAAGGAAAGAGATACAGAATTTATCAT
 CTTGCAACTTCAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAACTC
 AGTATCAACAACCTACCGTTTCAGATGAAATTTATTTCACTTTACCAGCCACGGGAGCCCTTCACTT
 CAGCAATTTTATAGATCCAGACTTTAGCCATCTTGTCTGAGGTGGACCTAATAGGATTTGTCGTTTCT
 GTTGTGAAAAAACAGGACTTGGCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAA
 AGTTTGGATAGACTTAATGAGGACATTATAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAGTG
 GCGTCCAGAATCCAAATCAGGCCTTCTACTTTATTTGCTGGAGATTTTCTGTGTTTTCTGCTAGTCCA
 AAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAACTGTTGAGAATATTGACATACTTTGCA
 ATGAAGCAGAAAAAAGCTTATGCATATACTGCATGCAATGATCCCAAGTGGTCCACCCCACTAAAGA
 CTGTACTTCAGGGCCGTACACTGCTCAAATCATTCTGGTACAGGAAACAAGCTTCTGATGTCTTCTCCT
 AATTGTGAGATATATTATCAAAGTCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTG
 TCTCAGCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAAGAACTGCAAAA
 GAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTT
 TCTCCGGCTGCACAGAAGGCATTTAGCCACCAAGGAGTTGTGGCACCATAACGAAACCCCATAAAGA
 AAAAAGAACTGAATTCCTCAGATGACTCCATTTAAAAAATCAATGAAATTTCTTTTGGAAAGTAA
 TTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAA
 CAATTTATATCTGTCACTGAAATCCACTAGGACTGCTCCACCAGTTTCAAGAAGATTATCTCAGACTGAAAC
 GACGTTGACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTATGGAAGAATGTGAGAAAAA
 TAAGCAGGACACAATTACAATAAAAAATATATC

AGCGGACCCACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

Protein Sequence:

>RC400766 representing NM_000059

Red=Cloning site Green=Tags(s)

MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSEAPPYNSEPAEESHKNNNYEPNLFKTPQRKPS
 YNQLASTPIIFKEQGLTLPYQSPVKELDKFKLDLGRNVPNSRHKSLRTVKTMDQADDVSCPLLNSCLS
 ESPVVLQCTHVTPQRDKSVVCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLI
 VRNEEASETVFPHDTTANVKSIFYSNHDESLKKNDRFIA SVTDSSENTNQREAASHGFGKTSNFSFKVNSCK
 DHIGKSMPNVLEDEVYETVVDTSEEDSFLCFSKCRTKNLQKVRTSKTRKKIFHEANADECEKSNQVKE
 KYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVP SLACEWSQLTSLGLNGAQMEKIPLLHISDC
 QNISEKDLLDTENKRKDFLTSNSLPRISLSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAIISG
 TSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDPNFKKETEASESGLEIHTVCSQKEDSLCPNLIDN
 GSWPATTTQNSVALKNAGLISTLKKTKNFYIAIHDETSYKGGKIPKDQKSELINCSAQFEANAFEAPLT
 FANADSGLLHSSVKRSCSQNDSEPTLSLTSSFGTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQL

FITPEADSL SCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQSLLYDHENASTLI
 LTPTSKDVL SNLVMISRGKESYKMSDKLKGNNYSDVELTKNIPMEKNQDVCALNENYKNVELLPPEKYM
 RVASPSRKVQFNQNTNLRVIQKNQEETTSISKITVNPDSEELFSDNENNFVFQVANERNLALGNTKELH
 ETDLTCVNEPIFKNSTMVL YGDTGDKQATQVSIKKDLVYVLAENKNSVKQHIKMTLGQDLKSDISLNDI
 KIPEKNNDYMNKWAGLLGPI SNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIIEEQYPTSLACVEIVNT
 LALDNQKLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHLTPSQKAEITELSTILEE
 SGSQFEFTQFRKPSYILQKSTFEVPENQMTILKTTSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKR
 KFAGLLKNDCKNSASGYLTDENEVGRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETS AEVHPISL
 SSSKCHDSVVSVMFKIENHNDKTVSEKNKNCQLILQNNIEMTTGTFVVEITENYKRNTENEDNKYTAASRN
 SHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKL SGQFMKEGNTQIKEDLSDLTFLEVAKAQEACH
 GNTSNKEQLTATKTEQNIKFETSDTFFQTASGKNISVAKESFNKIVNFFDQKPEELHNFSLNSELHSDI
 RKNKMDILSYEETDIVKHKILKESVPGTGNQLVTFQGGQPERDEKIKEPTLLGFHTASGKVKIAKESLD
 KVKNLFDEKEQGTSEITSFHQWAKTLKYREACKDLELACETIEITAAPKCKEMQNSLNNDKNLVSIETV
 VPPKLLSDNLCRQTENLKTSSIFLKVKHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCSRKTS
 VSQTSLL EAKKWLREGIFDQPERINTADYVGNLYENNSNSTIAENDKNHLSEKQD TYLSNSSMSNSYS
 YHSDEVYNDSGYL SKNKLDSGIEPVLKNVEDQKNTSF SKVISNVKDANAYPQTVNEDICVEELVTSSSPC
 KNKNAAIKLSISNSNFEVGPFAFRIASGKIVCVSHETIKKVKDIFTDSFSKVIKENNENKSKICQTKIM
 AGCYEALDDESEDILHNSLDNDECSTHSHKVFADIQSEEILQHNQNMGLEKYSKISPCDVSLETSDICKC
 SIGKLGKSVSSANTCGIFSTASGKSVQVSDASLQARQVFSEIEDSTKQVFSKVLFKSNEHSDQLTREEN
 TAIRTPPEHLISQKGFYNVNVSSAFSGFSTASGKQVSILESSLHKVKGVL EEFDLIRTEHSLHYSPTS RQ
 NVSKILPRVDKRNPEHCVNSEMEKTCSEKFKLSNNLNVEGGSSENNHSIKVSPYL SQFQDKQQLVLGTK
 VSLVENIHVLGKEQASPKNVKMEIGKTETTFSDVPVKTNIEVCSTYSKDSENYFETEAVEIAKAFMEDDEL
 TDSKLP SHATHSLFTCPENEEMVLSNSRIGKRRGEPLILVGEPSIKRNLNNEFDRIIENQEKSLKASKST
 PDGTIKDRRLFMHHSLEPITCVPFRTTKERQEIQNPNFTAPGQEFLSKSHLYEHLTLEKSSSNLAVSGH
 PFYQVSA TRNEKMRHLITTRPTKVFVPPFKTKSHFHRVEQCVRNINLEENRQKQNDIGHGSDSKNKIN
 DNEIHQFNKNSNQAAAVTFTKCEEEPLDLITSLQNARDIQDMRIKKKQRQRVFPQPSGLYLAKTSTLPR
 ISLKA AVGGQVPSACSHKQLYTYGVSKHCIKINSKNAESFQFHTEDYFGKESLWTGKGIQLADGGWLIPS
 NDGKAGKEEFYRALCDTPGVDPKLSRIWVYNHYRWIIWKLAA MECAFPKEFANRCLSPERVLLQLKYRY
 DTEIDRSRRSAIKKIMERDDTAAKTLVLCVSDIISLSANISETSSNKTSSADTQKVAIIELTDGWYAVKA
 QLDPPLLAVLKNGR LTVGQKIILHGAELVGSPDACTPLEAPESLMLKISANSTRPARWYTKLGFDPDRP
 FPLPLSSLFSDGGNVGCVDVIIQRAYPIQWMEKTS SGLYIFRNEREEEEKA AKYVEAQQKRL EALFTKIQ
 EEFEEHEENTTKPYLPSRALTRQQVRALQDGAELYEAVKNAADPAYLEGYFSEEQLRALNNHRQMLNDKK
 QAQIQLEIRKAMESAEQKEQGLSRDVTTVWKLRIVSYSKKEKDSVILSIWRPSSDLYSLLTEGKRYRIYH
 LATSKSKSERANIQLAATKKTQYQQLPVSD EILFQIYQPREPLHFSKFLDPDFQPSCSEVDLIGFVVS
 VVKKTGLAPFVYL SDECYNLLAIKFWIDLNEDI IKPHMLIAASNLQWRPESKSGLLTLFAGDFSVFSASP
 KEGHFQETFNKMKNTVENIDILCNEAENKLMHILHANDPKWSTPTKDC TSGPYTAQIIPGTGNKLLMSSP
 NCEIYYQSPLSLCMAKRKSVSTPVSAQMTSKSKCKEKEID DQKNCKRRALDFL SRLPLPPPVPSPICTFV
 SPAAQKAFQPPRSCGTYETPIKKKELNSPQMTPFKFFNEISLLESNSIADEELALINTQALLSGSTGEK
 QFISVSESTRTAPTSS ELYRLKRRCTTSLIKEQESSQASMECEKNKQDTITTKKYI

SGP TRRRLEQKLI 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]