



## LRRK2

Expressed:

**Flag LRRK2 C727D D2017A**

Plasmid:

**pCMV5 Flag LRRK2 C727D D2017A**

Parent Plasmid:

**pCMV5 FLAG**

DU Number:

**DU27085**

Species:

**Human**

Synonyms:

Sequence of Insert:

**GGATCCATGGCTAGTGGCAGCTGTCAGGGGTGCGAAGAGGACGAGGAAACTCTGAAGAAGTTG  
ATAGTCAGGCTGAACAATGTCCAGGAAGGAAAACAGATAGAAACGCTGGTCCAAATCCTGGAG  
GATCTGCTGGTGTTCACGTA CTCCGAGCACGCCTCCAAGTTATTTCAAGGCAAAAATATCCATGT  
GCCTCTGTTGATCGTCTTGGACTCCTATATGAGAGTCGCGAGTGTGCAGCAGGTGGGTTGGTCA  
CTTCTGTGCAAATTAATAGAAGTCTGTCCAGGTACAATGCAAAGCTTAATGGGACCCCAGGATG  
TTGGAAATGATTGGGAAGTCCTTGGTGTTACCAATTGATTCTTAAAATGCTAACAGTTCATAAT  
GCCAGTGTA AACTTGT CAGTGATTGGACTGAAGACCTTAGATCTCCTCCTAACTTCAGGTA AAT  
CACCTTGCTGATATTGGATGAAGAAAGTGATATTTTCATGTTAATTTTTGATGCCATGCACTCATT  
TCCAGCCAATGATGAAGTCCAGAACTTGGATGCAAAGCTTTACATGTGCTGTTTGAGAGAGTCT  
CAGAGGAGCAACTGACTGAATTTGTTGAGAACA AAGATTATATGATATTGTTAAGTGC GTTAACA  
AATTTTAAAGATGAAGAGGAAATTGTGCTTCATGTGCTGCATTGTTTACATTCCCTAGCGATTCT  
TGCAATAATGTGGAAGTCCTCATGAGTGGCAATGTCAGGTGTTATAATATTGTGGTGGAAAGCTAT  
GAAAGCATTCCCTATGAGTGAAGAATTCAAGAAGTGAGTTGCTGTTTGCTCCATAGGCTTACAT  
TAGGTAATTTTTCAATATCCTGGTATTAACGAAGTCCATGAGTTTGTGGTGA AAGCTGTGCAG  
CAGTACCAGAGAATGCAGCATTGCAGATCTCAGCGCTCAGCTGTTTGGCCCTCCTCACTGAGA  
CTATTTTCTTAAATCAAGATTTAGAGGAAAAGAATGAGAATCAAGAGAATGATGATGAGGGGGA  
AGAAGATAAATTGTTTTGGCTGGAAGCCTGTTACAAAGCATTAACTGATGAGGAGGAGGAGGAG  
CAGTGCAGGAGGCCGCATGCTGGGCACTAAATAATCTCCTTATGTACCAAACAGTTTACATG  
AGAAGATTGGAGATGAAGATGGCCATTTCCAGCTCATAGGGAAGTGATGCTCTCCATGCTGAT  
GCATTCTTCATCAAAGGAAGTTTTCCAGGCATCTGCGAATGCATTGTCAACTCTCTTAGAACAAA  
ATGTTAATTTAGAAAATACTGTTATCAAAGGAATACACCTGAATGTTTTGGAGTTAATGCAG  
AAGCATATACATTCTCCTGAAGTGGCTGAAAGTGGCTGTAAAATGCTAAATCATCTTTTTGAAGG  
AAGCAACTTCCCTGGATATAATGGCAGCAGTGGTCCCCAAAATACTAACAGTTATGAAACGT  
CATGAGACATCATTACCAGTGCAGCTGGAGGCGCTTCGAGCTATTTTACATTTTATAGTGCCTGG  
CATGCCAGAAGAATCCAGGGAGGATACAGAATTTATCATAAGCTAAATATGGTTAAAAAACAG  
TGTTTCAAGAATGATATTCACAAACTGGTCCTAGCAGCTTTGAACAGGTTTCATTGGAAATCCTGG  
GATTCAGAAATGTGGATTA AAGTAATTTCTTCTATTGTACATTTTCTGATGCATTAGAGATGTT**

ATCCCTGGAAGGTGCTATGGATTCAAGTCTTACACACTGCAGATGTATCCAGATGACCAAGAA  
ATTCAGTGTCTGGGTTAAGTCTTATAGGATACTTGATTACAAAGAAGAATGTGTTTCATAGGAAC  
TGGACATCTGCTGGCAAAAATTCTGGTTCCAGCTTATACCGATTTAAGGATGTTGCTGAAATAC  
AGACTAAAGGATTTTCAGACAATCTTAGCAATCCTCAAATTGTCAGCATCTTTTTCTAAGCTGCTG  
GTGCATCATTCAATTTGACTTAGTAATATTCCATCAAATGTCTTCCAATATCATGGAACAAAAGGAT  
CAACAGTTTCTAAACCTCTGTTGCAAGTGTGTTGCAAAAAGTAGCTATGGATGATTACTTAAAAAAT  
GTGATGCTAGAGAGAGCGTGTGATCAGAATAACAGCATCATGGTTGAAGACTTGCTTCTATTGG  
GAGCAGATGCCAATCAAGCAAAGGAGGGATCTTCTTTAATTTGTCAGGTATGTGAGAAAAGAGAG  
CAGTCCCAAATTGGTGGAACTCTTACTGAATAGTGGATCTCGTGAACAAGATGTACGAAAAGCG  
TTGACGATAAGCATTGGGAAAGGTGACAGCCAGATCATCAGCTTGCTCTTAAGGAGGCTGGCCC  
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CTTGGTCTTTATTTCCAGATAAGACTTCTAATTTAAGGAAACAAACAATATAGCATCTACACTA  
GCAAGAATGGTGTATCAGATATCAGATGAAAAGTGTGTGGAAGAAGGAACAGCCTCAGGCAGC  
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ATGGACAGTGTGTTTGTCAAAGTGTGACCTGGATAGTGAAGGAAGTGAAGGCTCATTCTTGT  
GAAAAGAAATCTAATCAATTAGTGTAGGAGAATTTTACCGAGATGCCGTATTACAGCGTTGCT  
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ATAGGAGAAGAATATTTGCTGGTTCCAAGCAGTTTGTCTGACCACAGGCCTGTGATAGAGCTTC  
CCCATTGTGAGAAGTCTGAAATTATCATCCGACTATATGAAATGCCTTATTTTCCAATGGGATTTT  
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CATCACAAACAGCAGGAATGCAAGCATTGGCTGGGCTGTGGGCACACCGACAGAGGACAGCTC  
TCATTTCTTGACTTAAATACTGAAGGATACACTTCTGAGGAAGTTGCTGATAGTAGAATATTGTG  
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CTCTCCTGGTCATCAATACCGAAGATGGGAAAAGAGACATACCCTAGAAAAGATGACTGATTC  
TGTCACTTGTGTTGATTGCAATTCCTTTTCCAAGCAAAGCAAACAAAAAATTTTCTTTTGGTTGG  
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TGAAGATACTAAATATAGGAAATGTCAGTACTCCATTGATGTGTTTGAGTGAATCCACAAATTCA  
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CATTCAGAACTCATTGAGACAAGAACAAGCCAAGTCTTTTCTTATGCAGCTTTTCAAGTATTCCA  
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GTGTGGGATAAGAAAACCTGAAAACCTCTGTGGACTAATAGACTGCGTGCACCTTTTAAAGGGAGG  
TAATGGTAAAAGAAAACAAGGAATCAAACACAAAATGTCTTATTCTGGGAGAGTGAAAACCTT  
CTGCCTTCAGAAGAACTGCTCTTTGGATAGGAACTGGAGGAGGCCATTTTTACTCCTGGATC  
TTTCAACTCGTCGACTTATACGTGTAATTTACAACCTTTTGTAAATTCGGTCAGAGTCATGATGACAG  
CACAGCTAGGAAGCCTTAAAAATGTCATGCTGGTATTGGGCTACAACCGGAAAATACTGAAGG  
TACACAAAAGCAGAAAGAGATACAATCTTGCTTGACCGTTTGGGACATCAATCTTCCACATGAA  
GTGCAAAATTTAGAAAACACATTGAAGTGAGAAAAGAATTAGCTGAAAAAATGAGACGAACAT  
CTGTTGAGTAAGAGAGAAATAGGCGGCCGCG

Amino Acid Sequence:

MDYKDDDDKGSMSAGSCQGCCEEDLTKKLVRLNNVQEGKQIETLVQILEDLLVFTYSEHASKLFG  
GKNIHVPLLVDSYMRVASVQVGVWSLLCKLIEVCPGTMQSLMGPQDVGNWVGLGVHQLILKMLT  
VHNASVNLVIGLKTLDLLTSGKITLLILDEESDIFMLIFDAMHSFPANDEVQKLGCKALHVLFERVSE  
EQLTEFVENKDYMILLSALTNFKDEEIVLHVLHCLHSLAIPCNNVEVLMMSGNVRVYNIVVEAMKAFPM  
SERIQEVSCLLHRLTLGNFFNILVLNEVHEFVVKAVQQYPENAALQISALSCLALLTETIFLNQDLEEK  
NENQENDDEGEEDKLFWLEACYKALTWHRKNKHVQEAACWALNLLMYQNSLHEKIGDEDGHFPA  
HREVMLSMLMHSSSKEVFQASANALSTLLEQNVNFRKILLSKGIHLNVLELMQKHIHSPEVAESGCK  
MLNHLFEFSNTSLDIMA AVVPKIL TVMKRHETSLPVQLEALRAILHFIVPGMPEESREDTEFHKLNMV  
KKQCFKNDIHKLVLAALNRFIGNPGIQKCGLKVIVSSIVHFPDALEMLSLEGAMDSVHLTLQMYPPDDQEI  
QCLGLSLIGYLITKKNVFIGTGHLLAKILVSSLYRFKDVAEIQTKGFQTLAILKLSASFSLKLVHHSFDL  
VIFHQSSNIMEQKQDQFLNLCCKCFKAVMDDYLKNVMLERACDQNSIMVEDLLLLGADANQAK  
EGSSLICQVCEKESPCLVELLLNSGSREQDVRKALTISIGKGDSSQIISLLRRLALDVANNSICLGGFC  
IGKVEPSWLGPLFPDKTSNLRKQTNIASTLARMVIRYQMKSAVEEGTAGSDGNFSEDVLSKFDEWT  
FIPDSSMDSVFAQSDDL DSEGSEGSFLVKKKSNSISVGEFYRDAVLQRCSPLQRHSNSLGPFDHED  
LLKRKRKILSSDDSLRSSKLQSHMRHSDSISSLASEREYITSLDLSANELRDIDALSQKCCISVHLEHL

EKLELHQNALTSFPQQLCETLKSLTHLDLHSNKFTSFPSYLLKMSCIANLDVSRNDIGPSVVDPTVK  
CPTLKQFNLSYNQLSFVPENLTDVVEKLEQLILEGNKISGICSPRLKELKILNLSKNHISSLSENFLEA  
CPKVESFSARMNFLAAMPFLPPSMTILKLSQNKFSCICEAILNPLHLRSLDMSSNDIQYLPGPAHWKS  
LNLRELLFSHNQISILDSEKAYLWSRVEKHLHSHNKLKEIPPEIGCLENLTSLDVSYNLELRSFPNEM  
GKLSKIWDLPLDELHLNFDKFKHIGCKAKDIIRFLQQRLKKAVPYNRMKLMIVGNTGSGKTTLLQQLMK  
TKKSDLGMQSATVGDVVDWPIQIRDKRKRDLVLNVWDFAGREEFYSTHPHFMTRALYLAVYDLSK  
GQAEVDAMKPWLFNIKARASSSPVILVGTHLDVSDEKQRKACMSKITKELLNKRGFPAIRDYHFVNA  
TEESDALAKLRKTIINESLNFKIRDQLVVGQLIPDCYVELEKIILSERKNVPIEFPVIDRKRLQLVRENQ  
LQLDENELPHAVHFLNESGVLLHFQDPALQLSDLYFVEPKWLCKIMAQILTVKVEGCPKHPKGIISRR  
DVEKFLSKKRKFPKNYMTQYFKLLEKFQIALPIGEEYLLVPSSLSDHRPVIELPHCENSEIIIRLYEMPYF  
PMGFWSRLINRLLLEISPYMLSGRERLRPNRMWYRQGIYLNWSPEAYCLVGSEVLDNHPESFLKITV  
PSCRKGCILLGQVVDHIDSLMEEWFPGLLEIDICGEGETLLKKWALYSFNDGEEHQKILLDDLMKKA  
EGDLLVNPDPQRLTIPISQIAPDLILADLPRNIMLNDELEFEQAPEFLLGDGSGSVYRAAYEGEEVA  
VKIFNKHTSLRLLRQELVVLCHLHPSLISLLAAGIRPRMLVMELASKGSLDRLLQQDKASLTRLQH  
RIALHVADGLRYLHSAMIYRDLKPHNVLLFTLYPNAIIAKIAAYGIAQYCCRMGIKTSEGTGPFRAPE  
VARGNVIYNQQADVYSFGLLLYDILTTGGRIVEGLKFPNEFDELEIQGKLPDPVKEYGCAPWPMVEKLI  
KQCLKENPQERPTSAQVFDILNSAELVCLTRRILLPKNVIVECMVATHHNSRNASIWLGCGHTRGQL  
SFLDLNTEGYTSEEVADSRILCLALVHLPVEKESWIVSGTQSGTLLVINTEDGKKRHTLEKMTDSVTCL  
YCNSFSKQSKQKNFLLVGTADGKLAIFEDKTVKLGAAPLKILNIGNVSTPLMCLSESTNSTERNVMW  
GGCGTKIFSFSNDFTIQKLIETRSTQLFSYAAFSDSNITVVVDTALYIAKQNSPVVEVWDDKTEKLCGLI  
DCVHFLREVMVKENKESKHKMSYSGRVKTLCQKNTALWIGTGGGHILLDLSTRRLIRVIYNFCNSV  
RVMMTAQLGSLKNVMLVLGYNRKNTEGTQKQKEIQSCLTVWDINLPHEVQNLEKHIEVRKELAEKM  
RTSVE\*

Antibiotic:

**Amp**

Comments:

**2 silent mutations G1624 K1637 Grow at or below 30°C Contains SNP S1647T**

Price per aliquot:

**£110.00**