

Product datasheet for **RC400500**

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:	Y42C
Affected Codon#:	42
Affected NT#:	125
Nucleotide Mutation:	BRCA2 Mutant (Y42C), 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:	>RC400500 representing NM_000059 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGCCTATTGGATCCAAAGAGAGGCCAACATTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGATT
TAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCCACCCTGTAATTCTGAACCTGC
AGAAGAATCTGAACATAAAAAACAACAATTACGAACCAAACCTATTTAAACTCCACAAAGGAAACCATCT
TATAATCAGCTGGCTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTC
CTGTAAGAATTAGATAAATTCAAATTAGACTTAGGAAGGAATGTTCCCAATAGTAGACATAAAGTCT
TCGCACAGTGAAGAACTAAATGGATCAAGCAGATGATGTTTCTGTCCACTTCTAAATCTTGTCTTAGT
GAAAGTCTGTTGTTCTACAATGTACACATGTAACACCACAAAGAGATAAGTCAGTGGTATGTGGGAGTT



[View online »](#)

TGTTTCATACACCAAAGTTTGTGAAGGGTCGTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGA
GGTGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACCACCCTTAGTTCTACTGTGCTCATA
GTCAGAAATGAAGAAGCATCTGAAACTGTATTTCTCATGATACTACTGCTAATGTGAAAAGCTATTTTT
CCAATCATGATGAAAGTCTGAAGAAAAATGATAGATTTATCGTCTCTGTGACAGACAGTGA AACACAAA
TCAAAGAGAAGCTGCAAGTCATGGATTTGGAAAAACATCAGGGAATTCATTTAAAGTAAATAGCTGCAAA
GACCACATTGGAAGTCAATGCCAAATGTCTAGAAGATGAAGTATATGAAACAGTTGTAGATACCTCTG
AAGAAGATAGTTTTTTCATTATGTTTTTCTAAATGTAGAACAAAAATCTACAAAAAGTGAAGCAAGCA
GACTAGGAAAAAATTTTCCATGAAGCAACGCTGATGAATGTGAAAAATCTAAAAACCAAGTGAAGAA
AAATACTATTTGTATCTGAAGTGAACCAATGATACTGATCCATTAGATTCAAATGTAGCAAATCAGA
AGCCCTTTGAGAGTGAAGTGACAAAATCTCCAAGGAAGTTGTACCGTCTTTGGCCTGTGAATGGTCTCA
ACTAACCTTTTCAAGTCTAAATGGAGCCAGATGGAGAAAAATACCCTATTGCATATTTCTTTCATGTGAC
CAAAATATTTTCAAGAAAAGACCTATTAGACACAGAGAACAAAAGAAAGAAAGATTTTCTTACTTCAGAGA
ATTCTTTGCCACGTATTTCTAGCCTACCAAAATCAGAGAAGCCATTAAATGAGGAAACAGTGGTAAATAA
GAGAGATGAAGAGCAGCATCTTGAATCTCATACTGACTGCATTCTTGCAGTAAAGCAGGCAATATCTGGA
ACTTCTCCAGTGGCTTTCATTTTCAAGGTATCAAAAAGTCTATATTCAGAATAAGAGAATCACCTAAAG
AGACTTTCAATGCAAGTTTTTCAAGTGCATATGACTGATCCAAACTTTAAAAAAGAAACTGAAGCCTCTGA
AAGTGGACTGGAATACATACTGTTTGCTCACAGAAGGAGGACTCCTTATGTCCAAATTTAATTGATAAT
GGAAGCTGGCCAGCCACCACACAGAATTCTGTAGCTTTGAAGAATGCAGGTTAATATCCACTTTTGA
AAAAGAAAAACAAATAAGTTTATTTATGCTATACATGATGAAACATCTTATAAAGGAAAAAATACCGAA
AGACCAAAAAATCAGAATAATTAAGTGTTCAGCCAGTTTGAAGCAATGCTTTTGAAGCACCATTACA
TTTGCAATGCTGATTCAGGTTTATTGCATTCTCTGTGAAAAGAAGCTGTTTACAGAATGATTCGAAG
AACCAATGCTGCTTAACTAGCTCTTTGGGACAATCTGAGGAAATGTTCTAGAAATGAAACATGTTT
TAATAATACAGTAATCTCTCAGGATCTTGATTATAAAGAAGCAAAATGTATAAAGGAAAAACTACAGTTA
TTTATTACCCAGAAGCTGATTCTGTGATGCCTGCAGGAAGGACAGTGTGAAAAATGCTCAAAAAAGCA
AAAAAGTTTCAAGATATAAAGAAGAGGTCTGGCTGCAGCATGTACCCAGTACAACATTCAAAAGTGGAA
ATACAGTGATACTGACTTTCAATCCCAGAAAAGTCTTTTATATGATCATGAAAAATGCCAGCACTCTTATT
TTAACTCTACTTCCAAGGATGTTCTGTCAAACCTAGTCATGATTTCTAGAGGCAAGAATCATACAAAA
TGTCAGACAAGCTCAAAGGTAACAATTATGAATCTGATGTTGAATTAACCAAAAAATTTCCCATGGAAAA
GAATCAAGATGTATGTGCTTTAAATGAAAATTAAAAAACGTTGAGCTGTTGCCACCTGAAAAATACATG
AGAGTAGCATCACCTTCAAGAAAGGTACAATTAACCAAAAACACAATCTAAGAGTAATCAAAAAAATC
AAGAAGAACTACTTCAATTTCAAAAAAATCACTGTCAATCCAGACTCTGAAGAATTTTCTCAGACATGA
GAATAATTTTGTCTTCCAAGTAGCTAATGAAAGGAATAATCTTGTCTTAGGAAATACTAAGGAATTCAT
GAAACAGACTTGACTTGTGTAACGAACCCATTTTCAAGAATCTACCATGGTTTTATATGGAGACACAG
GTGATAAAACAAGCAACCAAGTGTCAATTAAAAAAGATTTGGTTTATGTTCTTGCAGAGGAGAACAAAA
TAGTGTAAAGCAGCATATAAAAAATGACTCTAGGTCAAGATTTAAATCGGACATCTCCTTGAATATAGAT
AAAATACCAGAAAAAATAATGATTACATGAACAAATGGGCAGGACTCTTAGGTCCAATTTCAAATCACA
GTTTTGGAGGTAGCTTCAAGACAGCTTCAAATAAGGAAATCAAGCTCTCTGAACATAACATTAAGAAGAG
CAAAATGTTCTTCAAAGATATTGAAGAACAATATCCTACTAGTTTAGCTTGTGTTGAAATGTAATACC
TTGGCATTAGATAATCAAAAGAACTGAGCAAGCCTCAGTCAATTAATACTGTATCTGCACATTTACAGA
GTAGTGTAGTTGTTTCTGATTGTAAAAATAGTCATATAACCCCTCAGATGTTATTTTCCAAGCAGGATTT
TAATTCAAACCATAATTTAACACCTAGCCAAAAGGCAGAAATTACAGAATTTTCTACTATATTAGAAGAA
TCAGGAAGTCAAGTTGAAATTTACTCAGTTTAGAAAACCAAGCTACATATTGCAGAAGAGTACATTTGAAG
TGCTGAAAACAGATGACTATCTTAAAGACCCTTCTGAGGAATGCAGAGATGCTGATCTTTCATGTCAT
AATGAATGCCCATCGATTGGTCAGGTAGACAGCAGCAAGCAATTTGAAGGTACAGTTGAAATTAACGG
AAGTTTGTGCTGGCCTGTTGAAAAATGACTGTAACAAAAGTCTTCTGGTTATTTAACAGATGAAAAATGAAG
TGGGGTTTAGGGCTTTTATTCTGCTCATGGCACAAAACCTGAATGTTTCTACTGAAGCTCTGCAAAAAGC
TGTGAAACTGTTTAGTGATATTGAGAATATTAGTGAGGAACTCTGCAGAGGTACATCCAATAAGTTTA
TCTTCAAGTAAATGTCATGATTCTGTTGTTCAATGTTTAAAGATGAAAAATCATAATGATAAACTGTAA
GTGAAAAAATAATAATGCCAACTGATATTACAAAATAAATTTGAAATGACTACTGGCACTTTTGTGGA
AGAAATTAAGTAAAAATCAAGAGAAATGACTGAAAATGAAGATAACAAATATACTGCTGCCAGTAGAAAT
TCTCATAACTTAGAATTTGATGGCAGTGATTCAAGTAAAAATGATACTGTTTGTATTATAAAGATGAAA
CGGACTTGCTATTTACTGATCAGCACAACATATGTCTTAAATTAATCTGGCCAGTTTATGAAGGAGGGAAA

CACTCAGATTAAGAAGATTTGTGAGATTTAACTTTTTGGAAGTTGCGAAAGCTCAAGAAGCATGTCAT
 GGTAATACTTCAATAAAGAACAGTTAACTGCTACTAAAACGGAGCAAAATATAAAGATTTTGAGACTT
 CTGATACATTTTTTTCAGACTGCAAGTGGGAAAAATATTAGTGTGCGCCAAAGAGTCATTTAATAAAATTTG
 AAATTTCTTTGATCAGAAACCAGAAGAAATGCATAACTTTTCTTAAATTTCTGAATTACATTCTGACATA
 AGAAAGAACAAAATGGACATTCTAAGTTATGAGGAAACAGACATAGTTAAACACAAAATCTGAAAGAAA
 GTGTCCAGTTGGTACTGGAAATCAACTAGTGACCTCCAGGGACAACCCGAACGTGATGAAAAGATCAA
 AGAACCTACTCTATTGGGTTTTTCATACAGCTAGCGGGAAAAAAGTTAAATTTGCAAAGGAATCTTTGGAC
 AAAGTGAAAAACCTTTTTGATGAAAAAGCAAGGTAAGTAAATCACCAGTTTTAGCCATCAATGGG
 CAAAGACCCTAAAGTACAGAGAGGCTGTAAAGACCTGAATTAGCATGTGAGACCATTGAGATCACAGC
 TGCCCCAAAGTGTAAAGAAATGCAGAATTCTCTCAATAATGATAAAAACTTGTTTCTATTGAGACTGTG
 GTGCCACCTAAGCTCTAAGTGATAATTTATGTAGACAACTGAAAATCTCAAAACATCAAAAAGTATCT
 TTTTGAAGTTAAAGTACATGAAAATGTAGAAAAAGAACAGCAAAAAGTCTGCAACTTGTACACAAA
 TCAGTCCCCTTATTCAGTCATTGAAAATTCAGCCTTAGCTTTTTACACAAGTTGTAGTAGAAAACTTCT
 GTGAGTCAGACTTCATTACTGGAAGCAAAAAATGGCTTAGAGAAGGAATATTTGATGGTCAACCAGAAA
 GAATAAATACTGCAGATTATGTAGGAAATTTTGTATGAAAATAATTCAAACAGTACTATAGCTGAAAA
 TGACAAAAATCATCTCTCCGAAAAACAAGATACTTATTTAAGTAAACAGTAGCATGTCTAACAGCTATTCC
 TACCATTCTGATGAGGTATATAATGATTCAGGATATCTCTCAAAAAATAAACTTGATTCTGGTATTGAGC
 CAGTATTGAAGAATGTTGAAGATCAAAAAACACTAGTTTTTCCAAAGTAAATCCAATGTAAGAGATGC
 AAATGCATACCCACAACTGTAATGAAGATAATTTGCGTTGAGGAACTTGTGACTAGCTCTTACCCTGC
 AAAAAATAAAATGCAGCCATTAATTTGCCATATCTAATAGTAATAATTTTGGAGTAGGGCCACCTGCAT
 TTAGGATAGCCAGTGGTAAATCGTTTGTGTTTCATGAAACAATTAAGAAAGTAAAGACATATTTAC
 AGACAGTTTCAGTAAAGTAATTAAGGAAAAACAGGAGAATAAATCAAAAAATTTGCCAAACGAAAATATG
 GCAGTTGTTACGAGGCATTGGATGATTCAGAGGATATCTTCATAACTCTAGATAAGTAAAGTGA
 GCACGCATTCACATAAGGTTTTTGTGACATTCAGAGTGAAGAATTTTACAACATAACCAAAATATGTC
 TGGATTGGAGAAAGTTTCTAAAAATACCTTGTGATGTTAGTTTGGAACTTCAGATATATGAAATGT
 AGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGAA
 AATCTGTCCAGGTATCAGATGCTTATTACAAAACGCAAGACAAGTGTCTTGAATAGAAAGTAGTAC
 CAAGCAAGTCTTTTCCAAAGTATTGTTTAAAAGTAACGAACATTCAGACCAGCTCACAAGAGAAGAAAAT
 ACTGCTATACGTACTCCAGAACATTTAATATCCAAAAAGGCTTTTATATAATGTGGTAAATTCATCTG
 CTTTCTCTGGATTTAGTACAGCAAGTGGAAAGCAAGTTCCATTTTGAAGGTTCTTACACAAAGTTAA
 GGGAGTGTAGAGGAATTTGATTTAATCAGAAGTGGAGTATGCTTCACTATTCACCTACGTCTAGACAA
 AATGTATCAAAAAATCTCCTCGTGTGATAAGAGAAACCCAGAGCACTGTGAAACTCAGAAATGGAAA
 AAACCTGCAGTAAAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTCTTCAGAAAAATATCA
 CTCTATTAAGGTTTCTCCATATCTCTCAATTTCAACAAGACAAAACAACAGTTGGTATTAGGAACCAAA
 GTGTCACTTGTGAGAACATTCATGTTTTGGGAAAAAGAACAGGCTTCACTAAAAACGTAATAATGGAAA
 TTGGTAAAACGAACTTTTTCTGATGTTTCTGTGAAAACAAATAGAAAGTTTGTCTACTTACTCCAA
 AGATTCAGAAAACACTTTGAAACAGAAGCAGTAGAAATGCTAAAGCTTTTATGGAAGATGATGAAGT
 ACAGATCTAAACTGCCAAGTCATGCCACATTTCTTTTTACATGTCCGAAAATGAGGAAATGGTTT
 TGTCAAATCAAGAATTGGAAAAAGAAGAGGAGAGCCCTTATCTTAGTGGGAGAACCCCAATCAAAAAG
 AAACCTTAAATGAATTTGACAGGATAATAGAAAAATCAAGAAAAATCCTTAAAGGCTTCAAAAAGCACT
 CCAGATGGCACATAAAAAGATCGAAGATTGTTTATGCATCATGTTTCTTTAGAGCCGATTACCTGTGTAC
 CCTTTCGCACAACATAAGGAACGTCAAGAGATACAGAAATCCAAATTTTACCACCTGGTCAAGAAATTTCT
 GTCTAAATCTCATTTGTATGAACATCTGACTTTGGAAAAATCTTCAAGCAATTTAGCAGTTTTCAGGACAT
 CCATTTTATCAAGTTTCTGCTACAAGAAATGAAAAATGAGACACTTGATTACTACAGGCAGACCAACCA
 AAGTCTTTGTTCCACCTTTTAAACTAAATCACATTTTACAGAGTTGAACAGTGTGTTAGGAATATTA
 CTTGGAGGAAAACAGACAAAAGCAAAACATTGATGGACATGGCTCTGATGATAGTAAAAATAAGATTAAT
 GACAATGAGATTCATCAGTTTAACAAAAACAACCTCAATCAAGCAGCAGCTGAACTTTACAAAAGTGTG
 AAGAAGAACCTTTAGATTTAATTACAAGTCTTCAAGATGCCAGAGATATACAGGATATGCGAATTAAGAA
 GAAACAAGGCAACGCGTCTTTCCACAGCCAGGCACTGTATCTTGAAAAACATCCACTCTGCCTCGA
 ATCTCTCTGAAAGCAGCAGTAGGAGGCCAAGTTCCCTCTGCGTGTCTCATAAACAGCTGTATACGTATG
 GCGTTTCTAAACATTGCATAAAAATTAACAGCAAAAATGCAGAGTCTTTTTCAGTTTACACTGAAGATTA
 TTTTGGTAAGGAAAGTTTATGGACTGAAAAAGGAATACAGTTGGCTGATGGTGGATGGCTCATACCTCC

AATGATGGAAAGGCTGGAAAAGAAGAATTTTATAGGGCTCTGTGTGACACTCCAGGTGTGGATCCAAAGC
 TTATTTCTAGAATTTGGGTTTATAATCACTATAGATGGATCATATGAAACTGGCAGCTATGGAATGTGC
 CTTTCCTAAGGAATTTGCTAATAGATGCCTAAGCCCAGAAAGGGTGTCTTCAACTAAAATACAGATAT
 GATACGGAAATGATAGAAGCAGAAGATCGGCTATAAAAAAGATAATGAAAGGGATGACACAGCTGCAA
 AAACACTTGTCTCTGTGTTTCTGACATAATTTCACTGAGCGCAAATATATCTGAAACTTCTAGCAATAA
 AACTAGTAGTCAGATACCCAAAAAGTGGCCATTATTGAACTTACAGATGGGTGGTATGCTGTAAAGGCC
 CAGTTAGATCCTCCCCTTCTAGCTGTCTTAAAGAATGGCAGACTGACAGTTGGTCAGAAGATTATCTTTC
 ATGGAGCAGAACTGGTGGGCTCCTGATGCCTGTACACCTCTTGAAGCCCAGAACTCTTATGTTAAA
 GATTTCTGCTAACAGTACTCGGCCTGCTCGCTGGTATACCAAACCTGGATTCTTCTGACCCTAGACCT
 TTTCTCTGCCCTTATCATCGCTTTTCACTGATGGAGGAAATGTTGGTTGTGTTGATGTAATTATTCAAA
 GAGCATACCCTATACAGTGGATGGAGAAGACATCATCTGGATTATACATATTTGCAATGAAAGAGAGGA
 AGAAAAGGAAGCAGCAAAATATGTGGAGGCCAACAAAAGAGACTAGAAGCCTTATCTACTAAAATTCAG
 GAGGAATTTGAAGAACATGAAGAAAACACAACAAAACCATATTTACCATCACGTGCACTAACAGACAGC
 AAGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCAGCTTACCT
 TGAGGGTTATTTCACTGAAGAGCAGTTAAGAGCCTTGAATAATCACAGGCAAATGTTGAATGATAAGAAA
 CAAGCTCAGATCCAGTTGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAGGAACAAGGTTTATCAA
 GGGATGTCACAACCGTGTGGAAGTTGCGTATTGTAAGCTATTCAAAAAAGAAAAGATTCACTTATACT
 GAGTATTTGGCGTCCATCATCAGATTTATTTCTGTAAACAGAAGGAAAGAGATACAGAATTTATCAT
 CTTGCAACTTCAAATCTAAAAGTAAATCTGAAAGAGCTAACATACAGTTAGCAGCGACAAAAAACTC
 AGTATCAACAACCTACCGTTTCAGATGAAATTTATTTCACTTTACCAGCCACGGGAGCCCTTCACTT
 CAGCAAATTTTATAGATCCAGACTTTTCAAGCATCTTGTCTGAGGTGGACCTAATAGGATTTGCTGTTTCT
 GTTGTGAAAAAACAGGACTTGGCCCTTTCGTCTATTTGTCAGACGAATGTTACAATTTACTGGCAATAA
 AGTTTGGATAGACTTAATGAGGACATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAGTG
 GCGTCCAGAACTCAAATCAGGCCTTCTACTTTATTTGCTGGAGATTTTCTGTGTTTTCTGCTAGTCCA
 AAAGAGGGCCACTTTCAAGAGACATTCAACAAAATGAAAAACTGTTGAGAATATTGACATACTTTGCA
 ATGAAGCAGAAAAAAGCTTATGCATATACTGCATGCAATGATCCCAAGTGGTCCACCCCAACTAAAGA
 CTGTACTTCAGGGCCGTACACTGCTCAAATCATCCTGGTACAGGAAACAAGCTTCTGATGTCTTCTCCT
 AATTGTGAGATATATTATCAAAGTCTTTATCACTTTGTATGGCCAAAAGGAAGTCTGTTTCCACACCTG
 TCTCAGCCAGATGACTTCAAAGTCTTGTAAAGGGGAGAAAGAGATTGATGACCAAAAAGAACTGCAAAA
 GAGAAGAGCCTTGGATTTCTTGAGTAGACTGCCTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTT
 TCTCCGGCTGCACAGAAGGCATTTCAAGCCCAAGGAGTTGTGGCACCATAACGAAACCCCATAAAGA
 AAAAAGAACTGAATTCCTCAGATGACTCCATTTAAAAAATCAATGAAATTTCTTTTGGAAAGTAA
 TTCAATAGCTGACGAAGAACTTGCATTGATAAATACCCAAGCTCTTTTGTCTGGTTCAACAGGAGAAAA
 CAATTTATATCTGTCAGTGAATCCACTAGGACTGCTCCCACAGTTTCAAGAAGATTATCTCAGACTGAAAC
 GACGTTGACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAA
 TAAGCAGGACACAATTACAATAAAAAATATATC

AGCGGACCCACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

Protein Sequence:

>RC400500 representing NM_000059

Red=Cloning site Green=Tags(s)

MPIGSKERPTFFEIFKTRCNKADLGPISLWNFEELSSEAPPCNSEPAEESHKNNNYEPNLFKTPQRKPS
 YNQLASTPIIFKEQGLTLPYQSPVKELDKFKLDLGRNVPNSRHKSLRTVTKMDQADDVSCPLLNLSCLS
 ESPVVLQCTHVTPQRDKSVVCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSVTLI
 VRNEEASETVPFHDTTANVKSIFYSNHDESLKKNDRFIA SVTDSSENTNQREAAASHGFGKTSNGNSFKVNSCK
 DHIGKSMPNVLEDEVYETVVDTSEEDSFLCFSKCRTKNLQKVRTSKTRKKIFHEANADECEKSNQVKE
 KYSFVSEVEPNDDPLDSNVANQKPFESGSDKISKEVVP SLACEWSQLTSLGLNGAQMEKIPLLHISDCD
 QNISEKDLLDTENKRKKDFLTSNSLPRISLSEKPLNEETVVNKRDEEQHLESHTDCILAVKQAIISG
 TSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDPNFKKETEASESGLEIHTVCSQKEDSLCPNLIDN
 GSWPATTTQNSVALKNAGLISTLKKTKNFYIAIHDETSYKGGKIPKDQKSELINCSAQFEANAFEAPLT
 FANADSGLLHSSVKRSCSQNDSEPTLSLTSSFGTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQL

FITPEADSL SCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQSLLYDHENASTLI
 LTPTSKDVL SNLVMISRGKESYKMSDKLKGNNYSDVELTKNIPMEKNQDVCALNENYKNVELLPPEKYM
 RVASPSRKVQFNQNTNLRVIQKNQEETTSISKITVNPDSEELFSDNENNFVFQVANERNLALGNTKELH
 ETDLTCVNEPIFKNSTMVL YGDTGDKQATQVSIKKDLVYVLAENKNSVKQHIKMTLGQDLKSDISLNDI
 KIPEKNNDYMNKWAGLLGPI SNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIIEEQYPTSLACVEIVNT
 LALDNQKLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHLTPSQKAEITELSTILEE
 SGSQFEFTQFRKPSYILQKSTFEVPENQMTILKTTSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKR
 KFAGLLKNDCKNSASGYLTDENEVGRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETSAEVHPISL
 SSSKCHDSVVSVMFKIENHNDKTVSEKNKNCQLILQNNIEMTTGTFVVEITENYKRNTENEDNKYTAASRN
 SHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKL SGQFMKEGNTQIKEDLSLTFLEVAKAQEACH
 GNTSNKEQLTATKTEQNIKFETSDTFFQTASGKNISVAKESFNKIVNFFDQKPEELHNFSLNSELHSDI
 RKNKMDILSYEETDIVKHKILKESVPGTGNQLVTFQGGPERDEKIKEPTLLGFHTASGKVKIAKESLD
 KVKNLFDEKEQGTSEITSFHQWAKTLKYREACKDLELACETIEITAAPKCKEMQNSLNNDKNLVSIETV
 VPPKLLSDNLCRQNTENLKTSSIFLKVKHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCRKTS
 VSQTSLL EAKKWLREGIFDQPERINTADYVGNLYENNSNSTIAENDKNHLSEKQD TYLSNSSMSNSYS
 YHSDEVYNDSGYL SKNKLDSGIEPVLKNVEDQKNTSF SKVISNVKDANAYPQTVNEDICVEELVTSSSPC
 KNKNAAIKLSISNSNFEVGPFAFRIASGKIVCVSHETIKKVKDIFTDSFSKVIKENNENKSKICQTKIM
 AGCYEALDDESEDILHNSLDNDECSTHSHKVFADIQSEEILQHNQNMGLEKYSKISPCDVSLETSDICKC
 SIGKLGKSVSSANTCGIFSTASGKSVQVSDASLQARQVFSEIEDSTKQVFSKVLFKSNEHSDQLTREEN
 TAIRTPPEHLISQKGFYNVNVSSAFSGFSTASGKQVSILESSLHKVKGVL EEFDLIRTEHSLHYSPTS RQ
 NVSKILPRVDKRNPEHCVNSEMEKTCSEKFKLSNNLNVEGGSSENNHSIKVSPYL SQFQDKQQLVLGTK
 VSLVENIHVLGKEQASPKNVKMEIGKTETTFSDVPVKTNIEVCSTYSKDSENYFETEAVEIAKAFMEDDEL
 TDSKLP SHATHSLFTCPENEEMVLSNSRIGKRRGEPLILVGEPSIKRNLNNEFDRIENQEKSLKASKST
 PDGTIKDRRLFMHHSLEPITCVPFRTTKERQEIQNPNFTAPGQEFLSKSHLYEHLTLEKSSSNLAVSGH
 PFYQVSA TRNEKMRHLITTRPTKVFVPPFKTKSHFHRVEQCVRNINLEENRQKQNDIGHGSDSKNKIN
 DNEIHQFNKNSNQAAAVTFTKCEEEPLDLITSLQNARDIQDMRIKKKQRQRFVFPQPSGLYLAKTSTLPR
 ISLKAAVGGQVPSACSHKQLYTYGVSKHCIKINSKNAESFQFHTEDYFGKESLWTGKGIQLADGGWLIPS
 NDGKAGKEEFYRALCDTPGVDPKLSRIWVYNHYRWIIWKLAAAMECAFPEFANRCLSPERVLLQLKYRY
 DTEIDRSRRSAIKKIMERDDTAAKTLVLCVSDIISLSANISETSSNKTSSADTQKVAIIELTDGWYAVKA
 QLDPPLLAVLKNGR LTVGQKIILHGAELVGSPDACTPLEAPESLMLKISANSTRPARWYTKLGFDPDRP
 FPLPLSSLFSDGGNVGCVDVIIQRAYPIQWMEKTS SGLYIFRNEREEEEKA AKYVEAQQKRL EALFTKIQ
 EEFEEHEENTTKPYLPSRALTRQQVRALQDGAELYEAVKNAADPAYLEGYFSEEQLRALNNHRQMLNDKK
 QAQIQLEIRKAMESAEQKEQGLSRDVTTVWKLRIVSYSKKEKDSVILSIWRPSSDLYSLLTEGKRYRIYH
 LATSKSKSERANIQLAATKTKYQQLPVSDEILFQIYQPREPLHFSKFLDPDFQPSCSEVDLIGFVVS
 VVKKTGLAPFVYL SDECYNLLAIKFWIDLNEDI IKPHMLIAASNLQWRPESKSGLLTLFAGDFSVFSASP
 KEGHFQETFNKMKNTVENIDILCNEAENKLMHILHANDPKWSTPTKDC TSGPYTAQIIPGTGNKLLMSSP
 NCEIYYQSPLSLCMAKRKSVSTPVSAQMTSKSCKGEKEID DQKNCKRRALDFL SRLPLPPPVPSPICTFV
 SPAAQKAFQPPRSCGTYETPIKKKELNSPQMTPFKFFNEISLLESNSIADEELALINTQALLSGSTGEK
 QFISVSESTRAPTSSDYLR LKRRCTTSLIKEQESSQASTECEKKNKQDTITTKKYI

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]