



ASK2J00171_PINK1_P399L_D04_BB
 18,054 bp

5'
3'

AGAGGGCACCGCCCCAAGTTTGTGTGACCGGGCGGGGGACGCCGGTGGTGGCGGGCAGCGGGCGGCTGCGGGGGCACCGGGCCGCGGC
TCTCCGTGGCGGGGTTCAAACAACACTGGCCGCCCCCTGCGGCCACCACCGCCGTCGCCGCCGACGCCCCCGTGGCCCGGCGCCG

85

PINK1

PINK1-201

GCCACCATGGCGGTGCGACAGGCGCTGGGCGCGGCCTGCAGCTGGGTGCGAGCGCTGCTGCTGCGCTTCACGGGCAAGCCCGGCC
CGGTGGTACCGCCACGCTGTCCGCGACCCGGCGCCGGACGTGACCCAGCTCGCGACGACGACGCGAAAGTGCCCGTTCGGGCGCGG

170

PINK1

PINK1-201

1 5 10 15 20 25
Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly

ENSE00001465660

PINK1-201

GGGCCTACGGCTTGGGGCGGCCGGGCCCCGGCGGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGCCGCAGGACCGGGCGCGGA
CCCGGATGCCGAACCCCGCCGGGCCGGGCCGCCGCCGACACAGGCGCCCTCGCAGGTCCGACCCGGCGTCTCTGGCCCGCGCCT

255

PINK1

PINK1-201

30 35 40 45 50 55
Arg Ala Tyr Gly Leu Gly Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala Gly Pro Gly Ala Glu

ENSE00001465660

PINK1-201

GCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTTCTTCCGCCAGTCGGTGGCCGGGCTGGCGGGCGCGTTGACAGCGG
CGGAGCGTCCCAGCCGAGCCGAGGGATTGGCAGAGGCGAAGAAGGCGGTACGCCACCGGCCCGACCGCCGCGCCAACGTCGCC

340

PINK1

PINK1-201

60 65 70 75 80
Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg Leu Arg Phe Phe Arg Gly Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln Arg

ENSE00001465660

PINK1-201

CAGTTCGTGGTGGCGGCTGGGGCTGCGCGGGCCCTTGGCGCCGGGCAGTCTTTCTGGCCTTCGGGCTAGGGCTGGGCCTCATCG
GTCAAGCACCACGCCCGGACCCCGACGCGCCCGGGAACGCCGGCCCGTCCAGAAAGACCGGAAGCCCGATCCCGACCCGGAGTAGC

425

PINK1

PINK1-201

85 90 95 100 105 110
Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile

ENSE00001465660

PINK1-201

AGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCAGGTGAGCGGGGCGGGTCCTAAGCCGAGCGGAG
TCCTTTTTGTCCGCTCTCGGCCGCCCGCCAGAGCCGGACAGTCTCTAGGTCCACTCGCCCCGGCCAGGATTCGGCTCGCCTC

510

PINK1

PINK1-201

115 120 125
Glu Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln

ENSE00001465660

PINK1-201

GACGGAGCTAAGCGCGGGGGCGGGTCCCTCAGCTGGGTGGGGGCGGGGCTAGGTGTGGAGGCGGGGCTCTGAGCAGATCGAGGGCC
CTGCCCTCGATTGCGGCCCGCCAGGAGTGCACCCACCCCGCCCGATCCACACCTCCGCCCGGAGACTCGTCTAGCTCCCGG

595

PINK1

PINK1-201

PINK1-201

GAGGCGAGGGTCTTAAAGCTCATCTATTTACCACTACTGATCGGCTGCTATAAATAAAGCCAGCACCTCCCATTTGTTTTAAT
CTCCGCTCCAGGAATTTGAGTAGATAAAGTGGAATGACTAGCCGACGATATTTATTTTCGGTCGTGGAGGGTAAACAAAATTA

680

PINK1

PINK1-201

PINK1-201

GTTTCCCTTCCTCAAATGAAGACATGTTGCCGATTACAGCTCCTGTCGCAGCACAGCAAAGGCTTTGTGTAAATTTTCTAAAAT
CAAAGGGAAGGAGTTTACTTCTGTACAACGGCTAATGTGCGAGGACAGCGTCGTGTCGTTTTCCGAAACACATTTAAAAGATTTTA

765

PINK1

PINK1-201

PINK1-201

GTACGGACAACATAACATTCCTATCCCTTTGAGGTAGTTGCCGTCCCTAATTTATGGAGAAGGAAAGTCCTCAGGTGAA
CATGCCTGTTGATTTAGTATTGTAAGGATAGGGAACTCCATCAACGGCAGGGATTAAATACCTCTTCTTTTCAGGAGTCCACTT

850

PINK1

PINK1-201

PINK1-201

GGGACTTGCTCGAAGTCACACAGCTAATAAAATGCAGTGCCCTTAACCACTGAGCCAGGCTGCCTCCGCCGTTTAACCAAAGGAT
CCCTGAACGAGCTTCAGTGTGTCGATTATTTTACGTACGGGAATTGGTGACTCGGTCCGACGGAGGCGGCAAATTGGTTTCCTA

935

PINK1

PINK1-201

PINK1-201

TAGTAGTGACAGAGCTGAAACCGCAGTAAAACTATGAACGGCGAGAAAAACAGTCCTAACATTTTAGTTACCTGTGTAGAGTTA
ATCATCACTGTCTCGACTTTGGCGTCAATTTTGTACTTTGCCGCTCTTTTTGTGAGGATTGTAATAATCAATGGACACATCTCAAT

1020

PINK1

PINK1-201

PINK1-201

TCCCTGCTGACTGGATACACAAGGGTTCTTAGGGTTTTTAAATGCTTAAATAGCACAAGACTTCTCTTTTTGCCCAACCAAAGT
AGGGACGACTGACCTATGTGTTCCCAAGAATCCCAAAAAATTACGAATTTTATCGTGTTCTGAAGAGAAAAACGGGTTGGTTTCA

1105

PINK1

PINK1-201

PINK1-201

CTGTATTAGGGTTCTCAAATGGAATCAATAGGATGTGTCTATATAGAGGCAGGTTTATTTTGGAGACCTGGCTCCCTATGGGGA
GACATAATCCCAAGAGGTTTACCTTAGTTATCTACACAGATATATCTCCGTCCAAATAAACTCCTGGACCGAGGGATACCCCT

1190

PINK1

PINK1-201

PINK1-201

TTGGCAAAGTCTTAAAAGCCGCAGAGTAGGCCGGGCAGGCTGGAGAGCCAGGGAGGAGCCAGCGGTGCAGTTTCAGGTTTGAAGCCT
AACCgTTTCAGAAATTTTCGGCGTCTCATCCGCCCGTCCGACCTCTCGGTCCCTCCTCGGTTCGCCACGTCAAGTCCAAACTTCGGA

1275

PINK1

PINK1-201

PINK1-201

GGCCGCTGGCAGAATTCCATCTTCTTCCAGGGAGGTCACTCTTCTTCTCGGGGGTGTAGAACCCTCACTAAATTAGCATAGCCC
CCGGCGACCGTCTTAAGGTAGAAGAAGGTCCCTCCAGTGAGAAGAAGGACCCCCACATCTTGGTGAGTGATTTAATCGTATCGGG

1360

PINK1

PINK1-201

PINK1-201

CTGCATTTTACAGGTTAGGGCTGAGGTGGTGGAAAGAGGGAGTGACTTGCCCAAGGACACAGCTGTTAGGGCCAAGCAGTGGCTCC
GACGTAAAATGTCCAATCCCGACTCCACCACCTTCTCCCTCACTGAACGGGTTCTGTGTGCGACAATCCCGGTTTCGTACCCGAGG

1445

PINK1

PINK1-201

PINK1-201

TGGGTTTTCTGGTTTTCCATCCAGTTCTTATTGCTCATCACCCTGTCTCATGTTTGAGCTCTGGCCAGTTTGGGGTGACAGGTG
ACCCAAAGGACCAAAGGTAGGGTCAAGAATAACGAGTAGTGGTGACAGAGTACAAACTCGAGACCGGTCAAACCCCACTGTCCAC

1530

PINK1

PINK1-201

PINK1-201

ACATCTGGCCTAGTCCCCAGCCCCTGACCTTGTCTTTTGCCACAGCTTAACTGGCAGAAGCTAAGGATGGGAAATTTGACTAATC
TGTAGACCGGATCAGGGGTCTGGGGACTGGAACAGAAAACGGTGTGCAATTGACCGTCTTCGATTCTTACCCTTTAAACTGATTAG

1615

PINK1

PINK1-201

PINK1-201

CTGCTTAAACTAAAGAGGCTTTTTTAACTGAGGAGATTGATCCTCCTAACTTACCATTACACACACCTTCTTCGCACACTTC
GACGAATTTTGATTTCTCCGAAAAAATTGACTCCTCTAACTAGGAGGATTTGAATGGTAAGTGTGTGTGGAAGAAGCGTGTGAAG

1700

PINK1

PINK1-201

PINK1-201

ACCCTCCTATGCCTGAAAATGTTATTAGTTATCAATTAATTTACATTAATAAATTTTGGTCAGGCACTGTGGCTCATGC
TGGGAGGATACGGACTTTTACAATAATCAATAGTTAATTAAGTGTAATTTTTTAAAAAACCAGTCCGTGACACCGAGTACG

1785

PINK1

PINK1-201

PINK1-201

CTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCGGATCACGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGGAAACC
GACATTAGGGTCGTGAAACCCCTCCGACTCCGCCCGCCTAGTGCTCCAGTCTCTCAAACCTCTGGTTCGGACCGGTTGTACCACCTTGG

1870

PINK1

PINK1-201

PINK1-201

CTGTCTCTACTAAAAATACAAAAATTACCCGGGCGCAGTGTTGGGCGCCTGTAATCCCAGCTACTTGGGAGACTGAGGCAGGAGA
GACAGAGATGATTTTTATGTTTTTAATGGGCCCGCGTCAACCACCCGCGGACATTAGGGTCGATGAACCCCTCTGACTCCGTCCTCT

1955

PINK1

PINK1-201

PINK1-201

ATTCTTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCTGA
TAAGGAACTTGGGCCCTCCGCCTCCAACGTCACTCGACTCTAGTGCGGTGACGTGAGGTCGGACCCACTGTCTCGTTCTGAGACT

2040

PINK1

PINK1-201

PINK1-201

CTGGGGGGAGAAAAAGTTGTTTTCACTGGCTACTTTTTGCTGGAATTAATTTACATTTAAAAAATTCTGGGCCGGGCGGGGTGGC
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2125

PINK1

PINK1-201

PINK1-201

TCATGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCGGGCGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGT
AGTACGGACATTAGAGTCGTGAAACCCCTCCGGTTCCGCCCGCCTAGTACTCCAGTCTCTAGCTCTGGTAGGACCGATTGTACCA

2210

PINK1

PINK1-201

PINK1-201

GAAACCCCGCCTCTACTAAAAATACAAAAAATTAGCCAGGCATGGTGGCAGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAG
CTTTGGGGCGGAGATGATTTTTATGTTTTTTAATCGGTCCGTACCACCGTCCGCGGACATCAGGGTCGATGAGCCCTCCGACTC

2295

PINK1

PINK1-201

PINK1-201

GCAGGAGAATGGCGTGAACCCGGGAGGCAGGGCTTGCAGTGAGCCAAGATCGCGCCACTGCACTCCAGCCTAGAGGACAGAGTGA
CGTCTCTTACCGCACTTGGGCCCTCCGTCCCGAACGTCACTCGGTTCTAGCGCGGTGACGTGAGGTCGGATCTCCTGTCTCACT

2380

PINK1

PINK1-201

PINK1-201

GACTCCGTCTCAAAAAAAAAATAAAAAAAAAAAAAAAAAATAAAAAAAAAATTCTGAAGCCAGGCATGGTGACTCATGCCTATAATCCTGGTGCT
CTGAGGCAGAGTTTTTTTTTATTTTTTATTTTTTATTTTTTAAAGACTTCGGTCCGTACCACTGAGTACGGATATTAGGACCACGA

2465

PINK1

PINK1-201

PINK1-201

TTGGGAGGCCAAGGTGAGAGAATCTCTTGAGCCCAGGAGTTGAAGACCAGCTGGGACAACATAGTGAGACCTTGTTCACAAAA
AACCTCCGGTTCCACTCTCTTAGAGAACTCGGGTCTCAACTTCTGGTTCGACCCTGTTGTATCACTCTGGAACAAGGGTGT

2550

PINK1

PINK1-201

PINK1-201

TATTA AAAAGTTAGCTAGGCATGGTGGCACATGCCGATAGTCCAGCTACTTAGGAGGCTGAGGTGGGTGGATTGCTTGAGCCCA
ATAATTTTTCAATCGATCCGTACCACCGTGTACGGCTATCAGGGTCGATGAATCCTCCGACTCCACCCACCTAACGAACCTCGGGT

2635

PINK1

PINK1-201

PINK1-201

GGAGTTTGAGGCTGCAGTGAGCTGTAGTTGCAACACTGCACCCCATCCTGGGCAACTAGCAGGAGTGTGCTAGTAGCAAGCTCTA
CCTCAAACCTCCGACGTCACCTCGACATCAACGTTGTGACGTGGGGTAGGACCCGTTGATCGTCTCACACGATCATCGTTCGAGAT

2720

PINK1

PINK1-201

PINK1-201

AAAATTTATATTATAAAAAATATATATAATGTGTATATATGTATATGTGTATATATGTTGTGTATACTATAATATGTATGTT
TTTTAAATATAATTTTTTATATATATATTACACATATATATACATATACACATATATACAACACATATGATATTATACATACAA

2805

PINK1

PINK1-201

PINK1-201

CCATATAATAGTATATAGTATATTTTTATATATATACACACACACGTTGCTTCTGCTCCATGAAGTTTATAAGGGAAGTTGGATTT
GGTATATTATCATATATCATATAAAATATATATATGTGTGTGTGCAACGAAGACGAGGTA CTTCAAATATTCCTTCAACCTAAA

2890

PINK1

PINK1-201

PINK1-201

TCCTTTTTTTTTTTTTGATACGGAGTCTCACACCGTCGCCAGGCTGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCACCTC
AGGAAAAAAAAAAAACTATGCCTCAGAGTGTGGCAGCGGGTCCGACACGTTACCGTGCTAGAGTCGAGTGACGTTGGAGGTGGAG

2975

PINK1

PINK1-201

PINK1-201

CCAGATTCACGCAATTCTTCTGCCTCAGCCTCCTGAGTAGCTGGGATTACATGTGCACACCACCACACCCGGCTAATTTTTTTGTA
GGTCTAAGTGCGTTAAGAAGACGGAGTCTGGAGGACTCATCGACCTAATGTACACGTGTGGTGGTGTGGGCCGATTAAAAAACAT

3060

PINK1

PINK1-201

PINK1-201

TTTTTTAGTAGAGACGGGGTTTCACTATGTTGGCCAGGCTGGTCTTGAACCTCCTGACTTCATGATCCGCCTCCCTCGGCCTCCCA
AAAAAATCATCTCTGCCCAAAGTGATACAACCGGTCCGACCAGAACTTGAGGACTGAAGTACTAGGCGGAGGGAGCCGGAGGGT

3145

PINK1

PINK1-201

PINK1-201

AAGTGCTGGGATTACAGGCATGAGCCACCACGCCCGGCTGGACTTTTCATTTTTTTAAAAGTTCAAAGTTATAGTGCAAGGTTA
TTCACGACCCTAATGTCCGTACTCGGTGGTGCGGGCCGGACCTGAAAGTAAAAAATTTTCCAAGTTTCAATATCACGTTCCAAT

3230

PINK1

PINK1-201

PINK1-201

AGTTGCTTACAGATAGCAGGTGCTTTAGGAACCCTCTAGAAGGAAAGTTGCCATGGGCTGGGTTCATCAGGGCTGGTCACAGAGGA
TCAACGAATGTCTATCGTCCACGAAATCCTTGGGAGATCTTCTTTCAACGGTACCCGACCCAGTAGTCCCAGCCAGTGTCTCCT

3315

PINK1

PINK1-201

PINK1-201

AGGAGGAGCTTGAGTTGGGCTTGATGGCTGAGCAGGGATGAGCCAGACAGAGCAATACTATAGAAACAGGGGCTGGAAGGATGCT
TCCTCCTCGAACTCAACCCGAACTACCGACTCGTCCCTACTCGGTCTGTCTCGTTATGATATCTTTGTCCCCGACCTTCTTACGA

3400

PINK1

PINK1-201

PINK1-201

GTGAGCAGCTTTTCAGAGGGAGGCGTCCAAAGGATGAGTGCAGGCAGCGTGCAGACCAGCCTGGCAGCAGCCAGAACACAGATAAC
CACTCGTCGAAAAGTCTCCCTCCGCAGGTTTCTACTCACGTCCGTGCGACGTCTGGTCCGACCGTCTGTCGGTCTTGTGTCTATTG

3485

PINK1

PINK1-201

PINK1-201

CTCCTGGGCAGTCTGATGGACAGCCGAGTGACACATGAAAGCAACATATTTTGATGTGGCTCAGAGCAGGGGAAGGCACGGCACTG
GAGGACCCGTCAGACTACCTGTCGGCTCACTGTGTACTTTTCGTTGTATAAACTACACCGAGTCTCGTCCCTTCCGTGCCGTGAC

3570

PINK1

PINK1-201

PINK1-201

AGAGTGGGGTAGTCTAGAGATGGTGCCTGGTAGGCTATGGCCAAGGGGCATATGCAGAGCTGTGCCTGGCACCCAGGGGTGACTA
TCTCACCCCATCAGATCTCTACCACGGACCATCCGATACCGGTTCCCGTATACGTCTCGACACGGACCGTGGGTCCCCACTGAT

3655

PINK1

PINK1-201

PINK1-201

ACCTTGGAAAGGAAGAGCTCAGCAGATCAGACCATTTGAGAGGGAAAGCGGAGCCTGGGTGACTGGAAGAGTGACGTCACCGCTG
TGGAACCTTTCCTTCTCGAGTCGTCTAGTCTGGTAAACTCTCCCTTTCGCCTCGGACCCACTGACCTTCTCACTGCAGTGGCGAC

3740

PINK1

PINK1-201

PINK1-201

CCTGAAGCAGGGGAAGACCCACCAGATTTTTGTCACATGGCCTCTTTCCAGTGCAGCACTGCCCCAGCACCTGCACCTCCATC
GGACTTCGTCCCTTCTGGGTGGTCTAAAAACAGTGTACCGGAGAAAGGGTACGTCGTGACGGGGGTCGTGGACGTGGAGGTAG

3825

PINK1

PINK1-201

PINK1-201

TATTTCTGTCTGAACTCTTGTACTCTTGCTACCTTTCTGGACAGAGTAGCCTCATCGGGGCCCTAAGAGGCAGAGAGAGAAAGAC
ATAAAGACAGACTTGAGAACATGAGAACGATGGAAAGACCTGTCTCATCGGAGTAGCCCCGGGATTCTCCGTCTCTCTTTCTG

3910

PINK1

PINK1-201

PINK1-201

AGTACTGAATCCCTCTGCTCTGGGGATGCGCCTGATGTCACCCACTTGCCTGAGAGACCCTCTGAGATCACTGTGGATCACACAC
TCATGACTTAGGGAGACGAGACCCCTACGCGGACTACAGTGGGTGAACGGACTCTCTGGGAGACTCTAGTGACACCTAGTGTGTG

3995

PINK1

PINK1-201

PINK1-201

TCCTGCTAGTTGCCAGGAGCCGTCAGCCAAGGTCTTTGCAGAGCGAGCTGTCTCCATAATCAGACACCTCCAGAACTCTGCTGG
AGGACGATCAACGGGTCCTCGGCAGTCGGTTCAGAAACGTCTCGCTCGACAGAGGTATTAGTCTGTGGAGGTCTTGAGACGACC

4080

PINK1

PINK1-201

PINK1-201

AGAGTGAAGGCAGCAAGGAGAGGTGCACTGGCTGCGGGACGTGGGGTTTCTGACCTCTCAGATCATTGAGTATTGTGATCCCAGT
TCTCACTTCCGTTCCTTCTCCACGTGACCGACGCCCTGCACCCAAAGACTGGAGAGTCTAGTAACTCATAACACTAGGGTCA

4165

PINK1

PINK1-201

PINK1-201

GAAGCAACAGAGTTTGGAGAAAAATCATTCTGAATAATGAGAAAAGAAGATGGCCTGGACCCAGGCTGAGCAGTAGAACCTGGTTGG
CTTCGTTGTCTCAAACCTCTTTTTAGTAAGACTTATTACTCTTTCTTCTACCGGACCTGGGTCCGACTCGTCATCTTGGACCAACC

4250

PINK1

PINK1-201

PINK1-201

GTTGTGTTTTTCTGGTTTATTGATCTGGTCGACGTGGACCACGCCTTGCTGCACCTCTCTCTGCCTCCCCTGTTTCCCTTTTCTT
CAACACAAAAAGACCAAATAACTAGACCAGCTGCACCTGGTGCAGAACGACGTGGAGAGAGACGGAGGGGGACAAAGGGAAAAAGAA

4335

PINK1

PINK1-201

PINK1-201

GGGCCCTTCTAGGCTCCCTGGCTCACGGTGCATTCTTTTTCTCATCACAGGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGAC
CCCGGAAGGATCCGAGGGACCGAGTGCCACGTAAGAAAAGAGTAGTGTCCGTTAAAAATGGGTCTTTTCGTTCCGGCCCCGGACTG

4420

PINK1

PINK1-201

PINK1-201

130 135 140
Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp
ENSE00001041274

CCGTTGGACACGAGACGCTTGCAGGGCTTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGCTG
GGCAACCTGTGCTCTGCGAACGTCCCGAAAAGCCGACCTCCTCATAGACTATCCCGTCAGGTAACCATTCCCGACGTCACGACGAC

4505

PINK1

PINK1-201

PINK1-201

145 150 155 160 165
Pro Leu Asp Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile Gly Lys Gly Cys Ser Ala Ala

ENSE00001041274

TGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGGCCAGGTAC
ACATACTTCGGTGGTACGGATGTAACGGGGTCTTGGACCTCCACTGTTTCTCGTGGCCCAACGAAGGTCCCTCTCCGGGTCCATG

4590

PINK1

PINK1-201

PINK1-201

170 175 180 185 190 195
Val Tyr Glu Ala Thr Met Pro Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg Gly Pro Gly Thr

ENSE00001041274

CAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCCGGGGGCCCTGCCTTCCCTTGCCATCAAGATGATGTGGAACATCTCGGTA
GTCACGTGGTCTCTTCCCGTCTCGCTCGAGGCCCGGGGACGGAAGGGGAACCGGTAGTTCTACTACACCTTGTAGAGCCAT

4675

PINK1

PINK1-201

PINK1-201

200 205 210 215 220 225
Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly Ala Pro Ala Phe Leu Ala Ile Lys Met Met Trp Asn Ile Ser

AGCACCAGGCCTTTCATCTTTAAAGGAGATGTTCTCAAATGCCATCTTAGTGGGCCTGGTGAGGATTTTTTCCAGGAAGTAGG
TCGTGGTCCGGAAAGTAGAAATTTCTCTACAAGAGTTTTACGGGTAGAATCACCCGGACCACTCCTAAAAAAGGTCCTTCATCC

4760

PINK1

PINK1-201

PINK1-201

TAGGAAAAGACAGATTATCCACAGGAAAGGTGCCTGTATAGTCAGGTTACCTCCCCCTGTTACACAGAAGTCTAAACCAGAATGT
ATCCTTTTCTGTCTAATAGGTGTCTTTCCACGGACATATCAGTCCAATGGAGGGGGACAATGTGTCTTCAGATTTGGTCTTACA

4845

PINK1

PINK1-201

PINK1-201

TTGAAATTGTATTCTGCCACAGATCACCCAGAGATCAGGTTCAAAGGTAGATTTTGGCCAGGCCTGGTGGACCATGCCTGTAAT
AACTTTAACATAAGACGGGTGTCTAGTGGGTCTCTAGTCCAAGTTTCCATCTAAAACCGGTCCGGACCACCTGGTACGGACATTA

4930

PINK1

PINK1-201

PINK1-201

CCCAGCACTTTGGGAGGCCAATCACTTGAGCTCAGGAGTTTGGAGACCAGCCTGGGCAACATGATGAAACCCCATCTCTATGAAAA
GGGTTCGTGAAACCCCTCCGGTTAGTGAACCTCGAGTCCTCAAACCTCTGGTTCGGACCCGTTGTACTACTTTGGGGTAGAGATACTTTT

5015

PINK1

PINK1-201

PINK1-201

ATACAAAAATTAGCCGGGTGTGACAGCTTGCACCTGTATGTAGTCTTAGCTACTTGGGTGGCTGGTGGCTGAAAGTGGGAGGATCA
TATGTTTTTAATCGGCCACACTGTGGAACGTGGACATACATCAGAATCGATGAACCCACCGACCACCGACTTCACCTCCTAGT

5100

PINK1

PINK1-201

PINK1-201

CTTGAGTGCAAGAGGCAGAGGCTGCAGTGATCCAAGATTGTGGCACTGCACTCCAGCCTGGGTAACAGAGTAAGACCCTGTCTCA
GAACTCACGTTCTCCGTCTCCGACGTCAGTGGTTCTAACACCGTGACGTGAGGTCGGACCCATTGTCTCATTCTGGGACAGAGT

5185

PINK1

PINK1-201

PINK1-201

AAACAAAACAAACAAACAAAAAAACCCAAAGGTAGATTCTGATTCAGCAGGTCAGGGATGGGGCCTAAGATTGTGCCTTCCCAA
TTTGTGTTTGTGTTGTTGTTTTTTTTGGGTTTCCATCTAAGACTAAGTCGTCCAGTCCCTACCCCGGATTCTAACACGGAAGGGTT

5270

PINK1

PINK1-201

PINK1-201

TAAGCTCCCACGTGATACCAATGCCACTGCTCTGTCAACCACACTTTGAGTAACAAGTGCCTAAACCACTGATTTCTACCTTGAT
ATTCGAGGGTGCACATGTTACGGTGACGAGACAGTTGGTGTGAAACTCATTGTTACGGATTTGGTACTAAAGATGGAACATA

5355

PINK1

PINK1-201

PINK1-201

TGGTTAGTTCACCATCCCCTCCTTCTGCAACCTGCCTCACTGGAGAGGGGGAACTGGATCTCTTTTCCTTTAAGCTCACTCTGCA
ACCAATCAAGTGGTAGGGGAGGAAGGACGTTGGACGGAGTGACCTCTCCCCCTTGACCTAGAGAAAGGAAATTCGAGTGAGACGT

5440

PINK1

PINK1-201

PINK1-201

AGCCACCTCCAGCTCAGAGGCTTGCATGTCAACTCCCTACTCTCAACTCTTGGAAAGGACTCAAGACTTTGGGAAATTGAAGAGT
TCGGGTGGAGGTCGAGTCTCCGAACGTACAGTTGAGGGATGAGAGTTGAGAACCTTCTGAGTTCTGAAACCTTTAACTTCTCA

5525

PINK1

PINK1-201

PINK1-201

ATTTTTCCCCCACGAAAACAATTTCTGTCCACTTAATTTATTTACCTTGCCATTGCTAGGTAGGTTTTAAAAATGTATTAAGACC
TAAAAAGGGGGTGCTTTTGTAAAGACAGGTGAATTAATAAATGGAACGGTAACGATCCATCCAAAATTTTACATAATTCTGG

5610

PINK1

PINK1-201

PINK1-201

CGATGCTCTGTCTCCTGCCCATCCCTGGGCCCATCCATTCAAGGCCGCAGTGGGAAGTGGCCACAGCCGTTTCATGGTGGGCCCTA
GCTACGAGACAGAGGACGGGTAGGGACCCGGGTAGGTAAGTTCCGGCGTCAACCTTCACCGGTGTCGGCAAGTACCACCCGGGAT

5695

PINK1

PINK1-201

PINK1-201

GAGGATGCAGTTTCTTGTCTGATTTGGGGAATGAAGGTTATTAGACTGTTGCACTCCAAGCTGGGTTAATAGCTAACAAGTAGC
CTCCTACGTCAAAGAACAAGACTAAACCCCTTACTTCCAATAATCTGACAACGTGAGGTTTCGACCCAATTATCGATTGTTTCATCG

5780

PINK1

PINK1-201

PINK1-201

CAAATCCTTTGCCTGTGAAACATCCAGTCTTAGCATCAAACATGCCCTGGTTGGGGCATGACAGCTGTTGCATTACAGCAGCT
GTTTAGGAAACGGACACTTTGTAGGTCAGAATCGTAGTTTTGTACGGGACCAACCCCGTACTGTCGACAACGTAAGTGTCGTCGA

5865

PINK1

PINK1-201

PINK1-201

ACAAGATTGTTGATTCTTACCAGATCTTCTTGATACAGGTTTCATATGTCCTGAGAGCCCTTCCCAATACAATGAGGACAATAAG
TGTTCTAACAACATAAGAATGGTCTAGAAGAACTATGTCAAAGTATACAGGACTCTCGGGAAGGGTTATGTTACTCCTGTTATTC

5950

PINK1

PINK1-201

PINK1-201

GTGCTTTCCCACTCTTTGGTTTTTGTCTGTTTGTCTGCGTGGGGGATGGAGGAAGGCTGTTCTGTGATTCAGTACAACCTTCACCCAG
CACGAAAGGGGTGAGAAACCAAAAACAGACAAACAGCACCCCTACCTCCTTCCGACAAGACACTAAGTCATGTTGAAGTGGGTC

6035

PINK1

PINK1-201

PINK1-201

GGTGGAGCATGTCAGGCTCTGGCCTGGCTGCTGAAGGGAGCCTGCAGAATGAGTTAGTGATCCAGTGGTCAATTTTGAAGTGGTG
CCACCTCGTACAGTCCGAGACCGGACCGACGACTTCCCTCGGACGTCTTACTCAATCACTAGGTCACCCAGTTAAAACTTGACCAC

6120

PINK1

PINK1-201

PINK1-201



GGGACCAGAGGCCACCGATGGCAGGAAGCAGCACCCCATATCCTGATCACCTTGGCATCTCCTCCAGCCCTGGCATCTAGGCTGCA
CCCTGGTCTCCGTGGCTACCGTCCTTCGTCTGTTGGGTATAGGACTAGTGGAAACCGTAGAGGAGGTCGGGACCGTAGATCCGACGT

6205

PINK1

PINK1-201

PINK1-201

AGAGTTTGAGGAGTGTGAAGAATCCTCTGAGTTGGCATGGATGGTACCTCTGTCTGCCTCCCAGGAGTAACTAGTCTCAGCCTGC
TCTCAAACCTCCTCACACTTCTTAGGAGACTCAACCGTACCTACCATGGAGACAGACGGAGGGTCTCATTGATCAGAGTCGGACG

6290

PINK1

PINK1-201

PINK1-201

CAGTTAAGACAGGTCATCTTATCTCGAAGGTCAGAGCCAATTCTAGGCAGTAGCTGCCCTGCTCCAGGTTACAGGCAGGGCTTAC
GTCAATTCTGTCCAGTAGAATAGAGCTTCCAGTCTCGGTTAAGATCCGTTCATCGACGGGACGAGGTCCAATGTCCGTCCCGAATG

6375

PINK1

PINK1-201

PINK1-201

AAGGAACTTACCATTCTGCTCCGGCCTGTGTAACCCTGGGTTCCCTTGTGGGTGTTCCAGGCAGGTTCCCTCCAGCGAAGCCATCTT
TTCCCTTGAATGGTAAGACGAGGCCGGACACATTGGGACCCAAGGAACACCCACAAGGTCCGTCCAAGGAGGTGCGTTCGGTAGAA

6460

PINK1

PINK1-201

PINK1-201

Ala Gly Ser Ser Ser Glu Ala Ile Leu
ENSE00001041273

GAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGGTAAGTGCCC
CTTGTGTTACTCGGTCTCGACCAGGGTCTCGCTCGGCTCACCGGAACCGACCCCTCATACCTCGTCAGTGAATGTCCATTACAGGG

6545

PINK1

PINK1-201

235 240 245 250 255
Asn Thr Met Ser Gln Glu Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr Arg

ENSE00001041273

PINK1-201

TCTGCCTGCCAGACTGACTGGGACTTCTTTGAGAGCAACTTCATCCATCACTTATGTCCTCAGCACCTGGTACAGTGTCTGATAT
AGACGGACGGTCTGACTGACCCTGAAGAACTCTCGTTGAAGTAGGTAGTGAATACAGGAGTCGTGGACCATGTCCACAGACTATA

6630

PINK1

PINK1-201

PINK1-201

GACAGTAGATAATAAAGGCTTAATGTTGGTGATGGATTTTCAGTTAGTGGATAATTTCACTTGGGAAAGATTGCAGGTAATCTGA
CTGTCATCTATTATTTCCGAATTACAACCACTACCTAAAAGTCAATCACCTATTAAAGTGAACCCTTTCTAACGTCCATTAGACT

6715

PINK1

PINK1-201

PINK1-201

CCCCAAATGATGATGCACTTGCCTAATTCACATTGGAGCAGGGGAGAGGAGGCCCCCAAAAATGCCCAGTTCACAGTGTTCAT
GGGGTTTACTACTACGTGAACGCATTAAGTGTAACCTCGTCCCTCTCCTCCGGGGGGTTTTTACGGGTCAAGTGTCCACAACGTA

6800

PINK1

PINK1-201

PINK1-201

GATTGACTGGGGTTCTCAGATTCCTCCTAAGAAATGCACGGGTAGAGCGCCACCTATCGGAATAAACTGAACTCTGTCCCCACCA
CTAACTGACCCCAAGAGTCTAAGGAGGATTCTTTACGTGCCATCTCGCGGTGGATAGCCTTATTTGACTTGAGACAGGGGTGGT

6885

PINK1

PINK1-201

PINK1-201

GAGGGAACACTCATTTCACTAATAGTTATGTGCACTGATGGTGCCAAGAGATTTTAAAAAACA AAAAGTGGTCTGTTGGCCCA
CTCCCTTGTGAGTAAAGTGATTATCAATACACGTGACTACCACGGTTCTCTAAAATTTTTTTTTGTTTTTACCAGACAACCGGGT

6970

PINK1

PINK1-201

PINK1-201

GAGGTCTCAGTGTGGCAGCAGAGAGCCAGGGTGTAAGTGCTAGAATCGAGTATGCTTGGGCTGAGGGAGCCCAGGGGAGGCGTG
CTCCAGAGTCACACCGTCTGCTCTCGGGTCCACATTCACGATCTTAGCTCATACGAACCCGACTCCCTCGGGTCCCCTCCGCAC

7055

PINK1

PINK1-201

PINK1-201

TGCTGCAGAGGAGGGGCTGCTCAGAAAGCCTTCTCAAAGGGACAGTTTGTGCCACCTTGTGAAGGATGAATTGGCATTACTTGGG
ACGACGTCTCCTCCCGACGAGTCTTTCCGAAGAGTTTCCCTGTCAAACACGGTGGAACACTTCTACTTAACCGTAATGAACCC

7140

PINK1

PINK1-201

PINK1-201

CAGAGGAGTAGGGAAAGTGGCATTCCCAGCAGAGGGGAAGAGCAAGTGAACAGCAGCTACGCTTTCAGCTCAGAAAAGCCCCATGTCC
GTCTCCTCATCCCTTCACCGTAAGGGTCGTCTCCCTTCTCGTTCACTTGTCGTCGATGCGAAAAGTCGAGTCTTTTTCGGGTACAGG

7225

PINK1

PINK1-201

PINK1-201

ACCACCAGCCTCACCACAGGTGGTGAGGACTGACGCGCAGGCTATGACAGAGGAGATACTTGTGCCACCTCAATATTTACAGCC
TGGTGGTCGGAGTGGTGTCCACCACTCCTGACTGCGCGTCCGATACTGTCTCCTCTATGAACACGGGTGGAGTTATAAATGTCCG

7310

PINK1

PINK1-201

PINK1-201

TGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTAGGCAGATCACTTGAGCCCAGGAGTTCAAGAGCAGCCTGGGCAA
ACCGAGTACGGACATTAGGGTCGTGAAACCTCCGACTCCATCCGTCTAGTGAACCTCGGGTCCCTCAAGTTCTCGTCGGACCCGTT

7395

PINK1

PINK1-201

PINK1-201

CATGGTGAAACCCCGCCTTTACAAAAATAAATTTTAGCCGGGCATGGGGGCAAATGCCTGTGATCCCAGCTACTCAGGAGGCTG
GTACCACTTTGGGGCGGAAATGTTTTTTATTTAAAATCGGCCCGTACCCCGTTTACGGACACTAGGGTCGATGAGTCTCCGAC

7480

PINK1

PINK1-201

PINK1-201

AGGCGGGAGGATCATTTGAGTCCAGGGAGGTTGAGGCTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGCGACCTG
TCCGCCCTCCTAGTAAACTCAGGTCCCTCCAACCTCCGACGTCACCTCGGTTCTAGTACGGTGACGTGAGGTCCGACCCGCTGGGAC

7565

PINK1

PINK1-201

PINK1-201

GAGTGAGACCCTGTCTCTCATTTGTAGACCCACCAAGAAGAGGTGGGTCTGCTGCATTTTTGGTGATTTACTGGAGGGCTGGTTT
CTCACTCTGGGACAGAGAGTAAACATCTGGGTGGTTCTTCTCCACCCAGACGACGTAAAAACCACTAAATGACCTCCCGACCAA

7650

PINK1

PINK1-201

PINK1-201

ATAGATCTTCATTCTGTCAGAAGCAGGGAGGCAAAAGTATGAAATTAAGGGAGTGGTTGTGGAAAACCCCTTCCATGGTTTTGGAG
TATCTAGAAGTAAGACAGTCTTCGTCCCTCCGTTTTTCACTTTAATTCCCTCACCAACACCTTTTGGGGAAGGTACCAAACCTC

7735

PINK1

PINK1-201

PINK1-201

GTTTCCAATGTGACTGGGAGTCCCTGCAGGCCGGTGGAGGTAGCTGCTCAAGTGGCTGCTGCTTCTCCTGAGGCCTTTTTGGAGA
CAAAGGTTACTACTGACCCTCAGGGACGTCCGGCCACCTCCATCGACGAGTTCACCGACGACGAAGAGGACTCCGGAAAAACCTCT

7820

PINK1

PINK1-201

PINK1-201

AAGTGGACACCTGAATGTCAGCTGCTTTGGGGCTAACATGATCCTTGATGCCTCCTTTTTGTGGCATGAGTGGCAGCCGGCCGACG
TTCACCTGTGGACTTACAGTCGACGAAACCCGATTGTA TAGGAACTACGGAGGAAAAACACCGTACTCACCGTCGGCCGGCTGC

7905

PINK1

PINK1-201

PINK1-201

TGGTGCTGTCCTGCTGCCGGAGCACCATGATGTCTGCTGCTGAGACCTCCCATCTGACATAGTCCCTGTCCCTCTTCAGGGACTT
ACCACGACAGGACGACGGCCTCGTGGTACTACAGACGACGACTCTGGAGGGTAGACTGTATCAGGGACAGGGAGAAGTCCCTGAA

7990

PINK1

PINK1-201

PINK1-201

TGTTCCCTTTAGCAGTTCTCACTGTCTGGCCTCAAATAACACGTCTTTTTCTGTTGGTTCCTTTTTGCTCCAGCTGTACTGTAAAC
ACAAGGAAATCGTCAAGAGTGACAGACCGGAGTTTATTGTGCAGAAAAAGACAACCAAGGAAAAACGAGGTCGACATGACATTTG

8075

PINK1

PINK1-201

PINK1-201

ACTCTTTGTTTACTGCATACCCTCAGTAAATACCTGTTGAATGACCGGATAGATGTGGCAGCAGGTACATTACCTCAACTTCTGG
TGAGAAACAAATGACGTATGGGAGTCATTTATGGACAACCTACTGGCCTATCTACACCGTCGTCCATGTAATGGAGTTGAAGACC

8160

PINK1

PINK1-201

PINK1-201

TACACCTTGGGAGAAGCTTTCCCAAGAACACCCTGGGTTCAATTCCTCCTAGCCTCTGCTCTCCTG6GGGCCAGAGATTGAAGGC
ATGTGGAACCCTCTTCGAAAGGGTTCTTGTGGGACCCAAGTAAAGGAGGATCGGAGACGAGAGGACCCCGGGTCTCTAACTCCG

8245

PINK1

PINK1-201

PINK1-201

GCTTAACCTGCTCATCTCACCACGTCTCCCGCCTTATCTCTCACCTTCTCATCAGCACCCCTACACTCCACCACGCTGGCTTCAT
CGAATTGGACGAGTAGAGTGGTGCAGAGGGCGGAATAGAGAGTG6GAAGAGTAGTCGTGGGATGTGAGGTGGTGCACCGAAGTA

8330

PINK1

PINK1-201

PINK1-201

AGCTCCTTCCCCGAATGTGCCAGGCTTCTCTGTGACCATCTCTTGAGCGTACAGCTGGCTATACCTGGGCTGCCCTCCTCCCACA
TCGAGGAAGGGGCTTACACGGTCCGAAGAGACACTGGTAGAGAACTCGCATGTTCGACCGATATGGACCCGACGGGAGGAGGGTGT

8415

PINK1

PINK1-201

PINK1-201

TTTCAGGTCTCAGTTCAGACACCCGCAACCCACCATGTATCTCCCCAGTACAGCCATACTCCTCTGCCCTGAGCTCCCATGAC
AAAGTCCAGAGTCAAGTCTGTGGGCGTTGGGGTGGTACATAGAGGGGTCATGTTCGGTATGAGGAGACGGGGACTCGAGGGTACTG

8500

PINK1

PINK1-201

PINK1-201

ACCTGCTGGGGCCCTGACAGCCTGGGGCTGTGATCATGACTTGCCAGGGGGCCCGAGGGTGGAAACGATGCTCTGGCTCCTTTGA
TGGACGACCCCGGGACTGTTCGGACCCCGACACTAGTACTGAACGGGTCCCGGGCTCCACCTTTGCTACGAGACCGAGGAACT

8585

PINK1

PINK1-201

PINK1-201

TTGCATAGAACAGGGGCCACTCAGGTTGACTCAAGAGCAGGAGCAGCGCGTGGGCACACGTGGACTGCAGCCACACAGCCTGGGG
AACGTATCTTGTCCCCGGTGAGTCCAACCTGAGTTCTCGTCTCGTTCGCGCACCCGTGTGCACCTGACGTCGGTGTGTCGGACCCC

8670

PINK1

PINK1-201

PINK1-201

ACCATGCAGTGCTGGGAGAGGGCCGGTGCCCTGCTCTCTCCAGCACCCTAGGCTCTGCCCATTCGCTTCCCTCCACCATTG
TGGTACGTCACGACCCTCTCCGGCCACGGGACGAGAGAGGGGTCGTGGCAGATCCGAGACGGGGTAAGCGAAGGGAGGTGGTAAC

8755

PINK1

PINK1-201

PINK1-201

TTATGCAGCAAAGGGGGCTCTAGCCTGATGTGCTAGAAGCAGTCACACTGGATTTTTGAGAAAAGCCAAGCTTTCTATTGTGAGT
AATACGTCGTTTCCCCGAGATCGGACTACACGATCTTCGTAGTGTGACCTAAAAACTCTTTTCGGTTCGAAAGATAAACTCA

8840

PINK1

PINK1-201

PINK1-201

CGACTCATATGGAGACAGGAGTTGAATTCAACCCTGTCTCCCTGTGCTAGCTTTAAGGCGGTAATTTTATTAGAGGAGGTTTAAAG
GCTGAGTATACCTCTGTCTCAACTTAAGTTGGGACAGAGGGACACGATCGAAATTCGCCATTAAAATAATCTCCTCCAAATTC

8925

PINK1

PINK1-201

PINK1-201

GGGTGGATTCTAAGATTAGCAGGTGATTGATGGAAGGAAAGGAGAAGTCTGGACAGTCCCTTGGACATGCACAGTTATCTGTTTCAT
CCCACCTAAGATTCTAATCGTCCACTAACTACCTTCCTTTCTCTTCAGACCTGTCAGGAACCTGTACGTGTCAATAGACAAGTA

9010

PINK1

PINK1-201

PINK1-201

GCCAACTCATGGGTCCCCTGTGCAGATTTGGGAGGAGTGAGTATGAAACGTGCAGTGGCAATTCAGGCTTTGACATCAGCAA
CGGTTGAGTACCCAGGGGACACGTCTAAACCCTCCTCACTCATACTTTGCACGTCAACCGTTAAGTCCGAAACTGTAGTCGTTTGA

9095

PINK1

PINK1-201

PINK1-201

TGTTCTGTGCAAGCTGCAATTGGCCTTATTGGTTCCAACCAATTTTCAGCCAGTTCTTTTTATCTCATAAGCAGAGGGAGTTTCAGC
ACAAGACACGTTTCGACGTTAACCGGAATAACCAAGGTTGGTTAAAGTCGGTCAAGAAAATAGAGTATTCGTCTCCCTCAAAGTCG

9180

PINK1

PINK1-201

PINK1-201

CTTTCAGAAAAGTGGTTTCTGCAAACCTCAAATTTTCTTTTTATTTTTCTGAGACAGGGTCTTACTCTGTTGCCAGGCTGGAGAGCA
GAAAGTCTTTCACCAAAGACGTTTGAGTTTAAAAGAAAATAAAAAGACTCTGTCCAGAATGAGACAACGGGTCCGACCTCTCGT

9265

PINK1

PINK1-201

PINK1-201

GTGGCGTGATCTTGGCTCACTGCAGCCTCAACCTCCCTGGGCTCAAGTGATCCTCCCACCTCAGCCTCCCAAGTAGCTGGGTCTG
CACCGCCTAGAACCGAGTGACGTTCGGAGTTGGAGGGACCCGAGTTCACTAGGAGGGTGGAGTCGGAGGGTTTCATCGACCCAGAC

9350

PINK1

PINK1-201

PINK1-201

CAGGCACATGCCACCATGCCAGCTAATTTTTGTAGTTTTGTAGAGACAGAGTTTCTCCATGTTGCCCGGGCTGGCCTCGAACT
GTCCGTGTACGGTGGTACGGGTTCGATTAATAAACATCAAAAACATCTCTGTCTCAAAGAGGTACAACGGGGCCCGACCGGAGCTTGA

9435

PINK1

PINK1-201

PINK1-201

CCTGGGCTCAAGCAATTGCCTGCCTCAGCCTCCCAAATTGCTGGGATTACAGGAGTGAGCCACGGGAATTTCCATCAGTTACTGA
GGACCCGAGTTCGTTAACGGACGGAGTCGGAGGGTTTAAACGACCTAATGTCTCACTCGGTGCCCTTAAAGGTAGTCAATGACT

9520

PINK1

PINK1-201

PINK1-201

TTCTTGAACCTTGTAGGAACGTGGTTCCACTGTCCACATGCTGTTCTTTTCTCGCATCTCCTGTTTCTGCTTCCCTTTGGCCTGCT
AAGAACTTGAACATCCTTGACCAAGGTGACAGGTGTACGACAAGAAAGGAGCGTAGAGGACAAGGACGAAGGGAAACC GGACGA

9605

PINK1

PINK1-201

PINK1-201

CACCTCTGGCTCCTCATGGCCCCAGTGAAGTATCGTGGCTTCTCTCCACTGCAGACTGGCAGATTTCTTCACTCACACTCCCAA
GTGGAGACCGAGGAGTACCGGGGTCACCTTCATAGCACCGAAGGAGAGGTGACGTCTGACCGTCTAAAGAAGTGAGTGTGAGGGTT

9690

PINK1

PINK1-201

PINK1-201

AAAGAGAATCTACTTCCCTCCCTTCCCTTCGTCCAACCATCTGGGTCTCGAGTGTCACTGTAGGTTCACTGCCGTTGGGGCAGGT
TTTCTCTTAGATGAAGGGAGGGAAGGGAAGCAGGTTGGTAGACCCAGAGCTCACAGTGACATCCAAGTGACGGCAACCCCGTCCA

9775

PINK1

PINK1-201

PINK1-201

GACTCCTTGGGCCAGTCAGCTTTGGCTGAAGGGCAGGGCTGGCACACAGCTGGCAGAGCCACCCCATCCAAAATCCAGCCACTGT
CTGAGGAACCCGGTCAGTCGAAACCGACTTCCCGTCCCGACCGTGTGTGCGACCGTCTCGGTGGGGTAGGTTTTAGGTCGGTGACA

9860

PINK1

PINK1-201

PINK1-201

GCCTCAGCAGGGCTGTGGTTTGGGGGTCGGGGGGCGCTCCCCACAGGATAAGGAGCAGCCAGGGCAGGCAGATGACACTACCACT
CGGAGTCGTCCCGACACCAAACCCCGAGCCCCCGCGAGGGGTGTCTATTCTCGTCCGGTCCCGTCCGTCTACTGTGATGGTGA

9945

PINK1

PINK1-201

PINK1-201

ACTAGCTGCATCTGGATCTATTCACCTATTCAACAAAGGTTTATTACACCCATATTCTATGCCAACTACTGTACTAGACTTGGAA
TGATCGACGTAGACCTAGATAAGTGAATAAGTTGTTTCAAATAATGTGGGTATAAGATACGGTTGATGACATGATCTGAACCTT

10,030

PINK1

PINK1-201

PINK1-201

TAATGGAGAAAATTCAGGCACAGTCCTTGCTCTTAGGGAGCTCACATGATTACTCATTGATGAATATCTCTCTCCCCTGATAGAC
ATTACCTCTTTAAGTCCGTGTCAGGAACGAGAATCCCTCGAGTGTACTAATGAGTAACTACTTATAGAGAGAGGGGACTATCTG

10,115

PINK1

PINK1-201

PINK1-201

GACCTGGAATGCAAACCCAGGCAGTCTGATACCAGGGTTTCTCCACCTGTGTTCTGCCACATGGGATGGATAGGATGGATGGGTG
CTGGACCTTACGTTTGGGTCCGTCAGACTATGGTCCCAAAGAGGTGGACACAAGACGGTGTACCCTACCTATCCTACCTACCCAC

10,795

PINK1

PINK1-201

PINK1-201

TACGGATGGACGGACGGACAGACGGATGGACAAATGGATTGAAGGATGGGTAGGGGAGTCATCAGATGTGTTCTCCAACACCATG
ATGCCTACCTGCCTGCCTGTCTGCCTACCTGTTTACCTAACTTCTACCCATCCCCTCAGTAGTCTACACAAGAGGTTGTGGTAC

10,880

PINK1

PINK1-201

PINK1-201

TACAGTACCTGGCACATAGCAAATCTATGATAAACATTTGATAGTAAGTGAATAATGAATGTCAGTGCCAGTGTTGGTGTGGCCT
ATGTCATGGACCGTGTATCGTTTAGATACTATTTGTAACCTATCATTCACTTATTACTTACAGTCACGGTCACAACCACACCGGA

10,965

PINK1

PINK1-201

PINK1-201

TAGGTTATTCTTTCCAGGTGTTGTATCTGATGCTGGCCTCATATGTTTGTCTCACTTGGCTGACTAGAAAATCCAAGAGAGGTCC
ATCCAATAAGAAAGGTCCACAACATAGACTACGACCGGAGTATACAAACAGAGTGAACCGACTGATCTTTTAGGTTCTCTCCAGG

11,050

PINK1

PINK1-201

PINK1-201

260 265
Lys Ser Lys Arg Gly Pro
ENSE00003577628

CAAGCAACTAGCCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCCAGGGGCCCTGGTC
GTTTCGTTGATCGGGGAGTGGGGTTGTAGTAGGCCCAAGAGGCGCGGAAGTGGAGAAGGCACGGCGACGACGGTCCCCGGGACCAAG

11,135

PINK1

PINK1-201

PINK1-201

270 275 280 285 290
Lys Gln Leu Ala Pro His Pro Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly Ala Leu Val

ENSE00003577628

GACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGGCCATGGCCGGACGCTGTTCCCTCGTTATGAAGAAGTAAG
CTGATGGGACTACACGACGGGAGTGC GGAGGTGGGACTTCCGGACCCGGTACCGGCCTGCGACAAGGAGCAATACTTCTTCATTC

11,220

PINK1

PINK1-201

PINK1-201

295 300 305 310 315 320
Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn

ENSE00003577628

TGACAGCAGCGCGGCAGGGCCTGGAGCTGATACATCTCCAAAGGGGAGCTGGTTTCTGCCCTCCATGTGCACCTTGATCAGGGGG
ACTGTCGTCGCGCCGTCCCGGACCTCGACTATGTAGAGGGTTCCCTCGACCAAGGACGGGAGGTACACGTGGAAGTACTGCCCC

11,305

PINK1

PINK1-201

PINK1-201

TTTTGGAGAACAGGGTCATCACCCCTCCGGAGAAGAAAGCCATGCAAAGGGAACATATCTGCCCTGGAGAGCATTTCCTGTAG
AAAACCTCTTGTCCAGTAGTGGGAAGGCCTCTTCTTTTCGGTACGTTTCCCTTGTATAGACGGGACCTCTCGTAAAAGGGACATC

11,390

PINK1

PINK1-201

PINK1-201

GACGATTTTTTCATGGAAACAAACTCTCATCTTCATCCAGAACATACTTGTACCTAGTCCTTTTGGTCCATTTGACTGTTAACCT
CTGCTAAAAAGTACCTTTGTTTGAGAGTAGAAGTAGGTCTTGTATGAACAGTGGATCAGGAAAACCAGGTAAACTGACAATTGGA

11,475

PINK1

PINK1-201

PINK1-201

TTTCTGTGGCTGGACTTATCTGTTTTTAACATAAAAAACCGTTCTCCTTCCCTCACCCCTCTGTATCCCCCTAACTTTGCTATAGTGGG
AAAGACACCGACCTGAATAGACAAAAATTGTATTTTTGGCAAGAGGAAGGAGTGGGAGACATAGGGGATTGAAACGATATCACCC

11,560

PINK1

PINK1-201

PINK1-201

TATTTTATTTTAAGGAAATAATTATCTGCACCATTACTTTGAATATAGGGAGCCCCAACTCTTACTTCCTAATTTGAGGATGGTG
ATAAAATAAAATTCCTTTATTAATAGACGTGGTAATGAACTTATATCCCTCGGGGTTGAGAATGAAGGATTAAACTCCTACCAC

11,645

PINK1

PINK1-201

PINK1-201

AGTGGGAGGGAACAGAAAGGATGCTGGGGAAAAGTGGGAATCAAAGTGCTCCTGGAAGGGGAAGAGGAAACGGCCTAACCCCTAACA
TCACCCTCCCTTGTCTTTTCTACGACCCCTTTTACCCTTAGTTTTACGAGGACCTTCCCTTCTCCTTGCCGGATTGGGATTGT

11,730

PINK1

PINK1-201

PINK1-201

GTGATTAAGGTTATTAGGAGGCCGGGAATGGTGGCTGACGCCTGTAATCCCAGCACTTTGGAAGGCGGAGGTGGGTAGATCACTT
CACTAATCCAATAATCCTCCGGCCCTTACCACCGACTGCGGACATTAGGGTCTGTGAAACCTTCCGCCTCCACCCATCTAGTGAA

11,815

PINK1

PINK1-201

PINK1-201

GAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGATGAAACCCTGTATCTACTAAACATACAAAAATTAGCCTGGTGTGGTGGC
CTCCAGTCCCTCAAACCTCTGGTCGGACCGGTTGTACTACTTTGGGACATAGATGATTTGTATGTTTTAATCGGACCACACCACCG

11,900

PINK1

PINK1-201

PINK1-201

GGGCACCTATAATCCCAGCTACTCGGGAGGCTGAGGTAGGAGAATTGCTTGAACCTGGAAGGTGGAGGTTGCAGTGAGCCAAGAT
CCCCTGGATATTAGGGTCGATGAGCCCTCCGACTCCATCCTCTTAACGAACTTGGACCTTCCACCTCCAACGTCACCTCGGTTCTA

11,985

PINK1

PINK1-201

PINK1-201

CGTGCTACTGCACTCCAGCTTGGCGACAGAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAACGTATTGGGAGTCGTCGATGTGT
GCACGATGACGTGAGGTCGAACCGCTGTCTCACTCTGAGGTAGAGTTTTTTTTTTTTTTTTTGCATAACCCTCAGCAGCTACACA

12,070

PINK1

PINK1-201

PINK1-201

GGTAGCCAGAGGCCCTCTCCCCTCTCCGCCAGCTATCCCTGTACCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCGCC
CCATCGGTCTCCGGGAGAGGGGAGAGGCGGTCGATAGGGACATGGGACGCGGTCATGGAAACACACTTGTGTGGGTCGGGGGCGG

12,155

PINK1

PINK1-201

Tyr Pro Cys Thr ³²⁵ Leu Arg Gln Tyr Leu Cys Val ³³⁰ Asn Thr Pro ³³⁵ Ser Pro Arg
ENSE00003693654

PINK1-201

TCGCCGCATGATGCTGCTGCAGCTGCTGGAAGGCGTGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGA
AGCGGCGGTACTIONACGACGACGTCGACGACCTTCCGCACCTGGTAGACCAAGTTGTCCCGTAGCGCGTGTCTCTGGACTTTAGGCT

12,240

PINK1

PINK1-201

³⁴⁰ Leu Ala Ala Met Met ³⁴⁵ Leu Leu Gln Leu Leu Glu Gly ³⁵⁰ Val Asp His Leu Val ³⁵⁵ Gln Gln Gly Ile Ala ³⁶⁰ His Arg Asp ³⁶⁵ Leu Lys Ser Asp
ENSE00003693654

PINK1-201

CAACATCCTTGTGGAGCTGGACCCAGGTAGGAACCTGCTGCACCATCAGAGCTCTCCAGGGGCACTAGAGGGTGGGTCAGGAGCA
GTTGTAGGAACACCTCGACCTGGGTCCATCCTTGGACGACGTGGTAGTCTCGAGAGGTCCCCGTGATCTCCACCCAGTCTCTCGT

12,325

PINK1

PINK1-201

³⁷⁰ Asn Ile Leu Val Glu Leu Asp Pro
ENSE00003693654

PINK1-201

TTTAGGACTGACTCTTCAGGTCTCTCTGGTTTTGTGTTCTAAGTCATGTCTTTATTTAGTCCGCACACAAGAGGTTAGCAATC
AAATCCTGACTGAGAAGTCCAGGAGAGACCAAAACACAAGATTCAGTACAGAAATAAATCGAGGCGTGTGTTCTCCAATCGTTAG

12,410

PINK1

PINK1-201

PINK1-201

TCTCCCTTAGAACGGGGTTTTTTTTTCTCTCTTTGCAGAGAGACAGCACTTCCCAAGTTCCTTTCTCTAGCCCACTTAAAGAACA
AGAGGGAATCTTGCCCCAAAAAAAAAAGAGAGAAACGTCTCTCTGTCTGTAAGGGTTCAAGGAAAGAGATCGGGTGAATTTCTTGT

12,495

PINK1

PINK1-201

PINK1-201

AGGACCTCAGTGCTGCAAGTTTTCTAGGTAAATAAAGAGGGCCCGGCACAGTGGCTGACACCTGTAATCCCAACACTTTGGGAGG
TCCTGGAGTCACGACGTTCAAAGGATCCATTTATTTCTCCGGGCCGTGTACCCGACTGTGGACATTAGGGTTGTGAAACCCTCC

12,580

PINK1

PINK1-201

PINK1-201

CTTGCTTGAGGATTGCTTGAGGCCAGCAGTTTTGAGACCAGCCTGGGAAACAGAGTGAGATCCCTTCTCTACAAAAAAAATATG
GAACGAACTCCTAACGAACTCCGGTCGTCAAACCTCTGGTCGGACCCCTTTGTCTCACTCTAGGGAAGAGATGTTTTTTTTTATAC

12,665

PINK1

PINK1-201

PINK1-201

TTTTAAATTAGCCGGAAAAAAGTTAGCCAGGCATGGTGGCATGCACCTGTAGCCCCAGCTACTTGGGAGGCTGAGGTCGGAGGA
AAAATTTAATCGGCCCTTTTTTCAATCGGTCCGTACCACCGTACGTGGACATCGGGGTCGATGAACCCCTCCGACTCCAGCCTCCT

12,750

PINK1

PINK1-201

PINK1-201

TCACTTGAGCCTAGGAGTTAAGAGTCTGCAATGAGCTATGAATGTGCCACTGTACTCCAGCCTGGGCAGCAGAGTGAGATCCTAT
AGTGAACTCGGATCCTCAATTCTCAGACGTTACTCGATACTTACACGGTGACATGAGGTCGGACCCGTCGTCTCACTCTAGGATA

12,835

PINK1

PINK1-201

PINK1-201

CTCAAAAAATAATAAAAAATAATAAAGTAAAGAGAAAGTAGACTTTAGCTCATTATAAAAAATAACTTTCGGCCGGGGGTAGTG
GAGTTTTTTTATTATTTTTTATTATTTTCATTTTCTTTCATCTGAAATCGAGTAATATTTTTTATTGAAAGCCGGCCCCATCAC

12,920

PINK1

PINK1-201

PINK1-201

GCTCACGCCTGTAATCCCAGCACTTTGAGAGGCTGAGGCGGGCAGATCATGAGGTCAAGAGATCGAGACCATCCTGGCCAACATG
CGAGTGCGGACATTAGGGTCGTGAAACTCTCCGACTCCGCCCGTCTAGTACTCCAGTTCTCTAGCTCTGGTAGGACCGGTTGTAC

13,005

PINK1

PINK1-201

PINK1-201

GTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCGGGCGCCTGTAATCTCAGCTACTTGGGAAGCTGAG
CACTTTGGGGTAGAGATGATTTTTATGTTTTTAATCGACCCGTACCACCGCCCGCGGACATTAGAGTCGATGAACCCCTTCGACTC

13,090

PINK1

PINK1-201

PINK1-201

GCAGGAGAATTGCTTGAACCCGGGAGGCGGAGGTTGTAGTGTAGCCGAGATTGTGCCACTGCATTCCAGCCTGGCGACAGAGTGAG
CGTCCTCTTAACGAACTTGGGCCCTCCGCCTCCAACATCACTCGGCTCTAACACGGTGACGTAAGGTCGGACCGCTGTCTCACTC

13,175

PINK1

PINK1-201

PINK1-201

AGTCCATCTCAAATAAATTAATTAATTAATTAATTTTTTCAAACAATGAAAGCTGTCCAAATGTAAGCCCAGTTGCCTCTGGAA
TCAGGTAGAGTTTTATTTAATTAATTAATTAATTTAAAAAGTTTGTACTTTTCGACAGGTTTACATTTCGGGTCAACGGAGACCTT

13,260

PINK1

PINK1-201

PINK1-201

ATGAGTTGCCTACCACTGGAAGCATTCAAGTAGAAGCTGAATGGCCACTTGCCTAGGAAAATTGTAAGGAGATTACATACATCTGA
TACTCAACGGATGGTGACCTTCGTAAGTTCATCTTCGACTTACCGGTGAACGGATCCTTTTAACATTCTCTAAGTATGTAGACT

13,345

PINK1

PINK1-201

PINK1-201

TAAATTTTTGAACTAGAAGATTTAAAAATAATTGACTAGAGGAACTGGCTTTTATTATTTCTTTATTTATTTACTTATTTATTTAT
ATTTAAAAACTTGATCTTCTAAATTTTATTAAGTATCTCTTGACCGAAAATAATAAGAAAATAAATAAATGAATAAATAAATA

13,430

PINK1

PINK1-201

PINK1-201

TTATTTATTTGAGACAGAATCTTGCTTTGTTGCCAGGCTGGAGTGCAGTGGCGCCATCTCAGCTCACTGCAACCTCTGCTTCCC
AATAAATAAACTCTGTCTTAGAACGAAACAACGGGTCCGACCTCACGTACCCGCGGTAGAGTCGAGTGACGTTGGAGACGAAGGG

13,515

PINK1

PINK1-201

PINK1-201

AGGTTCAAGCAATTCTCGTGCCTCCGCCTCCTGAGTAGCTAGGATTACAGGCAGGTGCCACCACGCCTAGCTAATTTTTGATTTT
TCCAAGTTCGTTAAGAGCACGGAGGCGGAGGACTCATCGATCCTAATGTCCGTCCACGGTGGTGCGGATCGATTAATAAACTAAAA

13,600

PINK1

PINK1-201

PINK1-201

TTTTTTTTTTTTTTTTTTTGGAGACTGAGTCTCGCTCTGTCAACCCAGGCTGGAGTGCAATGGCATGATCTCGGCTCACTGCAAGCTCT
AAAAAAAAAAAAAAAAAACTCTGACTCAGAGCGAGACAGTGGGTCCGACCTCACGTTACCGTACTAGAGCCGAGTGACGTTTCGAGA

13,685

PINK1

PINK1-201

PINK1-201

ACCTCCCAGGTTACACACCATTTCTCCTGCTTCAGCCTCCCAGTAGCTGGGACTACAGGCGCCACCACCACGCCCGGCTAATTTT
TGGAGGGTCCAAGTGTGGTAAGAGGACGAAGTCGGAGGGCTCATCGACCCTGATGTCCGCGGGTGGTGGTGCGGGCCGATTAATA

13,770

PINK1

PINK1-201

PINK1-201

TTTGTATTTTTAGTACAGACGGGGTTTTACCATGTTAGCCAGGATGGTCTCTATCTCCTGACTTCGTGATCCACCTGCTTCGGCC
AAACATAAAAAATCATGTCTGCCCAAAGTGGTACAATCGGTCTTACCAGAGATAGAGGACTGAAGCACTAGGTGGACGAAGCCGG

13,855

PINK1

PINK1-201

PINK1-201

TCCCAAAGCGCTGGGATTATTATTTTTAGTGGAGATGGGGTTTTCACTGTTGGCCAGGCTGGTCTCAAACCTCCTGGCCTCAAGTGA
AGGGTTTTCGCGACCCTAATAATAAAAAATCACCTCTACCCCAAAGTGACAACCGGTCCGACCAGAGTTTGAGGACCGGAGTTCACT

13,940

PINK1

PINK1-201

PINK1-201

TCCACCCACCTCAGCCTCCAAAATGTTGGGATTACAGGTATGAGCCACCACGCCCAGCTGGGAGTTGGCTTTTTTTTTTTTTTTTT
AGGTGGGTGGAGTCGGAGGTTTTACAACCCTAATGTCCATACTCGGTGGTGCGGGTCCGACCCTCAACCGAAAAAAAAAAAAAAAA

14,025

PINK1

PINK1-201

PINK1-201

TTTTTTGAGACGGAGTCTCACTCTGTGCCAGGCTGGAGTGCAGTGGCATGATCTTGGCTCACTGCAACCCCTGCCTATCGGGT
AAAAAATCTGCCTCAGAGTGAGACAGCGGGTCCGACCTCACGTACCGTACTAGAACCGAGTGACGTTGGGGACGGATAGCCCA

14,110

PINK1

PINK1-201

PINK1-201

TCAAGCAATTCTCCGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACACGCCACTACACCTGGCTGATTTTTGTATTTTTAG
AGTTCGTTAAGAGGGCGGAGTCGGAGGACTCATCGACCCTAATGTCCGTGTGCGGTGATGTGGACCGACTAAAAACATAAAAAATC

14,195

PINK1

PINK1-201

PINK1-201

TAGAGACGGGGTTTTACCATGTTGGTCAGGCTGATCTGGAACCTCCTGACTTCGTGATCCGCCTGCCTCGGCCTCCCAAAGTTCTG
ATCTCTGCCCAAAGTGGTACAACCAAGTCCGACTAGACCTTGAGGACTGAAGCACTAGGCGGACGGAGCCGGAGGGTTTTCAAGAC

14,280

PINK1

PINK1-201

PINK1-201

GGATTACAGGCGTGAGCCACTGCGCCCAGCCAGGAACTGGCTTTTTAAAGGAATTTTGTGTGGACCCCTTTTACAAATAACCAATT
CCTAATGTCCGCACTCGGTGACGCGGGTCGGTCCTTGACCGAAAAATTTCTTAAAAACACACCTGGGAAAAATGTTTATTGGTTAA

14,365

PINK1

PINK1-201

PINK1-201

CTTTTTTATTTTTTCTGAGACAGAGTCTCGCTGTGTTGCTCAGGCTGAAGTGATTCTCCTGTCTCAGCCTCCTTCACCTCCCAG
GAAAAAATAAAAAAGACTCTGTCTCAGAGCGACACAACGAGTCCGACTTCACTAAGAGGACAGAGTCGGAGGAAGTGGAGGGTC

14,450

PINK1

PINK1-201

PINK1-201

GTTCAAGTAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGATACAGGCACACACCACCATGCCTGGCTAGTTTTTTTGTATTTT
CAAGTTCATTAAGAGGACAGAGTCGGAGGGCTCATCGACCCTATGTCCGTGTGTGGTGGTACGGACCGATCAAAAAACATAAAA

14,535

PINK1

PINK1-201

PINK1-201

TAGTAGAGACAGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATCTACCCGCCTCGGCCTCCCAAA
ATCATCTCTGTCCCAAAGTGGTACAACCGGTCCGACCAGAACTTGAGGACTGGAGTCCACTAGATGGGCGGAGCCGGAGGGTTT

14,620

PINK1

PINK1-201

PINK1-201

ATGTTGGCATTACAGGCCACCACACCCGGCAATAACTGATTCTTAATGCACCTGGTTCTTAGGTTTGGATTTGGGGTTTCAAATT
TACAACCGTAATGTCCGGTGGTGTGGGCCGTTATTGACTAAGAATTACGTGGACCAAGAATCCAAACCTAAACCCCAAAGTTTAA

14,705

PINK1

PINK1-201

PINK1-201

PCR Forward

aatcaaagtctcctgggggtataagg

CAAATCAAAGTCTCCTGGGGTATAAGGGCCCTTGGAGATCATTTGAACCAAGCTCTAGCTCCTTTGGTCTTGGGGACAGCTCCAA
GTTTAGTTTCAGAGGACCCCATATTCGCGGAACCTCTAGTAAACTTGGTTCGAGATCGAGGAAACCAGAACCCTGTGAGGGTT

14,790

PINK1

PINK1-201

PINK1-201

TTACTAGAACATGATTTAAATTGAGCCACACAGTCCTTTGCCTGGGGATTTTGCAGCCTGTACTTACTGGAGGCATTTCCGTGTT
AATGATCTTGTACTAAATTTAACTCGGTGTGTCAGGAAACGGACCCCTAAAACGTGCGACATGAATGACCTCCGTAAAGGCACAA

14,875

PINK1

PINK1-201

PINK1-201

Sanger Sequencing Primer
ccaacactgagccattagcc

CGCACAGCAGGCCCTTCTGATCAGCTCTCAGGCCTTGCTGACCTCCTGGGCCAACACTGAGCCATTAGCCCCTGTCAGCTATGTC
GCGTGTTCGTCGGGAAGACTAGTCGAGAGTCCGGAACGACTG6AGGACCCGGTTGTGACTCGGTAATCGGGGACAGTCGATACAG

14,960

PINK1

PINK1-201

PINK1-201

TTGCTGGTGGCTTTAGTAGGGACATAGGAGGGCCTCTCAGAG6GAAGGAGGGGAGGAGAAATGGTCACTTTGCTTGTCTCCTTCCC
AACGACCACCGAAATCATCCCTGTATCCTCCCGGAGAGTCTCCCTTCTCCCTCCTCTTTACCAGTGAAACGAACGAGGAAGGG

15,045

PINK1

PINK1-201

PINK1-201

gRNA Protospacer
TGCAGTTGCCCTTCAGCAGC

AGACGGCTGCCCTGGCTGGTGCATCGCAGATTTTGGCTGCTGCCTGGCTGATGAGAGCATCGGCCCTGCAGTTGCCTTCAGCAGC
TCTGCCGACGGGGACCGACCACTAGCGTCTAAAACCGACGACGGACCGACTACTCTCGTAGCCGGACGTCAACGGAAGTCGTCTG

15,130

PINK1

PINK1-201

375 Asp Gly Cys Pro Trp 380 Leu Val Ile Ala Asp Phe 385 Gly Cys Cys Leu Ala 390 Asp Glu Ser Ile 395 Gly Leu Gln Leu Pro 400 Phe Ser Ser
ENSE00003662034

PINK1-201

Donor Template WT -> SNV

Protospacer Sequence

SNV

GACTACTCTCGTAGCCGGACGTCAACGGAAGTCGTCTG

Donor Template

TGGTACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAAGAGGTGAGTCCCGAGTGTGTCATGCGCCATCGGCAGCCCTTCC
ACCATGCACCTAGCCCCGCCTTTGCCGACAGACTACCGGGGCTCCACTCAGGGCTCACACAGTACGCGGTAGCCGTCGGGAAGG

15,215

PINK1

PINK1-201

405 Trp Tyr Val Asp Arg Gly Gly 410 Gly Cys Leu Met Ala 415 Pro Glu
ENSE00003662034

PINK1-201

Donor Template WT -> SNV

PAM

ACCATGCACCTAGCCCCGCCTTTGCCGACAGACTACCGGGGCTCcaactcagggctcacaca

Donor Template

CCCACATGTCCACTGAATGCAGGAGACTCGATGCCTTGTGATAACCCAACACCTCCATCTTTTCTGACCCATAATTTGGCACAAG
GGGTGTACAGGTGACTTACGTCTCTGAGCTACGGAACACTATTGGGTTGTGGAGGTAGAAAAGACTGGGTATTAAACCGTGTTTC

15,300

PINK1

PINK1-201

PINK1-201

TTCTTCCCTGCCACTTTGCTTTCTCCGGCGTTCCCTCATGTTCCAGGAGAATGCAAGTCCTGTACATAAACCCAGGTGGTCTA
AAGGAAGGGACGGTGAAACGAAAGGAGGCCGCAAGGGAGTACAAGGTCTCTTACGTTTCAGGACAGTGTATTTGGTCCACCAGAT

15,385

PINK1

PINK1-201

PINK1-201

AGCAGACCCCTTCTGGGTCTGAGCCACAGCTCACTCAAGCTCTGGGTTTCCTTGGGACAGAGTTCAGATTAGCCCATGGATCAGGT
TCGTCTGGGGAAGACCCAGACTCGGTGTCGAGTGAGTTCGAGACCCAAGGAACCTGTCTCAAGTCTAATCGGGTACCTAGTCCA

15,470

PINK1

PINK1-201

PINK1-201

GATGTGCAGGACATGAAAAGGTTAGATGGGCGGGCAGCGTGATGTCTCACCCACTGCTTCTGAGCAGGTGTCCACGGCCCGTCTCT
CTACACGTCCTGTACTTTTCCAATCTACCCGCCCGTTCGCACTACAGAGTGGGTGACGAAGACTCGTCCACAGGTGCCGGGCAGGA

15,555

PINK1

PINK1-201

Val Ser Thr Ala Arg Pro
ENSE00003524815

PINK1-201

GGCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCTTGTCAATC
CCGGGGTCCCGTCACTAACTGATGTCGTTCCGACTACGGACCCGTCACCCTCGGTAGCGGATACTTTAGAAGCCCCGAACAGTTAG

15,640

PINK1

PINK1-201

Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val Asn
ENSE00003524815

PINK1-201

GATACTTTAGAAGCCCCGAACAGTTA
PCR Reverse

CCTTCTACGGCCAGGGCAAGGCCACCTTGAAAAGCCGCACTACCAAGAGGCTCAGCTACCTGCACTGCCCGAGTCAGTGCCTCC
GGAAGATGCCGGTCCCGTTCGGGTGGAACCTTCGGCGTCGATGGTCTCCGAGTCGATGGACGTGACGGGCTCAGTCACGGAGG

15,725

PINK1

PINK1-201

Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro
ENSE00003524815

PINK1-201

AGACGTGAGACAGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGGTGAGGCTGTCCCCGGCTTCGAGGGGACGGTGTGGG
TCTGCACTCTGTCAACCACTCCCGTGACGAGGTCGCTCTCCGGTCGTTCCACTCCGACAGGGGCGAAGCTCCCCTGCCACACCC

15,810

PINK1

PINK1-201

Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys
ENSE00003524815

PINK1-201

TAGAAACCTCTGTTCTCGTTCCAGAGTGAAGGTCAGGTTTGGGCCAGAGCCACAGTGACAGATCCTCTGTGTTAGGAAGGTAAAG
ATCTTTGGAGACAAGAGCAAGGTCTCACTTCCAGTCCAAACCCGGTCTCGGTGTCACTGTCTAGGAGACACAATCCTTCCATTTTC

15,895

PINK1

PINK1-201

PINK1-201

GCTAGTTACAAGAGAACAAAAACAGATTTTAATGTAGGTAGGAGTAGGAGCACTAGCCACCACAGCATAGTCAGAATCCTAGCA
CGATCAATGTTCTCTTGTTTTTTGTCTAAAATTACATCCATCCTCATCCTCGTGATCGGTGGTGTCTGATCAGTCTTAGGATCGT

15,980

PINK1

PINK1-201

PINK1-201

GTTCAACTCCTGTGGCTTTTTTAGTTGCTGAAAAAGTTGTTTCAGAGGCCAGACACGGTGGCTTACACCTATAATCACAGCACTTT
CAAGTTGAGGACACCGAAAAAATCAACGACTTTTTCAACAAGTCTCCGGTCTGTGCCACCGAATGTGGATATTAGTGTCTGAAA

16,065

PINK1

PINK1-201

PINK1-201

GGGAGGCTGAGGCGGGTGGATCACTTGGGACCAGGAGTTCCAGTCCAGCCTGGCCAACATGGTAAAACCCCGTCTGTACTAAAAA
CCCTCCGACTCCGCCACCTAGTGAACCCTGGTCTCAAGGTCAAGGTCAGGTCGGACCGGTTGTACCATTTTGGGGCAGACATGATTTTT

16,150

PINK1

PINK1-201

PINK1-201

TACAAAAATTAGCTGAGTGTCTGTTGGCACACGCCTGTAATTCAGGTA CTGGGAGGCTGAAGCAGGAGAATCGTTTGAACCCTGG
ATGTTTTTAATCGACTCACAGCACCGTGTGCGGACATTAAGGTCCATGAGCCCTCCGACTTCGTCTCTTAGCAAACTTGGGACC

16,235

PINK1

PINK1-201

PINK1-201

AGGCAGAGGTTGCAGTGAGCCAAGATCGCGCCACTGCACTCTGGCCTAGGTGACAGTGCAAGTCTTTGTCTCAAAAAAAAAAAAA
TCCGTCTCCAACGTCACCTCGGTTCTAGCGCGGTGACGTGAGACCGGATCCACTGTCACGTTTCAGAAACAGAGTTTTTTTTTTTTT

16,320

PINK1

PINK1-201

PINK1-201

AAAAAAAAAGGCTATTCAGAGAGAGAAAAGGAGGCATTTTTGAGAAATGTTTAAATGGAGATGTAGCTCATGGAAGCAGCTGAGAA
TTTTTTTTTCCGATAAGTCTCTCTTTTTCTCCGTAAAAACTCTTTACAAATTACCTCTACATCGAGTACCTTCGTCTGACTCTT

16,405

PINK1

PINK1-201

PINK1-201

CTGATCAGAGAGAGATGGAAAACATCTCCTGAGAGCAGATCTGGACATTGTGAAATTAATATAAAAGGAATGCAAAGGCAGACCTA
GACTAGTCTCTCTCTACCTTTTGTAGAGGACTCTCGTCTAGACCTGTAACACTTTAATTATATTTTCCTTACGTTTCCGCTCTGGAT

16,490

PINK1

PINK1-201

PINK1-201

TCCGAAGCCATAATTGGAGTGGCAGCTGGCTCAGGGGCAGGCTTAGTGCAAAGAGCTGAGCCATACCTGCACCCCAGCACTGTTC
AGGCTTCGGTATTAACCTCACCGTCGACCGAGTCCCCGTCCGAATCACGTTTCTCGACTCGGTATGGACGTGGGGTCTGTGACAAG

16,575

PINK1

PINK1-201

PINK1-201

TGCCACTCCGTTAACTGCTCTCTGTACGTGGCCTGCTATCTTGGTGCGCAGTGAAGGTTAGAACAACAGCTGCAACCAGTTATGA
ACGGTGAGGCAATTGACGAGAGACATGCACCGGACGATAGAACCACGCGTCACTTCCAATCTTGTGTGTCGACGTTGGTCAATACT

16,660

PINK1

PINK1-201

PINK1-201

AATGATAGAGGAGACTACTTACCTGGTTCAAGGGACCAGATAGCTGTGCACAAGAGGCACTAGGCTTTCCACCCAGGGGGAAAGG
TTACTATCTCCTCTGATGAATGGACCAAGTTCCTGGTCTATCGACACGTGTTCTCCGTGATCCGAAAGGTGGGTCCCCCTTTCC

16,745

PINK1

PINK1-201

PINK1-201

CTATTTCAACAATGCATGCTGCCCATGCAGAGGTGTACACATGGAAAAGCTTGGAGCACGGGCAGGGGACAGGCAGTATTTGTC
GATAAAGTTGTTACGTACGACGGGGTACGTCTCCACATGTGTACCTTTTCGAACCTCGTGCCCGTCCCCTGTCCGTCATAAACAG

16,830

PINK1

PINK1-201

PINK1-201

ACCTGAGTGAAGGGCATCAGTAGGAGATAGGGTAGAGGAAGAATTGGGTTGGGACCAGAGAAGGGAAGACCCTCACTAACAAAGC
TGGACTCACTTCCCAGTAGTCATCCTCTATCCCATCTCCTTCTTAACCCAACCCTGGTCTCTTCCCTTCTGGGAGTGATTGTTTCG

16,915

PINK1

PINK1-201

PINK1-201

AGGCTTTGGGTTGAGACTGTGTTAACAGATGTTCTAGCTACAGCTTCCCTTCTGTTGCAGAGACCATCTGCCCGAGTAGCCGCA
TCCGAAACCCAACCTCTGACACAATTGTCTACAAGATCGATGTCGAAGGGAAGGACAACGTCTCTGGTAGACGGGCTCATCGGCGT

17,000

PINK1

PINK1-201

PINK1-201

500
Arg Pro Ser Ala Arg Val Ala Ala
ENSE00001543152

AATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGGCTGGCTCCTCC
TTACACGAAGTAGATTTCGGAGACCCCACTTGTATAAGATCGGGACTTCTTAGACTTCAATCTGTTCTACCAACCGACCGAGGAGG

17,085

PINK1

PINK1-201

505 Asn Val Leu His Leu Ser Leu Trp Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp Leu Leu
510 515 520 525 530

ENSE00001543152

PINK1-201

AACAATCGGCCGCCACTTTTGTGGCCAACAGGCTCACAGAGAAGTGTGTGTGAAACAATAAATGAAGATGCTCTTTCTGGCTAA
TTGTTAGCCGGCGGTGAAACAACCGGTTGTCCGAGTGTCTCTTACAACACACCTTTGTTTTTACTTCTACGAGAAAGACCGATT

17,170

PINK1

PINK1-201

Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn
535 540 545 550 555 560

ENSE00001543152

PINK1-201

CCTGGAGTGTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGTG
GGACCTCACACTTTGCGAGACGGTCCGTCCGGAGGAGGAGACGAGTACCTCCCGTCGGGACACTACAGGGACGTACCTCGACCAC

17,255

PINK1

PINK1-201

Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg Ala Ala Leu
565 570 575 580

ENSE00001543152

PINK1-201

AATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAG
TTAATGATTTTTCTTGTACCCTAGGAGACACAGCACTACCAGACACTTACCACTCCACCCCTCAGTCTCTGTTCTGTGCGGTCTC

17,340

PINK1

PINK1-201

AGGGCTGGTTAGCCGAAAAGGCCTCGGGCTTGGCAAATGGAAGAAGTGTGAGTGTGAGAGTTTCAGTCTGCAGTCTCTGCTCACAGA
TCCCGACCAATCGGCCTTTTCCGGAGCCCGAACCGTTTACCTTCTTGAACCTCACTCTCAAGTCAGACGTGAGGAGACGAGTGTCT

17,425

PINK1

PINK1-201

CATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATCCACAGAGAGGATCCAG
GTAGACTTTTCACTTACCAGTTCGACCAGATCATCTACTCCGACCTGACTCCTCCCATCCGGACGTAGGTGTCTCTCTAGGTC

17,510

PINK1

PINK1-201

GCCAAGGCACTGGCTGTGTCAGTGGCAGAGTTTGGCTGTGACCTTTGCCCTAACACGAGGAAGTTCGTTTGAAGGGGGCAGCGTAGC
CGGTTCCGTGACCGACAGTACCGTCTCAAACCGACACTGGAACCGGGATTGTGCTCCTTGAGCAAACCTCCCCCGTCGCATCG

17,595

PINK1

PINK1-201

ATGCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGTCAGCACGTTTCAGTTACGGGAGTGGGAAATTACATGAGGCCT
TACAGACTAAACGGTGGACCTACTTCCGTCTGTAGTTGTACCCAGTCTGCAAGTCAATGCCCTCACCTTTAATGTACTCCGGA

17,680

PINK1

PINK1-201

GGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATCTCACTTAGCGAAAAGTGACGGATGAGCAGTAA

CCCGGAGACGCAAGGGTTTCGACACGCAAGACCTGGTTCGATGACTTAATAATTAGAGTGAATCGCTTTCACTGCCTACTCGTCATT

17,765

PINK1 >

PINK1-201 >

GTAAGTAAGTGTGGGGATTTAAACTTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAATT

CATTTCATTACACCCCTAAATTTGAACTCCCAAAGGGAGGACTGATCGGAGAGAATGTCCTTAACACTTTATAATTTACGTTTAA

17,850

PINK1 >

PINK1-201 >

TACAACTGCAGATGACGTATGTGCCTTGAAGTGAATATTTGGCTTTAAGAATGATTCTTATACTCTGAAGGTGAGAATATTTTGT

ATGTTGACGTCTACTGCATACACGGAAGTTGACTTATAAACCGAAATTCTTACTAAGAATATGAGACTTCCACTCTTATAAAACA

17,935

PINK1 >

PINK1-201 >

GGGCAGGTATCAACATTGGGGGAAGAGATTTTCATGTCTAACTAACTTTATACATGATTTTTAGGAAGCTATTGCCTAAATCA

CCCGTCCATAGTTGTAACCCCTTCTCTAAAGTACAGATTGATTGATTGAAATATGTACTAAAAATCCTTCGATAACGGATTTAGT

18,020

PINK1 >

PINK1-201 >

GCGTCAACATGCAGTAAAGGTTGTCTTCAACTGA

CGCAGTTGTACGTCATTTCCAACAGAAGTTGACT

3'

18,054

5'

PINK1 >

PINK1-201 >

Feature	Location	Size	Color	Symbol	Type
✓ PINK1	1 .. 18,054	18,054 bp	■	→	gene
/note	= gene ENSG00000158828 Protein coding				
✓ PINK1-201	1 .. 18,054	18,054 bp	■	→	prim_transcript
/note	= primary transcript ENST00000321556				
✓ PINK1-201	92 .. 17,234	17,143 bp	■	→	CDS
▶ 8 segments = 1746 bp					
/note	= coding sequence ENSP00000364204				
/translation	= MAVRQALGRGLQLGRALLRFTGKPGRAYGLGRPGPAA GCVRGERPGWAA GPGAEP RRVGLGLPNLRFFRQSVAGLAARLQRQFVVRAW GCAGPCGRAVFLAFGLGLG LIEEKQAESRRRAVSACQEIQ,,AIFTQKSKPGPDPLDTRRLQGFRLEEYLIQSIGKGC SAAVYEATMPTLPQNL EVTKSTGLLPGRPGTSAPEGGQERAPGAPAFPLAIKMMWNIS,,AGSSSEAILNTMSQELVPASRVALAGEYGAVTYR,,KSKRGPQKLA PHP NIIRVLRAFTSSVPLLPGALVDYPDVLP SRLHPEGLGHGRTLFLVMKN,,YPC TLRQYLCVNT P SPRLAAMMLLQLLEGVDHLVQQGIAHRDLK SDNILVELDP,,DGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPE,,VSTARPGPRAVIDYSKADA WAVGAIAYEIFGLV NPFY GQGKAHLESRSYQEAQLPALPESVPPDVRQLVRALLQREASK,,RPSARVAANV LHLSLWGEHILAKNLKLDKMGVWLLQQSAATLLANRLT 5'CGMFTAKNLELADLFCF LCQAALLCSWRAAL*				
MIR6084	222 .. 331	110 bp	■	→	gene
/note	= gene ENSG00000284005 miRNA				
MIR6084-201	222 .. 331	110 bp	■	→	prim_transcript
/note	= primary transcript ENST00000622012 miRNA				
PINK1-203	4672 .. 17,859	13,188 bp	■	→	prim_transcript
/note	= primary transcript ENST00000492302 protein_coding_CDS_not_defined				
PINK1-AS	9200 .. 18,736	9537 bp	■	←	gene
/note	= gene ENSG00000117242 lncRNA				
PINK1-AS-201	9200 .. 18,736	9537 bp	■	←	prim_transcript
/note	= primary transcript ENST00000451424 lncRNA				
PINK1-202	12,051 .. 18,053	6003 bp	■	→	prim_transcript
/note	= primary transcript ENST00000400490 protein_coding_CDS_not_defined				
✓ Donor Template WT -> SNV	15,093 .. 15,192	100 bp	■	⇌	misc_feature
✓ Protospacer Sequence	15,111 .. 15,130	20 bp	■	⇌	misc_feature
✓ SNV	15,120 .. 15,120	1 bp	■	⇌	misc_feature
/note	= WT = C SNV = T				
✓ PAM	15,131 .. 15,133	3 bp	■	⇌	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ gRNA Protospacer	20-mer	6062 .. 6073 15,111 .. 15,130	49°C 63°C	Mar 23, 2023
/sequence =	TGCAGTTGCCCTTCAGCAGC 60% GC / 6069.0 Da			
✓ PCR Foward	25-mer	14,708 .. 14,732	58°C	Mar 23, 2023
/sequence =	aatcaaagtctcctgggtataagg 44% GC / 7730.1 Da			
✓ Sanger Sequencing Primer	20-mer	14,926 .. 14,945	57°C	Mar 23, 2023
/sequence =	ccaacactgagccattagcc 55% GC / 6031.0 Da			
✓ Donor Template	100-mer	15,093 .. 15,192	82°C	Mar 23, 2023
/sequence =	acacactcgggactcacCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGAGCAACTGCAGGCCGATG 61% GC / 6000.8 Da			
✓ PCR Reverse	25-mer	15,615 .. 15,639	58°C	Mar 23, 2023
/sequence =	ATTGACAAGCCCGAAGATTTTCATAG 40% GC / 7674.1 Da			