

Product datasheet for **RC400741**

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:	R3052Q
Affected Codon#:	3052
Affected NT#:	9155
Nucleotide Mutation:	BRCA2 Mutant (R3052Q), 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:	SgfI-RsrII
ORF Nucleotide Sequence:	>RC400741 representing NM_000059 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGATT
TAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC
AGAAGAATCTGAACATAAAAAACAACAATTACGAACCAACCTATTTAAAACCTCCACAAAGGAAACCATCT
TATAATCAGCTGGCTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTC
CTGTAAGAATTAGATAAATCAAATTAGACTTAGGAAGGAATGTTCCCAATAGTAGACATAAAGTCT
TCGCACAGTGAAGAACTAAAATGGATCAAGCAGATGATGTTTCTGTCCACTTCTAAATCTTGTCTTAGT
GAAAGTCTGTTGTTCTACAATGTACACATGTAACACCACAAAGAGATAAGTCAGTGGTATGTGGGAGTT



[View online »](#)

TGTTTCATACACCAAAGTTTGTGAAGGGTCGTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGA
GGTGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACCACCCTTAGTTCTACTGTGCTCATA
GTCAGAAATGAAGAAGCATCTGAAACTGTATTTCTCATGATACTACTGCTAATGTGAAAAGCTATTTTT
CCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGTCTCTGTGACAGACAGTGA AACACAAA
TCAAAGAGAAGCTGCAAGTCATGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAA
GACCACATTGGAAAGTCAATGCCAAATGTCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTG
AAGAAGATAGTTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAATCTACAAAAAGTGAAGAACTAGCAA
GACTAGGAAAAAATTTTCCATGAAGCAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAAGAA
AAATACTCATTTGTATCTGAAGTGGAACCAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGA
AGCCCTTTGAGAGTGGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCA
ACTAACCTTTTCAAGTCTAAATGGAGCCAGATGGAGAAAAATACCCTATTGCATATTTCTTTCATGTGAC
CAAAATATTTTCAAGAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTTACTTCAGAGA
ATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGTAAATAA
GAGAGATGAAGAGCAGCATCTTGAATCTCATACTGACTGCATTCTTGCAGTAAAGCAGGCAATATCTGGA
ACTTCTCCAGTGGCTTTCATTTTCAAGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAG
AGACTTCAATGCAAGTTTTTCAAGTGCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGA
AAGTGGACTGGAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAAT
GGAAGCTGGCCAGCCACCACCACAGAAATCTGTAGCTTTGAAGAATGCAGGTTAATATCCACTTTTGA
AAAAGAAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAATACCGAA
AGACCAAAAAATCAGAATAATTAAGTGTTCAGCCAGTTTGAAGCAATGCTTTTGAAGCACCATTACA
TTTGCAAAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTTACAGAAATGATTTGAA
AACCAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTTACAGAAATGAAACATGTTT
TAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTAAATAAGGAAAAACTACAGTTA
TTTATTACCCAGAAGCTGATTCTGTGATGCCTGCAGGAAGGACAGTGTGAAAAATGCTCAAAAAAGCA
AAAAAGTTTCAAGATATAAAGAAGAGGTCTTGGCTGCAGCATGTACCCAGTACAACATTCAAAAAGTGA
ATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAAATGCCAGCACTCTTATT
TTAACTCTACTTCCAAGGATGTTCTGTCAAACCTAGTCATGATTTCTAGAGGCAAGAATCATACAAAA
TGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAAATTTCCCATGGAAAA
GAATCAAGATGTATGTGCTTTAAATGAAAATTAAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATG
AGAGTAGCATCACCTTCAAGAAAGGTACAATTCACCAAAAACACAATCTAAGAGTAATCAAAAAAATC
AAGAAGAACTACTTCAATTTCAAAAAAATCACTGTCAATCCAGACTCTGAAGAATTTTCTCAGACATGA
GAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGTCTTAGGAAATACTAAGGAATTCAT
GAAACAGACTTGACTTGTGTAACCGAACCCATTTTCAAGAATCTACCATGGTTTTATATGGAGACACAG
GTGATAAAACAAGCAACCCAAGTGTCAATTAAAAAAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAA
TAGTGTAAAGCAGCATATAAAAAATGACTCTAGGTCAAGATTTAAATCGGACATCTCCTTGAATATAGAT
AAAATACCAGAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACA
GTTTTGGAGGTAGCTTCAAGACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAG
CAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATGTAATACC
TTGGCATTAGATAATCAAAAGAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGA
GTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTT
TAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAATTTTCTACTATATTAGAAGAA
TCAGGAAGTCAAGTTGAAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAG
TGCTGAAAACAGATGACTATCTTAAAGACCCTTCTGAGGAATGCAGAGATGCTGATCTTTCATGTCAT
AATGAATGCCCATCGATTGGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAACGG
AAGTTTGTGCTGGCCTGTTGAAAAATGACTGTAACAAAAGTCTTCTGGTTATTTAACAGATGAAAAATGAAG
TGGGGTTTAGGGCTTTTATTCTGCTCATGGCACAAAACCTGAATGTTTCTACTGAAGCTCTGCAAAAAGC
TGTGAAACTGTTTAGTGATATTGAGAATATTAGTGAGGAACTCTGCAGAGGTACATCCAATAAGTTTA
TCTTCAAGTAAATGTCATGATTCTGTTGTTCAATGTTTAAAGATGAAAAATCATAATGATAAACTGTAA
GTGAAAAAATAATAATGCCAACTGATATTACAAAATAAATTTGAAATGACTACTGGCACTTTTGTGGA
AGAAATTAAGTAAAAATCAAGAGAAATGAAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAAT
TCTCATAACTTAGAATTTGATGGCAGTATTCAAGTAAAAATGATACTGTTTGTATTATAAAGATGAAA
CGGACTTGCTATTTACTGATCAGCACAACATATGTCTTAAATTTCTGGCCAGTTTATGAAGGAGGGAAA

CACTCAGATTAAGAAGATTTGTGAGATTTAACTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCAT
 GGTAATACTTCAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAAAGATTTTGAGACTT
 CTGATACATTTTTTTCAGACTGCAAGTGGGAAAAATATTAGTGTGCGCCAAAGAGTCATTTAATAAAATTTG
 AAATTTCTTTGATCAGAAACCAGAAGATTGCATAACTTTTCTTAAATTTCTGAATTACATTCTGACATA
 AGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTAAACACAAAATCTGAAAGAAA
 GTGTCCAGTTGGTACTGGAATCAACTAGTGACCTCCAGGGACAACCCGAACGTGATGAAAAGATCAA
 AGAACCTACTCTATTGGGTTTTTCATACAGCTAGCGGGAAAAAAGTTAAATTTGCAAAGGAATCTTTGGAC
 AAAGTGAAAAACCTTTTTGATGAAAAAGCAAGGTAAGTAAATCACCAGTTTTAGCCATCAATGGG
 CAAAGACCCTAAAGTACAGAGAGGCTGTAAAGACCTGAATTAGCATGTGAGACCATTGAGATCACAGC
 TGCCCCAAAGTGTAAAGAAATGCAGAATTCTCTCAATAATGATAAAAAACCTTGTTTCTATTGAGACTGTG
 GTGCCACCTAAGCTCTAAGTGATAATTTATGTAGACAACTGAAAATCTCAAAACATCAAAAAGTATCT
 TTTTGAAGTTAAAGTACATGAAAATGTAGAAAAAGAACAGCAAAAAGTCTGCAACTTGTACACAAA
 TCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAACTTCT
 GTGAGTCAGACTTCATTACTGGAAGCAAAAAATGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAA
 GAATAAATACTGCAGATTATGTAGGAAATTTTGTATGAAAATAATTCAAACAGTACTATAGCTGAAA
 TGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAACAGTAGCATGTCTAACAGCTATTCC
 TACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGC
 CAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAATATCCAATGTAAGAGATGC
 AAATGCATACCACAAACTGTAATGAAGATATTTGCGTTGAGGAACTTGTGACTAGCTCTTACCCTGC
 AAAAAATAAAATGCAGCCATTAATTTGCCATATCTAATAGTAATAATTTTGAGGTAGGGCCACCTGCAT
 TTAGGATAGCCAGTGGTAAATCGTTTTGTGTTTCATGAAACAATTAAGGAAAGTAAAGACATATTTAC
 AGACAGTTTCAGTAAAGTAATTAAGGAAAAACAGGAGAATAAATCAAAAAATTTGCCAAACGAAAATATG
 GCAGTTGTTACGAGGCATTGGATGATTCAGAGGATTTCTTCATAACTCTAGATAATGAAATGTA
 GCACGCATTCACATAAGGTTTTTGTGACATTCAGAGTGAAGAATTTTACAACATAACCAAAATATGTC
 TGGATTGGAGAAAGTTTCTAAAAATACCTTGTGATGTTAGTTTGGAACTTCAGATATATGAAATGT
 AGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGAA
 AATCTGTCCAGGTATCAGATGCTTCATTACAAAACGCAAGACAAGTGTCTTGAATAGAAAGTAGTAC
 CAAGCAAGTCTTTTCAAAGTATTGTTTAAAAGTAACGAACATTCAGACCAGCTCACAAGAGAAGAAAAT
 ACTGCTATACGTACTCCAGAACATTTAATATCCAAAAAGGCTTTTATATAATGTGGTAAATTCATCTG
 CTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTCCATTTTGAAGTTCTTACACAAAGTTAA
 GGGAGTGTAGAGGAATTTGATTTAATCAGAAGTGGAGTACTTCACTATTCACCTACGTCTAGACAA
 AATGTATCAAAAAATCTCCTCGTGTGATAAGAGAAACCCAGAGCACTGTGAAACTCAGAAATGGAAA
 AAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTCTTTCAGAAAATATCA
 CTCTATTAAGTTTCTCCATATCTCTCAATTTCAACAAGACAAAACAACAGTTGGTATTAGGAACCAAA
 GTGTCACTTGTGAGAACATTCATGTTTTGGGAAAAAGAACAGGCTTCACTAAAAACGTAATAATGGAAA
 TTGGTAAAACTGAAACTTTTTCTGATGTTCTGTGAAAACAAATAGAAAGTTGTTCTACTTACTCCAA
 AGATTCAGAAAACACTTTGAAACAGAAGCAGTAGAAATGCTAAAGCTTTTATGGAAGATGATGAAGT
 ACAGATCTAAACTGCCAAGTCATGCCACATTTCTTTTTACATGTCCGAAAATGAGGAAATGGTTT
 TGTCAAATTCAGAATTTGGAAAAAGAAGAGGAGAGCCCTTATCTTAGTGGGAGAACCCCAATCAAAAAG
 AAACCTTATAAATGAATTTGACAGGATAATAGAAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT
 CCAGATGGCACATAAAAAGATCGAAGATTGTTTATGCATCATGTTTCTTTAGAGCCGATTACCTGTGTAC
 CCTTTCGCACAACATAAGGAACGTCAAGAGATACAGAAATCCAAATTTTACCACCTGGTCAAGAAATTTCT
 GTCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCAATTTAGCAGTTTTCAGGACAT
 CCATTTTATCAAGTTTCTGCTACAAGAAATGAAAAATGAGACACTTGATTACTACAGGCAGACCAACCA
 AAGTCTTTGTTCCACCTTTTAAACTAAATCACATTTTACAGAGTTGAACAGTGTGTTAGGAATATTA
 CTTGGAGGAAAACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAATAAGATTAAT
 GACAATGAGATTCATCAGTTTAACAAAAACAACCTCAATCAAGCAGCAGCTGTAACCTTTCACAAAGTGTG
 AAGAAGAACCTTTAGATTTAATTACAAGTCTTCAAGATGCCAGAGATATACAGGATATGCGAATTAAGAA
 GAAACAAGGCAACGCGTCTTTCCACAGCCAGGAGTCTGTATCTTGAAAAACATCCACTCTGCCTCGA
 ATCTCTCTGAAAGCAGCAGTAGGAGGCCAAGTTCCCTCTGCGTGTCTCATAAACAGCTGTATACGTATG
 GCGTTTCTAAACATTGCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTTCAGTTTACACTGAAGATTA
 TTTTGGTAAGGAAAGTTTATGGACTGAAAAAGGAATACAGTTGGCTGATGGTGGATGGCTCATACCCTCC

AATGATGGAAAGGCTGGAAAAGAAGAATTTTATAGGGCTCTGTGTGACACTCCAGGTGTGGATCCAAAGC
 TTATTTCTAGAATTTGGGTTTATAATCACTATAGATGGATCATATGAAAAGTGGCAGCTATGGAATGTGC
 CTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCAGAAAGGGTGTCTTCAACTAAAATACAGATAT
 GATACGGAAATTTGATAGAAGCAGAAGATCGGCTATAAAAAAGATAATGAAAAGGGATGACACAGCTGCAA
 AAACACTTGTCTCTGTGTTTCTGACATAATTTTATTGAGCGCAATATATCTGAAAATCTAGCAATAA
 AACTAGTAGTGCAGATACCCAAAAGTGGCCATTATTGAACTTACAGATGGGTGGTATGCTGTTAAGGCC
 CAGTTAGATCCTCCCCTTCTAGCTGTCTTAAAGAATGGCAGACTGACAGTTGGTGCAGAAGATTATCTTTC
 ATGGAGCAGAAGTGGTGGGCTCCTGATGCCTGTACACCTCTTGAAGCCCAGAACTCTTATGTTAAA
 GATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAAGTGGATTCTTCTGACCCTAGACCT
 TTTCTCTGCCCTTATCATCGCTTTTTCAGTGTGGAGGAAATGTTGGTGTGTTGATGTAATTATTCAAA
 GAGCATACCCTATACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTGCAATGAAAGAGAGGA
 AGAAAAGGAAGCAGCAAAATATGTGGAGGCCAACAAAAGAGACTAGAAGCCTTATTCATAAAATTCAG
 GAGGAATTTGAAGAACATGAAGAAAACACAACAAAACCATATTTACCATCACGTGCACTAACAGACAGC
 AAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCAGCTTACCT
 TGAGGGTTATTTTTCAGTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAA
 CAAGCTCAGATCCAGTTGAAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAA
 GGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAGAAAAGATTTCAGTTATACT
 GAGTATTTGGCGTCCATCATCAGATTTATTTCTGTAAACAGAAGGAAAGAGATACAGAATTTATCAT
 CTTGCAACTTCAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAAACTC
 AGTATCAACAACCTACCGTTTCAGATGAAATTTTATTTTTCAGATTTACCAGCCACAGGAGCCCTTCACTT
 CAGCAATTTTATAGATCCAGACTTTTTCAGCCATCTTGTCTGAGGTGGACCTAATAGGATTTGTCGTTTCT
 GTTGTGAAAAAACAGGACTTGGCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAA
 AGTTTGGATAGACCTTAAAGAGCATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAGTG
 GCGACCGAATCCAAATCAGGCCTTCTACTTTATTTGCTGGAGATTTTCTGTGTTTTCTGCTAGTCCA
 AAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAATACTGTTGAGAATATTGACATACTTTGCA
 ATGAAGCAGAAAAAAGCTTATGCATATACTGCATGCAATGATCCCAAGTGGTCCACCCCAACTAAAGA
 CTGTACTTCAGGGCCGTACACTGCTCAAATCATTCTGGTACAGGAAACAAGCTTCTGATGTCTTCTCCT
 AATTGTGAGATATATTATCAAAGTCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTG
 TCTCAGCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAAGAACTGCAAAAA
 GAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTT
 TCTCCGGCTGCACAGAAGGCATTTACAGCCCAAGGAGTTGTGGCACCATAACGAAACCCCATAAAGA
 AAAAAGAACTGAATTCCTCAGATGACTCCATTTAAAAAATCAATGAAATTTCTTTTGGAAAGTAA
 TTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAA
 CAATTTATATCTGTGATGAAATCCACTAGGACTGCTCCACCAGTTTTCAGAAGATTATCTCAGACTGAAAC
 GACGTTGACTACATCTCTGATCAAAGAACAGGAGAGTTCCAGGCCAGTACGGAAGAATGTGAGAAAAA
 TAAGCAGGACACAATTACAATAAAAAATATATC

AGCGGACCGACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

Protein Sequence:

>RC400741 representing NM_000059
 Red=Cloning site Green=Tags(s)

MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSEAPPYNSEPAEESHKNNNYEPNLFKTPQRKPS
 YNQLASTPIIFKEQGLTLPYQSPVKELDKFKLDLGRNVPNSRHKSLRTVKTMDQADDVSCPLLNLSCLS
 ESPVVLQCTHVTPQRDKSVVCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLI
 VRNEEASETVFPHDTTANVKSIFYSNHDESLKKNDRFIA SVTDSSENTNQREAAASHGFGKTSNFSFKVNSCK
 DHIGKSMPNVLEDEVYETVVDTSSEDSFSLCF SKCRTKNLQKVRTSKTRKKIFHEANADECEKSNQVKE
 KYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVP SLACEWSQLTSLGLNGAQMEKIPLLHISDCD
 QNISEKDLLDTENKRKDFLTSNSLPRISL PKSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAIISG
 TSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDPNFKKETEASESGLEIHTVCSQKEDSLCPNLIDN
 GSWPATTTQNSVALKNAGLISTLKKTKNFIYAIHDETSYKGGKIPKDQKSELINCSAQFEANAFEAPLT
 FANADSGLLHSSVKRSCSQNDSEPTLSLTSSFGTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQL

FITPEADSLSCLQEGQCENDPKSKKVSIDIKEEVLAACHPVQHSKVEYSDTDFQSQKSLLYDHENASTLI
 LTPTSKDVL SNLVMISRKESYKMSDKLKGNNYSDVELTKNIPMEKNQDVCALNENYKNVELLPPEKYM
 RVASPSRKVQFNQNTNLRVIQKNQEETTSISKITVNPDSEELFSDNENNFVFQVANERNLALGNTKELH
 ETDLTVCNEPIFKNSTMVL YGDTGDKQATQVSIKKDLVYVLAENKNSVKQHIKMTLGQDLKSDISLNDI
 KIPEKNNDYMNKWAGLLGPI SNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIIEEQYPTSLACVEIVNT
 LALDNQKLLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHLTPSQKAEITELSTILEE
 SGSQFEFTQFRKPSYILQKSTFEVPENQMTILKTTSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKR
 KFAGLLKNDCKNSASGYLTDENEVGRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETSAEVHPISL
 SSSKCHDSVVSVMFKIENHNDKTVSEKNKNCQLILQNNIEMTTGTFVVEITENYKRNTENEDNKYTAASRN
 SHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKLSGQFMKEGNTQIKEDLSLTFLEVAKAQEACH
 GNTSNKEQLTATKTEQNIKDFETSDTFFQTASGKNISVAKESFNKIVNFFDQKPEELHNFSLNSELHSDI
 RKNKMDILSYEETDIVKHKILKESVPGTGNQLVTFQGGQPERDEKIKEPTLLGFHTASGKVKIAKESLD
 KVKNFLDEKEQGTSEITFSHQWAKTLKYREACKDLELACETIEITAAPKCKEMQNSLNDKNSLVSIEV
 VPPKLLSDNLCRQNTENLKTSSIFLKVKHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCRKTS
 VSQTSLLAEAKWLRREGIFDQPERINTADYVGNLYYENNSNSTIAENDKNHLSEKQDTYLSNSSMSNSYS
 YHSDEVYNDSGYL SKNKLDSGIEPVLKNVEDQKNTSFSKVISNVKDANAYPQTVNEDICVEELVTSSSPC
 KNKNAAIKLSISNSNFEVGPFAFRIASGKIVCVSHETIKKVKDIFTDSFSKVIKENNENKSKICQTKIM
 AGCYEALDDESEDILHNSLDNDECSTHSHKVFADIQSEEILQHNQNMGLEKYSKISPCDVSLETSDICKC
 SIGKHLKSVSSANTCGIFSTASGKSVQVSDASLQARQVFSEIEDSTKQVFSKVLFKSNEHSDQLTREEN
 TAIRTPPEHLISQKGFYNVNVSSAFSGFSTASGKQVSILESSLHKVKGVL EEFDLIRTEHSLHYSPTSQ
 NVSKILPRVDKRNPEHCVNSEMEKTCSEKFKLSNNLNVEGGSSENNHSIKVSPYL SQFQDKQQLVLGKTK
 VSLVENIHVLGKEQASPKNVKMEIGKTETTFSDVPVKTNIEVCSTYSKDSSENYFETEAVEIAKAFMEDDEL
 TDSKLP SHATHSLFTCPENEEMVLSNSRIGKRRGEPLILVGEPSIKRNLNDFDRIENQEKSLKASKST
 PDGTIKDRRLFMHHVSLLEPITCVPFRTTKERQEIQNPNFTAPGQEFLSKSHLYEHLTLEKSSSNLAVSGH
 PFYQVSA TRNEKMRHLITTRPTKVFVPPFKTKSHFHRVEQCVRNINLEENRQKQNDIGHGSDSKNKIN
 DNEIHQFNKNSNQAAAVTFTKCEEEPLDLITSLQNARDIQDMRIKKKQRQRVFPQPSGLYLAKTSTLPR
 ISLKAAVGGQVPSACSHKQLYTYGVSKHCIKINSKNAESFQFHTEDYFGKESLWTGKGIQLADGGWLIPS
 NDGKAGKEEFYRALCDTPGVDPKLSRIWVYNHYRWIIWKLAAAMECAFPEFANRCLSPERVLLQLKYRY
 DTEIDRSRRSAIKKIMERDDTAAKTLVLCVSDIISLSANISSETSSNKTSSADTQKVAIIELTDGWYAVKA
 QLDPPLLAVLKNGRLLTVGQKIILHGAELVGSDDACTPLEAPESLMLKISANSTRPARWYTKLGFDPDRP
 FPLPLSSLFSDGGNVGCVDVIIQRAYPIQWMEKTS SGLYIFRNEREEEEKAAKYVEAQQKRL EALFTKIQ
 EEFEEHEENTTKPYLPSRALTRQQVRALQDGAELYEAVKNAADPAYLEGYFSEEQLRALNNHRQMLNDKK
 QAQIQLEIRKAMESAEQKEQGLSRDVTTVWKLRIVSYSKKEKDSVILSIWRPSSDLYSLLTEGKRYRIYH
 LATSKSKSERANIQLAATKTKYQQLPVSDIILFQIYQPQEPLHFSKFLDPDFQPSCSEVDLIGFVVS
 VVKKTGLAPFVYL SDECYNLLAIKFWIDLNEDI IKPHMLIAASNQWRPESKSGLLTLFAGDFSVFSASP
 KEGHFQETFNKMKNTVENIDILCNEAENKLMHILHANDPKWSTPTKDCSTSGPYTAQIIPGTGNKLLMSSP
 NCEIYYQSPLSLCMAKRKSVSTPVSAQMTSKSCKGEKEIDQKNCKRRALDFLSRLPLPPPVPSPICTFV
 SPAAQKAFQPPRSCGTYETPIKKKELNSPQMTPFKFFNEISLLESNSIADEELALINTQALLSGSTGEK
 QFISVSESTRTAPTSSDYLRLLKRRCTTSLIKEQESSQASTECEKKNQDTITTKKYI

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]