

INK2J00028.1R_PSEN1_E276A_A12_AA
 27,076 bp

5'

3'

TAGTGGCACACACCTGTTGTCCCAGCTACTTAGGAGGCTGAGCTGGGAAGACCACCTGATCTCCGGAGGTAAAGACTGCAGTGAG
ATCACCGTGTGTGGACAACAGGGTCGATGAATCCTCCGACTCGACCCCTTCTGGTGGACTAGAGGCCTCCATTTCTGACGTCACCTC

85

PSEN1

PSEN1-201

CCGTGATTGCACCACTTTACTCCAGCCTGGGCAACAAAATGAGACCCTGGCTCAAAAACAAAACAAAACAAAAGAGTAAA
GGCACTAACGTGGTGAAATGAGGTCGGACCCGTTGTTTTACTCTGGGACCGAGTTTTTGTTTTTGTTTTGTTTTTCTCATTT

170

PSEN1

PSEN1-201

TTAATTTAAAGGGAAGTATTAATAAATAATAGCACAGTTGATATAGGTTATGGTAAAATTATAAAGGTGGGATATTAATATCTA
AATTAATTTCCCTTCATAATTTATTTATTATCGTGTCAACTATATCCAATACCATTTTAATATTTCCACCCTATAATTATAGAT

255

PSEN1

PSEN1-201

ATGTTTGGGAGCCATCACATTATTCTAAATAATGTTTTGGTGAAAATTATTGTACATCTTTTAAAATCTGTGTAATTTTTTTTCA
TACAAACCTCGGTAGTGAATAAGATTTATTACAAAACCACTTTAATAACATGTAGAAAATTTAGACACATTAAAAAAAAGT

340

PSEN1

PSEN1-201

GGGAAGTGTTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGAT
CCCTTCACAAAATTTTGGATATTGCAACGACACCTGATGTAATGACAACGTGAGGACTAGACCTTAAAACACACCACCTTACTA

425

PSEN1

PSEN1-201

185 190 195 200 205 210
E V F K T Y N V A V D Y I T V A L L I W N F G V V G M I

ENSE00003979383

PSEN1-201

TTCCATTCACCTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTATTATCAAG
AAGGTAAGTGACCTTTCCAGGTGAAGCTGAGGTCGTCCGTATAGAGTAATACTAATCACGGGAGTACCGGGACCACAAATAGTTC

510

PSEN1

PSEN1-201

215 220 225 230 235
S I H W K G P L R L Q Q A Y L I M I S A L M A L V F I K

ENSE00003979383

PSEN1-201

TACCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTTCAGTATATGGTAAAACCCAAGACTGATAATTTGTTTGTCA
ATGGAGGGGACTTACCTGACGCACCGAGTAGAACCGACACTAAAGTCATATACCATTTTGGGTTCTGACTATTAAACAAACAGTGT

595

PSEN1

PSEN1-201

240 245 250 255
Y L P E W T A W L I L A V I S V Y

ENSE00003979383

PSEN1-201

GGAATGCCCCACTGGAGTGTTTTCTTTCTCATCTCTTTATCTTGATTTAGAGAAAATGGTAAACGTGTACATCCCATAACTCTTC
CCTTACGGGGTGACCTCACAAAAGAAAGGAGTAGAGAAAATAGAACTAAATCTTTTTACCATTGCACATGTAGGGTATTGAGAAG

680

PSEN1

PSEN1-201

PSEN1-201

AGTAAATCATTAAATTAGCTATAGTAACTTTTTTCATTTGAAGATTTTCGGCTGGGCATGGTAGCTCATGCCTGTAATCTTAGCACTT
TCATTTTAGTAATTAATCGATATCATTGAAAAAGTAACTTCTAAAGCCGACCCGTACCATCGAGTACGGACATTAGAATCGTGAA

765

PSEN1

PSEN1-201

PSEN1-201

TGGGAGGCTGAGGCGGGCAGATCACCTAAGCCCAGAGTTCAAGACCAGCCTGGGCAACATGGCAAAACCTCGTATCTACAGAAAA
ACCCTCCGACTCCGCCCGTCTAGTGGATTTCGGGTCTCAAGTTCTGGTCCGACCCGTTGTACCGTTTTGGAGCATAGATGTCTTTT

850

PSEN1

PSEN1-201

PSEN1-201

TACAAAAATTAGCCGGGCATGGTGGTGCACACCTGTAGTTCCAGCTACTTAGGAGGCTGAGGTGGGAGGATCGATTGAGCCCAGG
ATGTTTTTAATCGGCCCGTACCACCACGTGTGGACATCAAGGTCGATGAATCCTCCGACTCCACCCTCCTAGCTAACTCGGGTCC

935

PSEN1

PSEN1-201

PSEN1-201

AGGTCAAGGCTGCAGTGAGCCATGATTGCATCACTGTATTCCAGCCTGGGTGATAGAACAAGACCTTGTCTCAAAAAAATTTGG
TCCAGTTCCGACGTCCTCGGTACTAACGTAGTGACATAAGGTCGGACCCACTATCTTGTCTGGAACAGAGTTTTTTTTAAACC

1020

PSEN1

PSEN1-201

PSEN1-201

TTTTTCAAGCTTTTTGAGGTTTTGACAAGCTGGCCAATATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGTGT
AAAAAGTTTGAAAAACTCCAAAACTGTTTCGACCGGTTATACCACTTTGGGGCAGAGATGATTTTTATGTTTTTAATCGACCCACA

1105

PSEN1

PSEN1-201

PSEN1-201

GGTGGCGTACCCTTGTATTCCAGCTACTTGAGAGGCTGAGGCAGGAGAATTATTTGAACCCAGGAAGTGAAGTGGAGGTTGCAG
CCACCGCATGGGAACATAAGGGTCGATGAACTCTCCGACTCCGTCCTCTTAATAAACTTGGGTCTTCACTTCACCTCCAACGTC

1190

PSEN1

PSEN1-201

PSEN1-201

TGAGCCGAGATGGTGCCACTGCACTCTAGCCTGGGTGACAGAGCGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGCAAAAAAAAAA
ACTCGGCTCTACCACGGTGACGTGAGATCGGACCCACTGTCTCGCTCTGAGACAGAGTTTTTTTTTTTTTTTCGTTTTTTTTTTT

1275

PSEN1

PSEN1-201

PSEN1-201

AGCACAAGCAGAGTGGTAGACACACAAAATGCTCAATTCATTTTTTAAACGATTTTTTTCCTTTATATCTTACTGCAGAAAGCTTT
TCGTGTTTCGTCTCACCATCTGTGTGTTTTACGAGTTAAGTAAAAAATTTGCTAAAAAAAAGGAAATATAGAATGACGTCTTCGAAA

1360

PSEN1

PSEN1-201

PSEN1-201

TTTCTTTTTTTTTGAGACAAAGTCTTGCTGTGTCACCCAGGCTGGGGTGCAGTGGCACAGTCATAGCTCACTGCAACCTTGAAGCTC
AAAGAAAAAAAACCTCTGTTTCAGAACGACACAGTGGGTCCGACCCACGTCACCGTGTGTCAGTATCGAGTGACGTTGGAACCTTGAG

1445

PSEN1

PSEN1-201

PSEN1-201

CCTGGCTCATGCGATCCTCCCACTTCAGCCTCTCAAGTAGCTAGAACTACAGGTGTGCACCACCATGCCTGACTAACTTGTTTTAT
GGACCGAGTACGCTAGGAGGGTGAAGTCGGAGAGTTTCATCGATCTTGATGTCCACACGTTGGTGGTACGGACTGATTGAACAAATA

1530

PSEN1

PSEN1-201

PSEN1-201

TTTTTGTAGAGAGAACGTCTTGCTATATTGCCTAGGCTGGTCTTGAAGCTCTTGGGCTCAAGCAATCCTCCTACCTTGGCCTCTCA
AAAAACATCTCTCTTGCAGAACGATATAACGGATCCGACCAGAAGCTTGAGAACCCGAGTTCGTTAGGAGGATGGAACCGGAGAGT

1615

PSEN1

PSEN1-201

PSEN1-201

AGGTATTGGGATTATAGGTGTGAGCCACTGCATCTGGCCTCAATTCACTTTTTAAAATCAAATAGGTTACCTACTTTTTATAAG
TCCATAACCCTAATATCCACACTCGGTGACGTAGACCGGAGTTAAGTGAAAATTTTAGTTTTAATCCAATGGATGAAAAATATTC

1700

PSEN1

PSEN1-201

PSEN1-201

GTAATGTATAGAATTATTCTTTTTAAAAATAAAACCGATTTGGACAGTGTGAGATTCACATTCTGTAACCACCAGTGTGACATGGG
CATTACATATCTTAATAAGAAAATTTTTATTTTGGCTAAACCTGTCACACTCTAAGTGTAAGACATTGGTGGTACACTGTACCC

1785

PSEN1

PSEN1-201

PSEN1-201

TCCTGAACAGTTAGAACATACTCCAGCCATTAACCCAGGCAGCTTTCAGGTACGTACTCTGTGGCTGTTGCCTTGTATGAAAGCC
AGGACTTGTCAATCTTGTATGAGGTCGGTAATTGGGTCCGTCGAAAGTCCATGCATGAGACACCGACAACGGAACATACTTTCCG

1870

PSEN1

PSEN1-201

PSEN1-201

AAAAAGAGATCCATTTTCAGAGATTAATATGTGACCCCTTCTATATTATAAGGCCATGGCCATACTCTTTTTTTTTTTCTTTTTGT
TTTTTCTCTAGGTAAAAGTCTCTAATTATACACTGGGGAAAGATATAATATTCCGGTACCGGTATGAGAAAAAAAAAAGAAAAACA

1955

PSEN1

PSEN1-201

PSEN1-201

TTTTTTCTTCCAAAGACAGGATCTCTCTCTGTCATCCACGCTAGAGTACAGTGGCATGAACGTGGCTTACTGCAGCCTCAAACCC
AAAAAAGAAGGTTTCTGTCCTAGAGAGAGACAGTAGGTGCGATCTCATGTCACCGTACTTGCACCGAATGACGTCGGAGTTTGGG

2040

PSEN1

PSEN1-201

PSEN1-201

TTGTCCTGGGCTCAAACAATCCTCCACCTCAGCCTTCAAAGTAGATAGAACTACAGGCATGCACTACCATGCCTAATTTTTTAA
AACAGGACCCGAGTTTGTAGGAGGGTGGAGTCGGAAGTTTTCATCTATCTTGATGTCCGTACGTGATGGTACGGATTAAAAAATT

2125

PSEN1

PSEN1-201

PSEN1-201

AAAAAAATTTTTTTTCAGAGATGAGATCTCACTGTGTTTTCCAGGCTTGTCCGGAACCTCTGGCCTCAAGCGATCCTCCACCTT
TTTTTTTAAAAAAGTCTCTACTCTAGAGTGACACAAAGGGTCCGAACAGGCCTTGAGGACCGGAGTTCGCTAGGAGGGTGGAA

2210

PSEN1

PSEN1-201

PSEN1-201

GGCCTGCCAAAGTGTGGGATTACAGGCATGAGCCACCATGCCTGGCCATACACTTTTTTTTTTTTTTTTTTTTCAAGACGGAGTC
CCGGACGGTTTTCAACAACCTAATGTCCGTA CTGCGGTGGTACGGACCGGTATGTGAAAAAAAAAAAAAAAAAAGTTCTGCCTCAG

2295

PSEN1

PSEN1-201

PSEN1-201

TGGCTCTGTCGCCAGACTGGAGTGCAGTGGCGTGATCTTGGCTCACTGCAAGCTTCGCCTCCCAGGTTTCATGCCGTTCTCCTGC
ACCGAGACAGCGGGTCTGACCTCACGTACCGCACTAGAACCGAGTGACGTTTCGAAGCGGAGGGTCCAAGTACGGCAAGAGGACG

2380

PSEN1

PSEN1-201

PSEN1-201

CTCAGCCTCCCAAGTAGCTGGGACTACAGGCATCTGCCACCACGCCCGGCTATTTTTTTGTATTTGTAGTAGAGACGGGGTTTCA
GAGTCGGAGGGTTTCATCGACCCTGATGTCCGTAGACGGTGGTGCGGGCCGATAAAAAAACATAAACATCATCTCTGCCCAAAGT

2465

PSEN1

PSEN1-201

PSEN1-201

CCATGTTAGCCAGGATGATCTCGATCTCCTGACCTCATGATTCACCTGCCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAG
GGTACAATCGGTCTACTAGAGCTAGAGGACTGGAGTACTAAGTGACGGAGCCGGAGGGTTTCACAACCCTAATGTCCGTA

2550

PSEN1

PSEN1-201

PSEN1-201

CCACCGTGCCCGGCCTGGCCATACACTTTTTGTCATTATTTACATACTTACTAAAATGTTTGGTGCCCTGTAATAGGAAACATCAT
GGTGGCACGGGCCGGACCGGTATGTGAAAACAGTAATAAATGTATGAATGATTTTACAAAACCACCGGACATTATCCTTTGTAGTA

2635

PSEN1

PSEN1-201

PSEN1-201

CCTCATTGATTGACGAAGAAGTCTGTGGAAATAGGATTGAACTGGTTCTGTTCTTGTATTTGAGTAATCAGTTGTGGAACATA
GGAGTAAACTAACTGCTTCTTCAGACACCTTTATCCTAACTTGACCAAGACAAGAACATAAACTCATTAGTCAACACCTTGATAT

2720

PSEN1

PSEN1-201

PSEN1-201

GAAGTCATATACTCTCTCTGACTTTCATAATTACCTTATGTTGTATAGTACTTGATGGTTTGC AAAAGTAACCATCTATTCTTGCT
CTTCAGTATATGAGAGAGACTGAAAGTATTAATGGAATACAACATATCATGAACTACCAAACGTTTCATTGGTAGATAAGAACGA

2805

PSEN1

PSEN1-201

PSEN1-201

TAGCTGTGAGTAAGAATGCCAGGTCTGGAGACAGAATGTCTGGGTTCAAATCTACTCATCACTTTTTATTTTTATTTTTTTTGA
ATCGACACTCATTCTTACGGTCCAGACCTCTGTCTTACAGACCCAAGTTTAAGATGAGTAGTGAAAAATAAAAAATAAAAAAACT

2890

PSEN1

PSEN1-201

PSEN1-201

GATAGAGTCTCGCTTTGTTGCCAGGCTGGAGTGCAGTGGCGTGATCTCAGCTCACTACAACCTCTCCCTCCCGGGATCAAGCGA
CTATCTCAGAGCGAAACAACGGGTCCGACCTCACGTCAACGACTAGAGTCGAGTGATGTTGGAGAGGGAGGGCCCTAGTTCGCT

2975

PSEN1

PSEN1-201

PSEN1-201

TTCTCCTGCCTCAGCCTTCCGAGTAGCTGGGACTACAAGTGCGCACCACCACGCCAGCTAATTTTTGTATTTTTAGTAGAGACG
AAGAGGACGGAGTCGGAAGGCTCATCGACCCTGATGTTACGCGTGGTGGTGC GGTCGATTAAAAACATAAAAAATCATCTCTGC

3060

PSEN1

PSEN1-201

PSEN1-201

AGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACCTCTGACCTCAAGTGATCTGCCTGCCTCAGCCTCCCAGAGTGCTGGGATTA
TCCAAAACGGTACAACCGGTCCGACCAGAGTTTGGAGACTGGAGTTCACTAGACGGACGGAGTCGGAGGGTCTCACGACCCTAAT

3145

PSEN1

PSEN1-201

PSEN1-201

CAGGCTTGAACCACTGCGCCCAGCCTACTCATCACTTACTAGCTATTTGACCACACAAGTTACTCAACTCCTATGTCAGTTATGA
GTCCGAACTTGGTGACGCGGGTCGGATGAGTAGTGAATGATCGATAAACTGGTGTGTTCAATGAGTTGAGGATACAGTCAATACT

3230

PSEN1

PSEN1-201

PSEN1-201

AGATTAAATTAATGATCCATTTAATACAATAATACACTTAGAACAAATGCTCTATCAGTAAATTTTTTCTGTTTTAAGAAACAGG
TCTAATTTAATTTACTAGGTAAATTATGTTATTATGTGAATCTTGTTACAGATAGTCATTTAAAAAAGACAAAATTTCTTTGTCC

3315

PSEN1

PSEN1-201

PSEN1-201

ATCTCACTCTGTCTCCCAGGCTGGAGTGAAGTGGCACGATTATAGCTCACTGTAGCTTCAAAGCCTGGGCTCAAGCAGTCCTCC
TAGAGTGAGACAGAGGGTCCGACCTCACTTACCCTGCTAATATCGAGTGACATCGAAGTTTTTCGGACCCGAGTTCGTCAGGAGG

3400

PSEN1

PSEN1-201

PSEN1-201

TGTCTCAGCCTCCCGAGTAGATAAGACTACAGGCACAGGTTGGTGTGACCTCCTAGCTTCAAGCAGCCTCCCAAAGTGCTGAGA
ACAGAGTCGGAGGGCTCATCTATTCTGATGTCCGTGTCCAACCACAACCTGGAGGATCGAAGTTCGTCGGAGGGTTTCACGACTCT

3485

PSEN1

PSEN1-201

PSEN1-201

TTACAGGTGTGAGCCACTATACCCAGCCCAGTGTTATATTTTTGTATAATCCTATGAAGTATCAAGGCAGTTATTATCCCTGTTT
AATGTCCACACTCGGTGATATGGGTCGGGTCACAATATAAAAACATATTAGGATACTTCATAGTTCGTCGAATAATAGGGACAAA

3570

PSEN1

PSEN1-201

PSEN1-201

TACTGCTAAGAACTTGAAGTTTACAGAGGTAAATTATTTGCCTAAGCCTAAACTCTGATCTCGAATCTGAATCCCAAGTCCAAT
ATGACGATTCTTTGAACTTCAAATGTCTCCATTTAATAAACGGATTCGGATTTGAGACTAGAGCTTAGACTTAGGGTTCAGGTTA

3655

PSEN1

PSEN1-201

PSEN1-201

ATTCTTTTCACCGTATTACAATATTTTTACCATCAACCCTCCATTCTGTCTGCACATCATACAAATGAGTATCTCTACAGAGCTT
TAAGAAAAGTGGCATAATGTTATAAAAAATGGTAGTTGGGAGGTAAGACAGACGCTGTAGTATGTTTACTCATAGAGATGTCTCGAA

3740

PSEN1

PSEN1-201

PSEN1-201

TGAGTTGCTTTTAAACAAAAGAGATTTTTGTACCCAATGTTTAGAGTAGTGATTCTCGGCTCCATTTTTACAAGATTTCAAGATT
ACTCAACGAAAATTTGTTTTCTCTAAAAACATGGGTTACAAATCTCATCACTAAGAGCCGAGGTA AAAATGTTCTAAAGTTCTAA

3825

PSEN1

PSEN1-201

PSEN1-201

TAATTTGTCAAAAAAGTTCTGAAATTTTCAAAGCAAAGCAATTTAATTTAATTGCTCTAAAAATAAGCAGATTTATCATTTA
ATTAACAGTTTTTTCAAGACTTTAAAAGTTTCGTTTTCGTTAAAATTAATTAACGAGATTTTTTATTTCGTCTAAATAGTAAAT

3910

PSEN1

PSEN1-201

PSEN1-201

GCAATTCCTTTAAGGGAGAGTGTATCATAAAACTGAAATAGTACTGAATGTGGCAGAATCAAACAAGTTGAAAATCTCATCACTTC
CGTTAAGAAATTCCTCTCACATAGTATTTTGACTTTATCATGACTTACACCGTCTTAGTTTGTTCAACTTTTAGAGTAGTGAAG

3995

PSEN1

PSEN1-201

PSEN1-201

AGAGCAGGGCAGACTTCTCATTCAAACAAATTGAGGTAGAAGTGGTGAGAGTAGAGATTTCTTTGTGTATGTGTGTTTTATTACT
TCTCGTCCCCTCTGAAGAGTAAGTTTGTTTAACTCCATCTTCACCACTCTCATCTCTAAAGAAACACATACACACAAAATAATGA

4080

PSEN1

PSEN1-201

PSEN1-201

GTACTATATTATATTATAGTTCTATATATACTATATTATATTGTACATATATATTATTATATGAAGAGACATGACCACTTTGAGG
CATGATATAATATAATATCAAGATATATATGATATAATATAACATGTATATATAATAATACTTCTCTGTACTGGTGAAACTCC

4165

PSEN1

PSEN1-201

PSEN1-201

CATGAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGGCACGGTCTTACTTTGTCACCTAGGCAGTGGCGCCATCTTGGCTCACTGC
GTACTTTAAAAA AAAAAAAAAAAAAAAAAAAAAA AACTCCGTGCCAGAATGAAACAGTGGATCCGTACCCGCGGTAGAACCGAGTGACG

4250

PSEN1

PSEN1-201

PSEN1-201

AGCCTCCACCTCCAGGGCTCAAGCAATCCTCCCACCTCAGCTTCTGAGTAGCTGGGACTATAGGCACCTGCCACCATGAGCTGC
TCGGAGGTGGAGGTCCCGAGTTCGTTAGGAGGGTGGAGTCTGAAGGACTCATCGACCTGATATCCGTGGACGGTGGTACTCGACG

4335

PSEN1

PSEN1-201

PSEN1-201

TAATTTTTTGTATTTTTGGTAGAGACGGGGTTTTGCCATCTTGCCAGGCTGGTCTCAAACCTCCTGAGCACAAGTGATCTGCTGC
ATTAATAAACATAAAAAACCATCTCTGCCCAAAACGGTAGAACCGGTCCGACCAGAGTTTGAGGACTCGTGTTCCTAGACGACG

4420

PSEN1

PSEN1-201

PSEN1-201

CTCAGCCTCCCCAAAGTGCTGGAATTACAAGCATAAGCCACTGTGCCTGGCAAGACATGAAATTTTTAAATGTAAATGCATTTAA
GAGTCGGAGGGGTTTCACGACCTTAATGTTTCGTATTTCGGTGACACGGACCGTTCTGTACTTTAAAAATTTACATTTACGTAAATT

4505

PSEN1

PSEN1-201

PSEN1-201

GTGACAATAATGTGAATACAAGTTATCAATTCTTCTTTACAAGTTTAGCTATACCTGTTTTATATTTTTTCAGTGTTTAAAATTA
CACTGTTATTACACTTATGTTCAATAGTTAAGAAGGAAATGTTCAAATCGATATGGACAAAATATAAAAAGTCACAAATTTTAAAT

4590

PSEN1

PSEN1-201

PSEN1-201

TTTTTATATTTTTATATTCTGAATTTTCTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTCGCTGTATTGCCAG
AAAAATATAAAAATATAAGACTTAAAAGAAAGAAAGAAAGAAAAAAAAAAAAAAAAAAAACTCTGCCTCAGAGCGACATAACGGGTC

4675

PSEN1

PSEN1-201

PSEN1-201

GCTGGAGTGCAGTGGCGCAATCTCGGCGCACTGCAAGCTCCGCTTCCCGGGTTCACGCCGTTCTCCTGCCTCAGCCTCCCGAGTA
CGACCTCACGTACCAGCGTTAGAGCCGCGTGACGTTTCGAGGCGAAGGGCCCAAGTGCGGCAAGAGGACGGAGTCGGAGGGGCTCAT

4760

PSEN1

PSEN1-201

PSEN1-201

GCTGGGACTACAGGCACGCGCCACCACACCCAGCTAATTTTTTGTATTTTTTAGTAGAGACAGGGTTTCACCGTGTTAGCCAGGA
CGACCCTGATGTCCGTGCGCGGTGGTGTGGGTCGATTAAAAACATAAAAAATCATCTCTGTCCCAAAGTGGCACAATCGGTCTCT

4845

PSEN1

PSEN1-201

PSEN1-201

TGGTCTTGATCTCCTGACCTTGTGATCCGCCACCTCGGCCTCCCAAAGTGCTGGGATTGCAGGCCTGAGCCACTGCGCCCGGCC
ACCAGAACTAGAGGACTGGAACACTAGGCGGGTGGAGCCGGAGGGTTTCACGACCCTAACGTCCGCACTCGGTGACGCGGGCCGG

4930

PSEN1

PSEN1-201

PSEN1-201

TATATGCTGAATTTTCATGACAGAGAATGAAAGAAAAAGTGCAGTTGATCGAAAGAAATGGTGGTATAAACAGGAATAACAGGCA
ATATACGACTTAAAAGTACTGTCTCTTACTTTCTTTTTCACGTCAACTAGCTTTCTTTACCACCATATTTGTCCTTATTGTCCGT

5015

PSEN1

PSEN1-201

PSEN1-201

TGTTGTTTCCTCTCTGATTTATTATTTTTGTAAAATAAGCTACTTTTTAGCACCACATACATATGTTCTGAGACCTGAATATTTG
ACAACAAAGGAGAGACTAAATAATAAAAACATTTTATTTCGATGAAAAGTCGTGGTGTATGTATACAAGACTCTGGACTTATAAAC

5100

PSEN1

PSEN1-201

PSEN1-201

TGACCAAAGAGTAAAGAAGTAATAAACTTTATCTCGCAAAGAGTTATTATTGTGTTTTATTTAAATTTACTGCCCTCTTACTTCA
ACTGGTTTCTCATTTCTTCATTATTTGAAATAGAGCGTTTCTCAATAATAACACAAAATAAATTTAAATGACGGGAGAATGAAGT

5185

PSEN1

PSEN1-201

PSEN1-201

AGTACTTCTCAGTAGTACGTAATACTGCTTTTAAAAAGGAGAAGGGATGAATTTCTTCTACTCTGCTCTTCATATTTGAAAAGT
TCATGAAGAGTCATCATGCATTATGACGAAAATTTTCTCTTCCCTACTTAAAGAAGATGAGACGAGAAGTATAAACTTTTCA

5270

PSEN1

PSEN1-201

PSEN1-201

PCR Forward

TT

TCAGTCAAATCCCCTTTATTTAAATTCATCTCAGAGTAATCTTTTTAATTTGTAGTTTCATATCCGTGATTAGTTTAGAAGTGACTT
AGTCAGTTTAGGGGAAATAATTTAAGTAGAGTCTCATTAGAAAAATTAACATCAAGTATAGGCACTAATCAAATCTTCACTGAA

5355

PSEN1

PSEN1-201

PSEN1-201

PCR Forward

CTCCCTGTTTCTGCTCACTGTAG

CTCCCTGTTTCTGCTCACTGTAGGTTGACAACTGCTTAAAATAGTCTATCTCATCATTATCTCTGCAGCTTTTCTTTAACTAGG
GAGGGACAAAGACGAGTGACATCCAACCTGTTGACGAATTTTATCAGATAGAGTAGTAATAGAGACGTCGAAAGGAAATTTGATCC

5440

PSEN1

PSEN1-201

PSEN1-201

AAGACTTGTTTCCTATACCCAGTAACGATACACTGTACACTAAGCAAATAGCAGTCAAACCCAAATGAAATTTTTACAGATGTTCT
TTCTGAACAAGGATATGGGGTCATTGCTATGTGACATGTGATTTCGTTTATCGTCAGTTTTGGGTTTACTTTAAAAATGTCTACAAG

5525

PSEN1

PSEN1-201

PSEN1-201

TGTGTCATTTTTATTTTGTGTTATGTTGTCTCCCCACCCCCACCCAGTTCACCTGCCATTTATTTTCATATTCATTCAACGTCTTTTT
ACACAGTAAAAATAAAACAAATACAACAGAGGGGGTGGGGGTG6TCAAGTGGACGGTAAATAAAGTATAAGTAAGTTGCAGAAAAA

5610

PSEN1

PSEN1-201

PSEN1-201

GTGTA AAAAGAGACAAAAAACATTA AACTTTTTCTTCGTTAATTCCTCCCTACCACCCATTTACAAGTTTAGCCCATACATTT
CACATTTTTCTCTGTTTTTTGTAATTTGAAAAAAGGAAGCAATTAAGGAGGGATGGTGGGTAAATGTTCAAATCGGGTATGTAAA

5695

PSEN1

PSEN1-201

PSEN1-201

gRNA Protospacer

TATGCTGGTTGAAAC

TATTAGATGTCTTTTTATGTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAAC
ATAATCTACAGAAAATACAAAAAGAAAAAGATCTAAATCACCGACAAAACACAGGCTTCCAGGTGAAGCATACGACCAACTTTG

5780

PSEN1

PSEN1-201

PSEN1-201

D L V 260 A V L C P 265 K G P L R 270 M L V E T
ENSE00003979367

Protospacer Sequence

AGGCTTTCCAGGTGAAGCATACGACCAACTTTG

Donor Template SNV -> REV

gRNA Protospacer

AGC GC

AGC T CAGGAGAGAAATG A AACGCTTTTTCCAGCTCTCATTTACTCCTGTAAGTATTTGAGAAGGATATTGAATTAGTAATCAGTG
TCG A GTCCTCTCTTTACT T T T GCGAAAAAGGTGCGAGAGTAAATGAGGACATTCATAAACTCTTCCTATAACTTAATCATTAGTCAC

5865

PSEN1

PSEN1-201

PSEN1-201

275 A Q E R N 280 E T L F P 285 A L I Y S

ENSE00003979367

Prot... PAM

SNV

Silent SNV

TCGAGTCCTCTCTTTACTTTTGCGAAAAAGGTGCGAGAGTAAATGAGGACATTCATAAACTCTTCCTAT

Donor Template SNV -> REV

TAGAATTTATCGGAACTGAAGCACATGTAACATGTTTTCATGGTACTTGTTCATCTTAAATGCACAGCATTCTGGAA
ATCTTAAATAGCCTTGACTTCGTGTACATTGATACCAGTAAAAGTACCATGAACAAGAGTAGAATTTACGTGTCGTAAGGACCTT

5950

PSEN1

PSEN1-201

PSEN1-201

CGTGTGCGTAAGGACCTT
Sanger Sequencing

CTCCTGCAGATCTCTTTGTTTCCTTGCAAGCAATTGTCTTCTACCTGATGTTGATTCAAGAGAGTTTTCAATATGAATAGAAAAGA
GAGGACGTCTAGAGAAAACAAAGGAACGTTTCGTTAACAGAAGATGGACTACAACCTAAGTTCTCTCAAAAAGTTATACTTATCTTTCT

6035

PSEN1

PSEN1-201

PSEN1-201

GAG

Sanger Sequencing

AAGAAAATGTTTAGATATTGGGGAACCAGCATTCCCATTTTTAAACCTGTTAGGAGTTGTTGATTAGGGCAAGCTCAAGGATTCC
TTCTTTTACAAATCTATAACCCCTTGGTTCGTAAGGGTAAAATTTGGACAATCCTCAACAACCTAATCCCCTTCGAGTTCCCTAAGG

6120

PSEN1

PSEN1-201

PSEN1-201

TTTGAGTGACTGGTTTAGATGTCTTTCTGCTATTCGGTGACCACTGGGGAACCTGAGATTGTTGAGCAGAAGGGTAATGTGAGCAG
AAACTCACTGACCAAATCTACAGAAAGACGATAAGCCACTGGTGACCCCTTGACTCTAACAACCTCGTCTTCCCATTACACTCGTC

6205

PSEN1

PSEN1-201

PSEN1-201

AGCCGTGCCTTTGTAAGCTGGCAGCACTGTGTGAGATGAATTGGTGGGTTGGATACTGAGATCATGAGAGGCATACTAAGCATAA
TCGGCACGGAAACATTTCGACCGTTCGTGACACACTCTACTTAACCACCCAACCTATGACTCTAGTACTCTCCGTATGATTTCGTATT

6290

PSEN1

PSEN1-201

PSEN1-201

TTAAGATGATATTGCCATGATCTAGGTGGAAAGTAATGGGGGTTTGAATTATGGTAGTGGCAGTAGCAATCAAGGGAAAGAGTTG
AATTCTACTATAACGGTACTAGATCCACCTTTCATTACCCCAAACTTAATACCATCACCGTCATCGTTAGTTCCTTTCTCAAC

6375

PSEN1

PSEN1-201

PSEN1-201

CCACCTTTCATTACCCCAAACTTA
PCR Reverse

ATCAGAGGATTCAGAGGTAGAATCAATAGTTCTAGCAACTGAGGAGAGAAAGTTGTAAGCTTGAAGGAAAAGGTGATGAAGAAAAAA
TAGTCTCCTAAGTCTCCATCTTAGTTATCAAGATCGTTGACTCCTCTCTTCAACATTCGAACTTCCTTTCCACTACTTCTTTTTT

6460

PSEN1

PSEN1-201

PSEN1-201

TGCTTTCCTGTGTTTTCTTGTGTTGTTGTTGTTGAGATAGGGTCTCACTCCCATCCAGGATGGAGTACAGTAGTGTGATCATGGCTC
ACGAAAAGGACACAAAAGAACAACAACAACACTCTATCCCAGAGTGAGGGTAGGTCTACCTCATGTCATCACACTAGTACCGAG

6545

PSEN1

PSEN1-201

PSEN1-201

ACTGCAGCCTCGACCTCCCAGGCTCAGGTGATCCACCCACCTCAGCCTCCCGAGTAGCTGTGACTACAGGCACGCACTACCAGGC
TGACGTCGGAGCTGGAGGGTCCGAGTCCACTAGGTGGGTGGAGTCGGAGGGCTCATCGACACTGATGTCCGTGCGTGATGGTCCG

6630

PSEN1

PSEN1-201

PSEN1-201

CTGGCTAATTTTTTGTGTTGTGTGTAGAGACTGGGTTTTGCCATGTGCCCAGGCTGGTCTTGAACCTCCTCGGCTTAAGCGATCC
GACCGATTAAAAAACACAACACACATCTCTGACCCAAAACGGTACACGGGTCCGACCAGAACTTGAGGAGCCGAATTCGCTAGG

6715

PSEN1

PSEN1-201

PSEN1-201

TCCTGCCTTGACTTCACAAAGTGCTTGAGTTACAGGTGTGAGCTACCACGCCTGGCCATGTTTTCTTGTGTGAAGGATCTGTTTA
AGGACGGAACTGAAGTGTTTACGAACTCAATGTCCACACTCGATGGTGC GGACCGGTACAAAAGAACACACTTCTTAGACAAAT

6800

PSEN1

PSEN1-201

PSEN1-201

GTTTTATATCTTTCTGTGGCTCATATCTAATTTAGTTGACAGTACCTGTGGGTCCTAGGTAGACATTGCTAGCAGACGTTTAGA
CAAAATATAGAAAAGACACCGAGTATAGATTAAATCAACTGTCATGGACACCCAGTGATCCATCTGTAACGATCGTCTGCAAATCT

6885

PSEN1

PSEN1-201

PSEN1-201

AATGAAATACTAGAGCTTGGGAAAAAGTTGATATTTGAGATAGAGACTTGAAGAACATTAGCAGAGAGTTGGTAGTTAAGGTCTG
TTACTTTATGATCTCGAACCTTTTTCAACTATAAACTCTATCTCTGAACTTCTTGTAAATCGTCTCTCAACCATCAATTCAGAC

6970

PSEN1

PSEN1-201

PSEN1-201

TGAGCTGGTGAGCAATTCAAATAAAAAGCAGAAGAGAAGAGGAAGACAAGGGTCAAACCTTTGTCAACTACTGTGTTTAGAGAATGA
ACTCGACCACTCGTTAAGTTTATTTTCGTCCTTCTCTTCTCTTCTGTTCCAGTTTGAAACAGTTGATGACACAAATCTCTTACT

7055

PSEN1

PSEN1-201

PSEN1-201

GACAAGAGAGGATACTACAGGAAGTAGAGGAAAATAGTGGAAAATTGGGCAAGCCAGTATTTTTCACTTAAGAATATCATTACTG
CTGTTCTCTCCTATGATGTCCTTCATCTCCTTTTATCACCTTTAACCCTGTCGGTCATAAAAAAGTGAATTCTTATAGTAATGAC

7140

PSEN1

PSEN1-201

PSEN1-201

TTTTTTGATGTCAGCACATGAAATGGCTGCATAGTGTCTTACGTAGATATTCAGTGGTGGGTATCCTCATTGATAGACATTT
AAAAAACTACAGTCGTGTACTTTACCGACGTATCACAAGAGAATGCATCTATAAGTCACCACCCATAGGAGTAACATATCTGTA

7225

PSEN1

PSEN1-201

PSEN1-201

AGATCATTTCCATTTATTTTCTATCACAGACAGCACTTACAGAGTGCATCCATGAACTTATGAATATTATTATAAAAATGTATTCT
TCTAGTAAAGGTAAATAAAAAGATAGTGTCTGTCGTGAATGTCTCACGTAGGTACTTGAATACTTATAATAATATTTTACATAAGA

7310

PSEN1

PSEN1-201

PSEN1-201

TACAGTAGAATTGCTAAGTCAAAGGATGTATTTAAATTTTGATAGTTTGCCATATTGCCTCCTAAAAAAGCTGTGCCTGTTTACA
ATGTCATCTTAACGATTCAGTTTCTTACATAAAATTTAAAACCTATCAAACGGTATAACGGAGGATTTTTTTCGACACGGACAAATGT

7395

PSEN1

PSEN1-201

PSEN1-201

TTCCCTTCAGTAATATGAAAGTATCAATTTCTTACCCCTTTGGTGTGTTTGGTTTGTGTTTGGAGACTGAGTCTCGCTCTG
AAGGGAAGTCATTATACTTTCATAGTTAAAGGAATGGGGAAACCACAAAACCAAACAAAACCTCTGACTCAGAGCGAGAC

7480

PSEN1

PSEN1-201

PSEN1-201

TCATGCAGGCTGGAGTGCAGTGGTGCATCTCGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCAGTTCTCCTGCCTCAGCCT
AGTACGTCCGACCTCACGTACCACGCTAGAGCCGAGTGACGTTGGAGGCGGAGGACCCAAGTTCGTCAAGAGGACGGAGTCGGA

7565

PSEN1

PSEN1-201

PSEN1-201

CCGGAGTGGCTGGGATTACAGGCGTGTGCCACCACACCCAGCTAATTTTTTGTATTTTTAGTGGAGACACGGTTTTACCATGTTG
GGCCTCACCGACCCTAATGTCCGCACACGGTGGTGTGGGTTCGATTAAAAAACATAAAAAATCACCTCTGTGCCAAAGTGGTACAAC

7650

PSEN1

PSEN1-201

PSEN1-201

ACCAGGCTGGTCTCGAACTCCTGACTTCAGGTGATCCGCCTGCCTAGGCCTCCCAAATGCCAGGATTATAGCTGTGAGCCACCA
TGGTCCGACCAGAGCTTGAGGACTGAAAGTCCACTAGGCGGACGGATCCGGAGGGTTTTACGGTCCTAATATCGACACTCGGTGGT

7735

PSEN1

PSEN1-201

PSEN1-201

TGCCCGGCCACTGCTTTGTTAATGCTTGCCTGTGTCTGTGCATACATGCATGTGTGTGTGTCTGAGAGAGAAAGAGATCTAATAG
ACGGGCCGGTGACGAAACAATTACGAACGGACACAGACACGTATGTACGTACACACACACAGACTCTCTCTTTCTCTAGATTATC

7820

PSEN1

PSEN1-201

PSEN1-201

GCAAAAAATAACATCTTGTTTTATTTTTATTGTTTGTCTAATGCTTTGGGTGATTATTTGAACTTTTTTTCATGTGTTTCTTA
CGTTTTTTTATTGTAGAACAATAAAAAATAACAAACAGATTACGAAACCCACTAATAAAGTTGAAAAAAGTACACAAAGAAT

7905

PSEN1

PSEN1-201

PSEN1-201

GTTACAGATCTGAATTTATTTTGTAACTGGCTTGGTATAATCTTTTTCATATTTGTGAAATTAATCTTTTTTGTGTGTGTGAG
CAATGTCTAGACTTAAATAAACATTGACCGAACCATATTAGAAAAAGTATAAACACTTTAATTAGAAAAAACACACACACTC

7990

PSEN1

PSEN1-201

PSEN1-201

ACAGTCTCTCTCTGTCACCCAAGCTGGAGTACAGTGGCGCAATCTCAACTCACTGCAACCTCCATCTCCAGGTTCAAGCAATTC
TGTCAGAGAGAGACAGTGGGTTTCGACCTCATGTCACCGCGTTAGAGTTGAGTGACGTTGGAGGTAGAGGGTCCAAGTTCGTTAAG

8075

PSEN1

PSEN1-201

PSEN1-201

TCCTCTCTCAGCCTCCCAAGTAGCTGGAATTACAGGCGCATGCCACCACGCCTGGCTGATTTTTGTATTTTTAGTAGAGACGGGA
AGGAGAGAGTCGGAGGGTTCATCGACCTTAATGTCCGCGTACGGTGGTGC GGACCGACTAAAAACATAAAAAATCATCTCTGCCCT

8160

PSEN1

PSEN1-201

PSEN1-201

TTTCACCACGTTGGCCAGGCTGGTCTCAAGTGATCCAAGTGCCTCAGACTCCCAAAGCATTAGTATTACAGGTGTGAGCCACTGC
AAAGTGGTGCAACCGGTCCGACCAGAGTTCACTAGGTTGACGGAGTCTGAGGGTTTCGTAATCATAATGTCCACACTCGGTGACG

8245

PSEN1

PSEN1-201

PSEN1-201

TCCCAGCCCTGTAAAATTAATCTTAATTATACAAGTAATTCATTATCCTTGAAAAAGGATAAACATTACAGATAAAAAATAAATTT
AGGGTCGGGACATTTTAATTAGAATTAATATGTTTCATTAAGTAATAGGAACTTTTTCTATTGTAAATGTCTATTTTTATTAAA

8330

PSEN1

PSEN1-201

PSEN1-201

CACGGTAACTATCATCTCTAATCTTAATGCCTTATCAAGTACTTACCCTGTTGTCAGTTTGTGTATATCCTTGTAGATTTTTT
GTGCCATTGATAGTAGAGATTAGAATTACGGAATAGTTTCATGAATGGGGACAACAGTCAAACAACATATAGGAACATCTAAAAA

8415

PSEN1

PSEN1-201

PSEN1-201

TTGCCAATTTTTCTGTTGAGTTACTGGAAAAGCAGTTTCAAGAAGGAGAGAGGCTGGGCGTGGTGGCTAACACCTGTAATCCCAG
AACGGTTAAAAAGACAACCTCAATGACCTTTTCGTCAAAGTCTTCTCTCTCCGACCCGCACCACCGATTGTGGACATTAGGGTC

8500

PSEN1

PSEN1-201

PSEN1-201

CACTTTGGGAGGCCTAGGTGGGCGGATCACTTGAGGTCAGGAGTTTGAAACCAGCCTGGCCAACATGGTGAAACTCTGTCTTTAC
GTGAAACCCTCCGGATCCACCCGCCTAGTGAACCTCCAGTCTCAAACCTTTGGTTCGGACCGGTTGTACCACCTTTGAGACAGAAATG

8585

PSEN1

PSEN1-201

PSEN1-201

TAAAAATATAAAAATCAGCTGGGTGTGGTGGTGCACACTTGTAAATCCCAGTTACTTGGGAGGCTGAGGTGGGAGGATCACTTGAA
ATTTTTATATTTTAGTCGACCCACACCACCGTGTGAACATTAGGGTCAATGAACCCTCCGACTCCACCCTCCTAGTGAACCTT

8670

PSEN1

PSEN1-201

PSEN1-201

CCCAGGAGGCGGAGGTTACAGTGAGCCATGATCGTGCCACTGCACTCCAGCCTGAGTGACAGCAAGGCTTCATCCCCACCCTCCC
GGGTCTCCGCCTCCAATGTCACTCGGTACTAGCACGGTGACGTGAGGTTCGGACTCACTGTCGTTCCGAAGTAGGGGTGGGAGGG

8755

PSEN1

PSEN1-201

PSEN1-201

AAAAAAAAAGAGAATATCTTTTTGTTTGTGGCAGAGTCTTGCTGTGTCGCCAGGCTGGAGTT
TTTTTTTCTCTTATAGAAAAACAACAACAACAACAACAACAACAACAACAACAACACCGTCTCAGAACGACACAGCGGGTCCGACCTCAA

8840

PSEN1

PSEN1-201

PSEN1-201

CAGTGGGGCGATCTCGGCTCACTGCAAGCTCCGCCTCCTGGGTTTCAGCCATTCTCCTGCCTCAGCCTCCCCAGCAGCTGGGACTA
GTCACCCCGCTAGAGCCGAGTGACGTTTCGAGGCGGAGGACCCAAGTCGGTAAGAGGACGGAGTCGGAGGGGTTCGTCGACCTGAT

8925

PSEN1

PSEN1-201

PSEN1-201

CAGGCACACGCCGCCACGCCCGGCTAATTTTTGTATTTTTAGTAGCAACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCT
GTCCGTGTGCGGCGGTGCGGGCCGATTAATAAACATAAAAAATCATCGTTGCCCAAAGTGGTACAATCGGTCCTACCAGAGCTAGA

9010

PSEN1

PSEN1-201

PSEN1-201

CCTGACCTTGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGGCCGAGAATATCATT
GGACTGGAACACTAGGCGGGCGGAGCCGGAGGGTTTCACGACCTAATGTCCGCACTCGGTGGCGCGGACCGGCTCTTATAGTAA

9095

PSEN1

PSEN1-201

PSEN1-201

TTTTATAAAGAAGTCAAAGGTAATGAGGACTAAGTAAAACCATACAGTATTTGCTGTCTAAGATGTCATTAGTGACATTGAAGAG
AAAATATTTCTTCAGTTTCCATTACTCCTGATTCATTTTGGTATGTCATAAACGACAGATTCTACAGTAATCACTGTAACCTTCTC

9180

PSEN1

PSEN1-201

PSEN1-201

AGCAGTTTCAGTAGAGTGATAGAACCAGAAGCAGTACTCCAAAGGGAAGGTGCGTATGTGTGCATGCATGTCTCTGTGTTTTGCC
TCGTCAAAGTCATCTCACTATCTTGGTCTTCGTCATGAGGTTTCCCTTCCACGCATACACACGTACGTACAGAGACACAAAACGG

9265

PSEN1

PSEN1-201

PSEN1-201

AGTGCTGGCAGTGGAAGTGATGGTGTAGGCAGAGAATGGGTGGTGAAGAAGGAGAGGTATAGTAAATGTCATGTACTACATCAA
TCACGACCGTCACCTTCACTACCACATCCGTCTTTACCCACCACTTCTTCCCTCTCCATATCATTTACAGTACATGATGTAGTTT

9350

PSEN1

PSEN1-201

PSEN1-201

GATTCCTGTCTCACAGGCAGAGCAGGTGGTGACCTGACAGGAGAACAGGTTTCAGGAAAAGGTGTTTCAAGGAGAGGGGAAGGTTCC
CTAAGGACAGAGTGTCCGTCTCGTCCACCACTGGACTGTCTCTTGTCCAAAGTCCTTTCCACAAAGTTCTCTCCCTTCCAAGG

9435

PSEN1

PSEN1-201

PSEN1-201

ATTTTATTTTATTTATTTATTTTTTTTTGAAACAGAGTCTTGCTCTGTTGCTCGGGCTAGAGTGCAGTGGTGTGATCTTGGCTCAC
TAAAAATAAAATAAAATAAAAAAACTTTGTCTCAGAACGAGACAACGAGCCCGATCTCACGTCAACCACTAGAACCAGGTG

9520

PSEN1

PSEN1-201

PSEN1-201

TGCAACCCCGCCTCCCAAGTTCAAGCAATGGTCTGTCTCAGCCTCCGGAGTAGCTGGGATTATAGGCACCCACCACCATCC
ACGTTGGGGGCGGAGGGTTCAAGTTCGTTACCAGGACAGAGTCGGAGGCCTCATCGACCCTAATATCCGTGGGTGGTGGTGTAGG

9605

PSEN1

PSEN1-201

PSEN1-201

GGCTAATGTTTGTATTTTATTTAGTAGAGTTGGGGTTTTCGCCACATTGGCCAGGCTGGCCTTGAACCTCCCCACCTCAAGTGATCCACC
CCGATTACAAACATAAAAAATCATCTCAACCCCAAAGCGGTGTAACCGGTCCGACCGGAACCTTGAGGGGTGGAGTTCCTAGGTGG

9690

PSEN1

PSEN1-201

PSEN1-201

TGCTCGGCCTCCCAAAGTGCTGGGATTACAGACGTGAGCCACTGCACCCGACCTGTTTTATTTTATTTTGGAGGTAAGTCTTGC
ACGGAGCCGGAGGGTTTTACGACCCTAATGTCTGCACTCGGTGACGTGGGCTGGACAAAATAAAAAAACTCCATTGAGAACG

9775

PSEN1

PSEN1-201

PSEN1-201

TCTGTTGCCAGGCTGGAGTGCAGTGGCGCAATCTCAGCTCACTGCAACCTCCATCTCCTGGGTTTCAAGGCAATTCTCCTGCCTCA
AGACAACGGGTCCGACCTCACGTCAACCGGTTAGAGTGCAGTGCAGTGGAGGTAGAGGACCCAAGTCCGTTAAGAGGACGGAGT

9860

PSEN1

PSEN1-201

PSEN1-201

GCCTCCCGAGTAGTTGAGATTACAAGCATGCGCCACTATACCTGGCTAATTTTTTTTTTCCATATTTTATTTAGTTGAGCCACAGGTT
CGGAGGGCTCATCAACTCTAATGTTTCGTACGCGGTGATATGGACCGATTAAAAAAAAGGTATAAAAAATCAACTCGGTGTCCAA

9945

PSEN1

PSEN1-201

PSEN1-201

GATACAGATGATTTGCATGTATTTTTTTTAAAAAGTTCTCAAGTCTATTTAATAACCACAGAATATGAGACATTCTGAGATGTTTTA
CTATGTCTACTAAACGTACATAAAAAAATTTTCAAGAGTTTCAAGATAAATTATTGGTGTCTTATACTCTGTAAGACTCTACAAAAT

10,625

PSEN1

PSEN1-201

PSEN1-201

GAAACAGTTCAACATATGTGGGAAAATAGGAGTATAAACCCCTTACCTCCTGTGTAGATCAGGTAGGTTCAAGATTGCATCTGTTC
CTTTGTCAAGTTGTATACACCCTTTTATCCTCATATTTGGGAATGGAGGACACATCTAGTCCATCCAAGTTCTAACGTAGACAAG

10,710

PSEN1

PSEN1-201

PSEN1-201

TTTTGTAATACTAAATGTCTGGTGAAGATTTGAGGATTTTATATAAATCATTGAGTTTGAGAGGTTTTTTTTGTTTTTGTTTTTGA
AAAACATTATGATTTACAGACCACTTCTAAACTCCTAAAATATATTTAGTAACTCAAACCTCTCCAAAAAACAAAAACAAAACT

10,795

PSEN1

PSEN1-201

PSEN1-201

GATGGAGTTTCACTCTTGTGGCCAGGCTGAAGTGCAATGGCACAATCTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCG
CTACCTCAAAGTGAGAACAACGGGTCCGACTTACGTTACCGTGTAGAGCCGAGTGACGTTGGAGGCGGAGGGTCCAAGTTCGC

10,880

PSEN1

PSEN1-201

PSEN1-201

ATTCTCCTGCCTCGGCCTCCTGAGTAGCTGGGATTACAGACGCCTGCCACCACGCCAGCTAATTTTTTGTATTTTTGTATTTTT
TAAGAGGACGGAGCCGGAGGACTCATCGACCCTAATGTCTGCGGACGGTGGTGCGGGTGCGATTAAAAAACATAAAAAACATAAAAA

10,965

PSEN1

PSEN1-201

PSEN1-201

AGTAGAGAGAGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTTGTGACCTCAGGTGATCTACCCGCCTCACCTCCCAAAGT
TCATCTCTCTCCCAAAGTGGTACAACCGGTCCGACCAGAGTTTGAACACTGGAGTCCACTAGATGGGCGGAGTGGGAGGGTTTCA

11,050

PSEN1

PSEN1-201

PSEN1-201

GCTGGGATTACAGGCATGAGCCACCGCACCTGGCCTTCGTTTTGTTTTTCAACAGAATGTAAGAATTTTTTCTTACATTTTTCT
CGACCCTAATGTCCGTACTCGGTGGCGTGGACCGGAAGCAAACAAAAAAGTTGTCTTACATTCTTAAAAAAGAATGTAAAAAGA

11,135

PSEN1

PSEN1-201

PSEN1-201

TACATTTTAAACAGAATGTAAGAAAACCAACGCAATGCCGATGAGTACTTTTTCCCTGAAGTGGATATAAGCATGAATATAAA
ATGTAAAAATTGCTTACATTCTTTTGGTGTTCGTTACGGCTACTCATGAAAAAGGGACTTCACCTATATTCGTACTTATATTT

11,220

PSEN1

PSEN1-201

PSEN1-201

AAGTTTTAAATCAGTCATCCTGGCTATTTGTTCTCTAAAAATCAATAAATAATTCTTTCATGCATTTTAATACTGTCTCCCAGTT
TTCAAAATTTAGTCAGTAGGACCGATAAAACAAGAGATTTTGTATTATTTAAGAAAAGTACGTAAAAATTATGACAGAGGGTCAA

11,305

PSEN1

PSEN1-201

PSEN1-201

AAGGGTATTCAGTTTGC AAAATGCTCTTACTGACAGGAAATGTATGAGCATT TTTGTTTTTACTTCTGTCGTTTGACAGAAAAA
TTCCATAAGTCAAACGTTTTACGAGAATGACTGTCTTTACATACTCGTAAAAACAAAAAATGAAGACAGCAAACGTCTTTTT

11,390

PSEN1

PSEN1-201

PSEN1-201

ATATACACCTACTCTTTGAGCTAATTTATTCTTACCTAGTGGTCATTAGTAGAAGTGGTTCACTCTGGGAGCTTAACTAGAAGGG
TATATGTGGATGAGAACTCGATTAAATAAGAATGGATCACCAGTAATCATCTTCACCAAGTGAGACCCCTCGAATTGATCTTCCC

11,475

PSEN1

PSEN1-201

PSEN1-201

AAACTAACAATTCCTTGAGGTAGATCATTTTATCTAAAGCTTTTTGATTTCATATCAGTTGGGGGCGGGTATATTATGTTAATTT
TTTGATTGTTAAGGAACTCCATCTAGTAAAAATAGATTTTGAAAAACTAAAGTATAGTCAACCCCGCCCATATAATACAATTTAA

11,560

PSEN1

PSEN1-201

PSEN1-201

TTAAATCTGCATATTTTCCAGCCAGGCATGACTATAATCCCAGGACTTTGGGAGGTAGAAGCAGGAGGATTGCTTGAGCCCAGGA
AATTTAGACGTATAAAAAGGTCGGTCCGTA CTGATATTAGGGTCTGAAACCCTCCATCTTCGTCTCCTAACGAACTCGGGTCTT

11,645

PSEN1

PSEN1-201

PSEN1-201

ATTCAAGACCACCCTAGACTACATTA AAAAACATATTTTTTTGTATTTATTTTTTATTTTTTTTTTTGAGACAGAGTTTCGCTC
TAAGTTCTGGTGGGATCTGATGTAATTTTTGTATAAAAAACATAAATAAAAAATAAAAAAATAAAAAA ACTCTGTCTCAAAGCGAG

11,730

PSEN1

PSEN1-201

PSEN1-201

TCATTGCCAGGCTGGAGTGCAATGGCACGATCTCGGCTCACCACAGCCTCCGCCTCCTGGATTCAAGCAATTCTCCTGCCTCAG
AGTAACGGGTCCGACCTCACGTTACCGTGCTAGAGCCGAGTGGTGTCTGGAGGCGGAGGACCTAAGTTCGTTAAGAGGACGGAGTC

11,815

PSEN1

PSEN1-201

PSEN1-201

CCTCCCGAGTCGCCGGGATTATAGACATGCACCACCACACCGGGCTAATTTTGTATTTTGTAGTAGAGACAGGGTTTCTCCATGTT
GGAGGGCTCAGCGGCCCTAATATCTGTACGTGGTGGTGTGGCCCGATTAAAACATAAAAAATCATCTCTGTCCCAAAGAGGTACAA

11,900

PSEN1

PSEN1-201

PSEN1-201

GGTCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCCACCTCCGACTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACC
CCAGTCCGACCAGAACTTGAGGACTGGAGTCCACTAGGTGGGTGGAGGCTGAGGGTTTCACGACCCTAATGTCCACACTCGGTGG

11,985

PSEN1

PSEN1-201

PSEN1-201

ATGCCTGGCCTTTTTTTTTTTTTTAATTTAAACGAAATCTGCTTATTTTCTGTTGATGTAAGGTGTTTGTGTTAAGGTGAAAT
TACGGACCGGAAAAAAAAAAAAAAAAAATTAAATTTGCTTTAGACGAATAAAAGGACAACCTACATTCCACAAACACAATTCCACTTTA

12,070

PSEN1

PSEN1-201

PSEN1-201

GAAAAGTGATTTTTAAAAAATATTATTTTAGGACTATTTAACAAATATACTATTTATGATAATTAACATGGGGTTAGCAAACCTA
CTTTTCACTAAAAATTTTTTATAATAAAATCCTGATAAATTGTTTATATGATAAATACTATTAATTGTACCCCAATCGTTTGAT

12,155

PSEN1

PSEN1-201

PSEN1-201

CTGCTTGAAGCCAAATATGGCCCATGGCTTGTGTTTTGTACAGCTTATAAGCTAAAAATGCTTTTTACATTTAAAAAAAAAAAAA
GACGAACTTCGGTTTATACCGGTTACCGAACAAAAACATGTCGAATATTCGATTTTTACGAAAAATGTAATTTTTTTTTTTTTT

12,240

PSEN1

PSEN1-201

PSEN1-201

AGAACAAGGAAGAATATGTGACACACAAAACCTGAAATGTTTACTCCCTGGCCATTTACAGAAAAAGTTAGCTGGACATTGATTT
TCTTGTTCCCTTCTTATACACTGTGTGTTTTGGACTTTACAAATGAGGGACCGGTAAATGTCTTTTTCAATCGACCTGTAACCTAAA

12,325

PSEN1

PSEN1-201

PSEN1-201

TCATGTTACTATTAAGTCTGCTAAAAACAAAGGAGCTTGTAGCTATATTTTTTTCATACTTGCATAAAGAAAGAAAACCTAATAAATCG
AGTACAATGATAAATTGACGATTTTGTTCCTCGAACATCGATATAAAAAAGTATGAACGTATTTCTTTCTTTTGGATTATTTAGC

12,410

PSEN1

PSEN1-201

PSEN1-201

CTGGTGGCTTCATTTCCAAAAGGCTATGGAAATCCATAAACAGGCTGGGTGCAGTGGCTCATGCCTGTAATCCTAGCACTTTGGG
GACCACCGAAGTAAAGGTTTTCCGATACCTTTAGGTATTTGTCCGACCCACGTCACCGAGTACGGACATTAGGATCGTGAAACCC

12,495

PSEN1

PSEN1-201

PSEN1-201

AGGCTGAGGC GGGAGGATTGCTTGAGCCCAAGGAGTTT GAGTCTGGCCTGGGCAACGTAGTGAGACCTGTTTTTAGAAAAATGA
TCCGACTCCGCCCTCCTAACGAACCTCGGGTCTCAAACCTCAGACCGGACCCGTTGCATCACTCTGGGACAAAAATCTTTTTTACT

12,580

PSEN1

PSEN1-201

PSEN1-201

AGATAAAAACTAATCCATAAACCTCATACTTGGTGGTTGCCCTTCAGTTTTTCTTCTTTAGATCTGGATTTAGTTAAACAGTGT
TCTATTTTTTGATTAGGTATTTGGAGTATGAACCACCAACGGGAAGTCAAAAAGAAGAAATCTAGACCTAAATCAATTTGTCACA

12,665

PSEN1

PSEN1-201

PSEN1-201

ATTGCCTGCCTGGTTTCTGTTAACTTTTGATCATTGGTTGGGTTATCCTATAATGAAACTTGGTTGACCTCAGAAATAACAAGG
TAACGGACGGACCAAAGACAATTGAAAACCTAGTAAACCAACCCAATAGGATATTACTTTGAACCAACTGGAGTCTTTATTGTTCC

12,750

PSEN1

PSEN1-201

PSEN1-201

TGGTCGTT CAGCTTCTTTGATTGTGTGTTTCTTTCATAAGTTCTTCAAGAAGCCTGAGTATTAGAAACATGGATAAAATTATTGT
ACCAGCAAGT CGAAGAACTAACACACAAAAGAAAGTATTCAAGAAGTTCTTCGGACTCATAATCTTTGTACCTATTTAATAACA

12,835

PSEN1

PSEN1-201

PSEN1-201

GATAAAAAGCCAGAGAGACATAAATGTCAAGTATCTTGTTTTAAAATTACTGTGACCAGGCCGGGCGTGGTGGCTCACGCCTGTAA
CTATTTTTCGGTCTCTCTGTATTTACAGTTCATAGAACAAATTTAATGACACTGGTCCGGCCCGCACCACCGAGTGC GGACATT

12,920

PSEN1

PSEN1-201

PSEN1-201

TCCCAGCACTTTGGGAGGCTGAGGCGGGCGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACAGTGAAACCCACCT
AGGGTCGTGAAACCTCCGACTCCGCCCGCCTAGTGCTCCAGTCTCTAGCTCTGGTAGGACCGATTGTGTCACTTTGGGGTGGA

13,005

PSEN1

PSEN1-201

PSEN1-201

CTACTAAAAAATACAAAAATTAGCCAGGCATGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAT
GATGATTTTTTTTATGTTTTTAAATCGGTCCGTACCACCGCCCGGACATCAGGGTCGATGAGCCCTCCGACTCCGTCCTCTTA

13,090

PSEN1

PSEN1-201

PSEN1-201

GGCGTGAACCCAGGAGACGGAGCTTGCAGTGAGCCGAGATCATGCCACTGTACTCCAGCCTGGGTGACAGAGCAAGACTCTGTCT
CCGCACTTGGGTCCTCTGCCTCGAACGTCCTCGGCTCTAGTACGGTGACATGAGGTCGGACCCACTGTCTCGTTCTGAGACAGA

13,175

PSEN1

PSEN1-201

PSEN1-201

CAAAAAAAAAAAAAAAAAAAAAAAAAAATTACTGTGACCAGATTGGACTCAGCTTGCTGCTGGCATTGGTTCCACCATAACTCATA
GTTTTTTTTTTTTTTTTTTTTTTTTAATGACACTGGTCTAACCTGAGTCGAACGACGACCGTAAACCAAGGGTGGTATTGGAGTAT

13,260

PSEN1

PSEN1-201

PSEN1-201

TGTCATGTGTTTGCTTATATGTACTTTTGTGTTATTGTTGGTGTATCTTCAGGATAAGTTCCAAAATGTAATATTGCTGGGTTAA
ACAGTACACAAACGAATATACATGAAAACACAATAACAACCACATAGAAGTCCTATTCAAGGTTTTACATTATAACGACCCAATT

13,345

PSEN1

PSEN1-201

PSEN1-201

AGGATTAATGCACATGTAGTTTTATTAGATGTTACCAAATTTCCCTCCAGTGGGGATTATACCATTTTTTCATTCTGCCTGAAAT
TCCTAATTACGTGTACATCAAAAATAATCTACAATGGTTTTAAAGGGAGGTCACCCCTAATATGGTAAAAAGTAAGGACGGACTTTA

13,430

PSEN1

PSEN1-201

PSEN1-201

ATATGAGAGAAGCACCATTTTTAAAGTTTTTACAATGTCTCTGAACTAAAATGTGGTAGAGATGCACATGTGTATATCTAGATCTA
TATACTCTCTTCGTGGTAAAAATTTCAAAGTGTACAGAGACTTGATTTTACACCATCTCTACGTGTACACATATAGATCTAGAT

13,515

PSEN1

PSEN1-201

PSEN1-201

GATTGATATATTGATATACATGTATTTTTGTAGAAAGGGGGCACAGAGGAGGCCTCTTGACTATCCCTATTATGTTTATTGCTTTTA
CTAACTATATAACTATATGTACATAAAAAACATCTTCCCCGTGTCTCCTCCGGAGAAGCTGATAGGGATAATACAAATAACGAAAAT

13,600

PSEN1

PSEN1-201

PSEN1-201

ACGTTTTTTTCTCACGCCGGGTTTTAAACATGGTTTAGCATTATTGAACATTCTAAAAATGAGACATAATATGAAGGAAATTTACT
TGCAAAAAAGAGTGCGGCCCAAATTTTGTACCAAATCGTAATAACTTGTAAGATTTTTACTCTGTATTATACTTCCTTTAAATGA

13,685

PSEN1

PSEN1-201

PSEN1-201

CTGTGCATCTTTTGAATTATAATCACCATCTGAGGCTTTTGTGAGCTCCAGTTTGTCTCGAATTTAGAACATTCAACTAGTCCA
GACACGTAGAAAACCTTAATATTAGTGGTAGACTCCGAAAACACTCGAGGTCAAACAGGACCTTAAATCTTGTAAGTTGATCAGGT

13,770

PSEN1

PSEN1-201

PSEN1-201

GCTATTGTTTCAGTGGAATCTTGCTGGCCTGAACAGTTTTCTTCTGGTTCCTTTTCAGGGACTAAAAATGATGAAGAGTTTTGT
CGATAACAAAGTCACCTTAGAACGACCGGACTTGTCAAAGGAAGACCAAGGAAAAGTCCCTGATTTTTACTACTTCTCAAACA

13,855

PSEN1

PSEN1-201

PSEN1-201

GATAGCAGGTGCAGTTTTGAGTACTACAGTAAACATTCAAGTTTCAGAACTTCTTCTTACCTGCTAAAAACAAAGAGAACCTTTT
CTATCGTCCACGTCAAACCTCATGATGTCATTTGTAAGTCAAAGTCTTGAAGAAGAGAATGGACGATTTTTGGTTTTCTTTGGAAAA

13,940

PSEN1

PSEN1-201

PSEN1-201

TTTTATTTTTACTTCTGATTGTTGAACAGTCTTAAGGCAGCATTAGGAAGACTGGCGATTTGTGTGGAGAAATGATGGCTTGTTG
AAAATAAAAAATGAAGACTAACAACCTTGTGAGAATTCGGTCGTAATCCTTCTGACCGCTAAACACACCTCTTTACTACCGAACAAC

14,025

PSEN1

PSEN1-201

PSEN1-201

TTGTCTATGCATACTTTGTGTGTCCAGTGCTTACCTGGAATTTTGTCTTTCCCAACAGCAACAATGGTGTGGTTGGTGAATATGG
AACAGATACGTATGAAACACACAGGTCACGAATGGACCTTAAAACAGAAAGGGTTGTCGTTGTTACCACACCAACCCTTATACC

14,110

PSEN1

PSEN1-201

PSEN1-201

290 S T M V W L V N M 295
ENSE00003979370

CAGAAGGAGACCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAGAAAGTAGGTAACCTTTTATTAGATAAATAT
GTCTTCCTCTGGGCCTTCGAGTTTCTCTCATAGGTTTTTAAGGTTTCATATTACGTCTTTTCATCCATTGAAAAATAATCTATTATA

14,195

PSEN1

PSEN1-201

300 305 310 315
A E G D P E A Q R R V S K N S K Y N A E

ENSE00003979370

PSEN1-201

CTTGATTTTTTCAGGGTCACTGTTATAAGCTAACAGTATAGCAATGTTTTTATCGTCTTTCTTTGGTCATAGACTCCTTTGAGAAT
GAACTAAAAAGTCCCAGTGACAATATTCGATTGTCATATCGTTACAAAAATAGCAGAAAGAAACCAGTATCTGAGGAAACTCTTA

14,280

PSEN1

PSEN1-201

PSEN1-201

CTCTTGAGAACTATGATAATGCCAGTAAATACACAGATAAGTATTTAAGGAGTTCAGATACTCAAAACCCAACAATACAGTCAA
GAGAACTCTTGATACTATTACGGGTCATTTATGTGTCTATTATAAATTCCTCAAGTCTATGAGTTTTGGGTTGTTATGTCAGTT

14,365

PSEN1

PSEN1-201

PSEN1-201

AGCATCCTAGGTTAAGACACCTCCCATTAATAACAGAATACCAGCATGGAAAGGTTTCAGGCTGAGGTTATGATTTTTGTTTTGTT
TCGTAGGATCCAATTCTGTGGAGGGTAATTTATGTCTTATGGTCGTACCTTTCCAAGTCCGACTCCAATACTAAAAACAAAAACAA

14,450

PSEN1

PSEN1-201

PSEN1-201

TTTTGTTTGTTTTTTATAAGTCATGATTTTTAAAAAGAAAAAATAAACTCTCTCCAACATGTAAAAGTAAGAATCTCCTAAAAGA
AAAACAAACAAAAAATATTCAGTACTAAAATTTTTCTTTTTTATTGAGAGAGGTTTGTACATTTTCATTCTTAGAGGATTTTCT

14,535

PSEN1

PSEN1-201

PSEN1-201

AACAAAAAGAAACAGACAATAAAGGAAAAATAAGTAAACAAAAAAGCAAAATATAAACAAACATAAAAAATGAGAACCTCTTGTC
TTGTTTTTTCTTTGTCTGTTATTTCTTTTTATTCAATTTGTTTTTTTCGTTTTATATTTGTTGTATTTTTACTCTTGGAGAACAG

14,620

PSEN1

PSEN1-201

PSEN1-201

TAAATGACCAGAAATAACTGAAATATGATTTGAGATGTGCTGATGTGTATACTGAGAAGATCAAAATATTCTAGGTGGATATGACT
ATTGTACCGGCTTATTGACTTTATACTAAACTCTACACGACTACACATATGACTCTTCTAGTTTTATAAGATCCACCTATACTGA

14,705

PSEN1

PSEN1-201

PSEN1-201

TTTTAGAAGAGGATAAGAATGACTTAGGATGAGCTGGGTGACAGTGATGTGTGCCTGTAGTCCCAGCTACATGGCCAAGGCAAGAG
AAAATCTTCTCCTATTCTTACTGAATCCTACTCGACCCACGTCACTACACACGGACATCAGGGTTCGATGTACCGGTTCCGTTCTC

14,790

PSEN1

PSEN1-201

PSEN1-201

GATCACTTGAGCTAAGGAGTTCCGGATTACCCTGGGCAACTTATACCTTACCTCAAAAAATAATAATAATAATGAATAATAATAAT
CTAGTGAACCTCGATTCCCTCAAGGCCTAATGGGACCCGTTGAATATGGAATGGAGTTTTTATTATTATTACTTATTATTATTA

14,875

PSEN1

PSEN1-201

PSEN1-201

GACTTAGGATAAGAGAGTGAAAGGCCCTCTAAGGATACTACAGAACATATTAAGGAGAACACAAGTTAGAAGTTGTTATTAGATG
CTGAATCCTATTCTCTCACTTTCCGGGAGATTCCCTATGATGTCTTGTATAATTCCCTCTTGTGTTCAATCTTCAACAATAATCTAC

14,960

PSEN1

PSEN1-201

PSEN1-201

GAGTTGAGGGGGAGCTTTCATTCAGTTTTCTGGAATGGAGGCTACCTTCCCACACACACTAAAAAAAAAAGAAAGGGTTGAGGA
CTCAACTCCCCCTCGAAAGTAAGTCAAAAGACCTTACCTCCGATGGAAGGGTGTGTGTGATTTTTTTTTTTCTTTCCCAACTCCT

15,045

PSEN1

PSEN1-201

PSEN1-201

ATAACAGCACAAATATAAATAGTCTAAAAAAGGGCTAACTTTTTATGAGGAATCTGAAAAACAACAGGCACAGTAAATATTGGTGA
TATTGTCGTGTTATATTTATCAGATTTTTTTTCCCGATTGAAAAACTCCTTAGACTTTTTTGTGTCGGTGTCAATTTATAACCACT

15,130

PSEN1

PSEN1-201

PSEN1-201

GGAAAAAAGGCCTTAATTGAGTTGCTGTTTGTTCAGGAAAGGGAGAGTTTATGTTTTATAAAGCCAGGAAATCTACAGAGTTAGC
CCTTTTTTTCCGGAATTAACCTCAACGACAAACAGTCCTTTCCCTCTCAAATACAAAATATTTTCGGTCTTTAGATGTCTCAATCG

15,215

PSEN1

PSEN1-201

PSEN1-201

ATTTAGGCAACTGCAAGGAAGATACTTTCAACCAGGAATTCCTATTTGGAACCTCAGAGATGTGAGTCTTTATTATACAGTAAGCA
TAAATCCGTTGACGTTCCCTTCTATGAAAGTTGGTCCTTAAGGATAAACCTTGAGTCTCTACACTCAGAAATAATATGTCATTTCGT

15,300

PSEN1

PSEN1-201

PSEN1-201

AGGCAGCAGAACAAGGTCATGTTAGACTCTCACGGGATCCTTAGGGTGTGACTTTGCTAGCCAGAAACCTCTGTGGCTGGTGGCA
TCCGTCGTCCTTGTCCAGTACAATCTGAGAGTGCCCTAGGAATCCACACTGAAACGATCGGTCTTTGGAGACACCGACCACCGT

15,385

PSEN1

PSEN1-201

PSEN1-201

CCTTTTCCTGAGATTTGCTCAGGCCCACTGGGCTCATTCCACCTACTCAGCCTAGCTGGCTATGCTTGGCTTTCTCTACCAGCTG
GGAAAAGGACTCTAAACGAGTCCGGGTGACCCGAGTAAGGTGGATGAGTCGGATCGACCGATACGAACCGAAAGAGATGGTTCGAC

15,470

PSEN1

PSEN1-201

PSEN1-201

GACCCCATGCCTGCCAAAGGCAAGCCAGGCATGGAGCAGCGAGGAGTGCATGAGCAAGTGAGTGCAGGGTCCAGCCACTGCACAC
CTGGGGTACGGACGGTTTCCGTTCCGGTCCGTACCTCGTCGCTCCTCACGTAICTCGTTCACTCACGTCCCAGGTCGGTGACGTGTG

15,555

PSEN1

PSEN1-201

PSEN1-201

AGCCAGGCATGCTGGCTGCAGCAGGGCAGGCAGCCTCAGGTAICTAGCTCCCTGCTGCAGCTAGACCAGGCATTACCTAAGCAGCT
TCGGTCCGTACGACCGACGTCGTCCCGTCCGTCCGAGTCCATGATCGAGGGACGACGTCGATCTGGTCCGTAATGGATTTCGTCGA

15,640

PSEN1

PSEN1-201

PSEN1-201

TTGACTACAGGCCACTACCACTAGTAAACCTGATAGAAAAGTAAGAAATATACTGGAAAAGTAATGCCACAAGCCTGGCTCTTGTG
AACTGATGTCCGGTGATGGTGATCATTGGACTATCTTTTCATTCTTTATATGACCTTTCTTAACGGTGTTCGGACCGAGAACAC

15,725

PSEN1

PSEN1-201

PSEN1-201

TTAACCTTGTGTTAACCTGGGGAACACAGGGGCACCCAGAAGCTTGGAGATGCCAGGAACTGCAGAACCCCAAAGAGGGGGGTCA
AATTGGAACACAATTGGACCCCTTGTGTCCCGTGGGTCTTCGAACCTCTACGGTCTTGACGCTTGGGGTTTCTCCCCCAAGT

15,810

PSEN1

PSEN1-201

PSEN1-201

TAGCCCTGGCTTAGGGAACTCCTGAGTCTGGACTCCCCGAAGGGCCACATCTCTTCACTCCTCTCTTCTCTCCTTCTCGCCACCT
ATCGGGACCGAATCCCTTGAGGACTCAGACCTGAGGGGCTTCCCGGTGTAGAGAAGTGAGGAGAGAAGAGAGGAAGAGCGGTGGA

15,895

PSEN1

PSEN1-201

PSEN1-201

GCAACGTGGCAAGTGGGGGGCACGTTTCAGCCCTGTTTGTCTTACGGTCTTTCAATCCTGCCATTCAATGGGTCCCAAGTTCTT
CGTTGCACCGTTACCCCCCGTGCAAAGTCGGGACAAACAGAATGCCAAGAAAGTTAGGACGGTAAGTTACCCAGGGTTCAAGAA

15,980

PSEN1

PSEN1-201

PSEN1-201

GTCCTGCATCCAGGAAGAATGAAGTACGTGGACAGCTGGAGGGAGAGCAAGATGAAAAGGTGCTTTATTGAGCAACAGTACAGCT
CAGGACGTAGGTCCTTCTTACTTCATGCACCTGTCGACCTCCCTCTCGTTCTACTTTCCACGAAATAACTCGTTGTCATGTCGA

16,065

PSEN1

PSEN1-201

PSEN1-201

CTCAGGAGACCCTATCTGCAGGCAGGTCGTCCCATTTGTCTCTGCAGCTCTCAGTGGAGAGGAGACCTGGAGTGGGTAGCTCCTGT
GAGTCCTCTGGGATAGACGTCCGTCCAGCAGGGTAACAGAGACGTCGAGAGTCACCTCTCCTCTGGACCTCACCCATCGAGGACA

16,150

PSEN1

PSEN1-201

PSEN1-201

CTGCAGGCAGGTCATCCTGATGTCTGTAATCCTCAGTGGAGAGGAGACCCGGAATGGGTATCTCCTATCCACAAGCAGGTCATCC
GACGTCCGTCCAGTAGGACTACAGACATTAGGAGTCACCTCTCCTCTGGGCCTTACCCATAGAGGATAGGTGTTTCGTCCAGTAGG

16,235

PSEN1

PSEN1-201

PSEN1-201

CATCATCTCTGCAGCCCTCAGTGGAGAGGAGACCCGGAGTGGGTAGCTTCTTTCTGCAGGCAGGTTGTCCTTCATCTGCCAAG
GTAGTAGAGACGTCGGGAGTCACCTCTCCTCTGGGCCTCACCCATCGAAGAAAGACGTCCTGTC AACAGGGGAAGTAGACGGGTTTC

16,320

PSEN1

PSEN1-201

PSEN1-201

TCTGACTGAGTCTGGGGTTTTTATGGGCTTCAGAGGGGAGGAAGTACATGCTGATGGGTCCATGGGTGGCCATGAGCAGGCCCCAG
AGACTGACTCAGACCCCCAAAAATACCCGAAGTCTCCCTCCTTCATGTACGACTACCCAGGTACCCACCGGTA CTGTCGGGTC

16,405

PSEN1

PSEN1-201

PSEN1-201

AAAATGCACCATAAGTTCTCACTGTGGTCTGTGGA ACTGGGAGCTTGGCCTCCAGGCTTCAGGCTTTCCCTGACTTGAGGTGGTG
TTTTACGTGGTATTCAAGAGTGACACCAGACACCTTGACCTCGAACCGGAGGTCCGAAGTCCGAAAGGGACTGAACTCCACCAC

16,490

PSEN1

PSEN1-201

PSEN1-201

CTTCACCAGGGAACTTCCCCTTTCCGCCTAGGAGCCTGTCTGCCTCCTGCTGCCATCAACCTGCTGTCTATAGCTCCCATGGCAC
GAAGTGGTCCCTTGAAGGGGAAAAGGCGGATCCTCGGACAGACGGAGGACGACGGTAGTTGGACGACAGATATCGAGGGGTACCGTG

16,575

PSEN1

PSEN1-201

PSEN1-201

CCAGGCTGTTTCATGCCAAAGGGTGCCTGCAGGCCACGGTAAGCTGCCTTCAGCCCCCTCCTCAGTCTCCCTCCCATGCTTGTGAG
GGTCCGACAAGTACGGTTTCCCACGGACGTCCGGGTGCCATTCGACGGAAGTCGGGGAGGAGTCAGAGGGGAGGGTACGAACAGTC

16,660

PSEN1

PSEN1-201

PSEN1-201

CACCCAAAGTCCAGAGGGGGCCAAGGTGGCAGGGGGCTGGCATGTGTCAGTGTGCCCAAGCGCCCGCACACCCGGCCAGGTCATG
GTGGGTTTCAGGCTCCCCCGGTTCCACCGTCCCCGACCGTACAGTACGACGCGGGTTCGCGGGCGTGTGGGCCGGTCCAGTAC

16,745

PSEN1

PSEN1-201

PSEN1-201

ACAGCACCCAGCCTCAGCCACAACCTTTGCTCTGAAATCGGAGCCTGCAGACGCAAGGGGCTTCTGGACCCCTGAGAGCACAGGG
TGTCGTGGGTCGGAGTCGGTGTGAAACGAGACTTTAGCCTCGGACGTCTGCGTTCCCCGAAGGACCTGGGGACTCTCGTGTCCC

16,830

PSEN1

PSEN1-201

PSEN1-201

ATGCCAGGTCTACAGCCACAGCTGGGAAGCTGCAGCTGTGGGAGTGCGGGACTTCTGCCCCACCAACTCAGAAGGGGGCAGGAC
TACGGGTCCAGATGTCGGTGTGACCCCTTCGACGTGACACCCCTCACGCCCTGAAGACGGGGTGGTTGAGTCTTCCCCCGTCTCTG

16,915

PSEN1

PSEN1-201

PSEN1-201

TCCCGCCTGTTCCCTGGCTCCTGCCAGCTCACAGAGCATGCTGCCCCAGCTGCACCTCCCCTGCTGCAGCTGCCATCTTTGCAGCA
AGGGCGGACAAGGACCGAGGACGGTCGAGTGTCTCGTACGACGGGGTCGACGTGGAGGGGACGACGTGACGGTAGAAAACGTCGT

17,000

PSEN1

PSEN1-201

PSEN1-201

GCCACTCCAGATGGGCCGCTGCTGCCATCAAGACCACTAGTAAACCTGATAGAAAAGTAAGAAATATACTGGAAAGAATTGCCAC
CGGTGAGGTCTACCCGGCGACGACGGTAGTTCTGGTGATCATTTGGACTATCTTTTCATTCTTTATATGACCTTTCTTAACGGTG

17,085

PSEN1

PSEN1-201

PSEN1-201

AAGCCTGGCTCTTGTGTTAACCTGTGTTAAGCTAAAGAAAATCAAATGATTGTCTGTGAGCATGTAGGTATATATGTATGTGAGT
TTCGGACCGAGAACAACAATTGGACACAATTCGATTTCTTTTAGTTTACTAACAGACACTCGTACATCCATATATACATACACTCA

17,170

PSEN1

PSEN1-201

PSEN1-201

GAGTGATACAACAGAATTTCAATTCATTTTACAGATGTTGACTGAGCACCTGACTATGTGCTAGGCCCTGGGGATATAGCACTGAA
CTCACTATGTTGTCTTAAAGTAAAGTAAAATGTCTACAACCTGACTCGTGGACTGATACACGATCCGGGACCCCTATATCGTGACTT

17,255

PSEN1

PSEN1-201

PSEN1-201

CAAGATTTCCCCTGCCCTTGTGGAGCTTATAGTCTATTTGGAGAGATAGATGGTCAACAAATTATTACATAAATAATTCATACAG
GTTCTAAAGGGGACGGGAACACCTCGAATATCAGATAAACCTCTCTATCTACCAGTTGTTTAAATAATGTATTTATTAAGTATGTC

17,340

PSEN1

PSEN1-201

PSEN1-201

TTGTGATAGGTACTACAAAGAAGACGTATAAGTTGCTATGAAAGTTTATAATAGGGGAATTTTACGTATCCTGGAAAAGTCAAGGG
AACACTATCCATGATGTTTCTTCTGCATATTC AACGATACTTTCAAATATTATCCCCTTAAATGCATAGGACCTTTCAGTTCCC

17,425

PSEN1

PSEN1-201

PSEN1-201

GTGCTTCCCTGAGGAAGTGGAATAGGGGACGGCCCGCTGAAGGATGGAGGAAGAGCTTTCCAAGAGAGGGACAACATGAGCAAG
CACGAAGGGACTCCTTCACCATTATCCCCTGCCGGGCGACTTCTTACCTCCTTCTCGAAAGGTTCTCTCCCTGTTGTAICTCGTTTC

17,510

PSEN1

PSEN1-201

PSEN1-201

GGCTTTGAAATGAGAAGGCTGGATGAACTGCAGGCTTCTCAGTGAGAATGCTGCTGGTATTTTGGGGGACACAGTTCTTTGTGG
CCGAAACTTTACTCTTCCGACCTACTTGACGTCCGAAGGAGTCACTCTTACGACGACCATAAAACCCCGTGTC AAGAAACACC

17,595

PSEN1

PSEN1-201

PSEN1-201

GACTTTCCTCATATTGCAAGATATTTAACATCCCTGGCCCTCACCCACTAAATGCCAATAATGGCTTTAAGGCTTTGCAATAA
CTGAAAGGGAGTATAACGTTCTATAAATTGTAGGGACCGGGAGTGGGTGATTTACGGTTATTACCGAAATTCCGAAACGTTATT

17,680

PSEN1

PSEN1-201

PSEN1-201

TCAAAAACTCCTCCATCCTAGTTATTTCCAAACACTCCCCGGAAGGGAGGTGCTATCCCTAGTTGAAAAATCACTGTGTTAACGG
AGTTTTTTGAGGAGGTAGGATCAATAAAGGTTTGTGAGGGGCCTTCCCTCCACGATAGGGATCAACTTTTTTAGTGACACAATTGCC

17,765

PSEN1

PSEN1-201

PSEN1-201

AACTAGAAGTTACATTGGAACAAAAGGGCATAGGGCTCCAAGAGGGATATCTGTGTAAGGAAAAACAAACAAAAGAACTGAGAG
TTGATCTTCAATGTAACCTTGTTCCTCGTATCCCGAGGTTCTCCCTATAGACACATTCCTTTTTTGTGTTTCTTGACTCTC

17,850

PSEN1

PSEN1-201

PSEN1-201

ATTACCTGATGTGGTTGAGCTCTGTCAGAGCATTTCAGGATAAATTAGTCATAGATAATAATATAAAATTCATCAGTGGAAAAA
TAATGGACTACACCAACTCGAGACAGTCTCGTAAAGTCTATTTAATCAGTATCTATTATTATTTTTAAGTAGTCACCTTTTTT

17,935

PSEN1

PSEN1-201

PSEN1-201

ATGAGGCAGTTTTCCAAAGAAAAACAAAACTTGCTCAAAAAAGCAAATGTAATTATAGTATATTCTGGCTATAGCAAAGTAGTTT
TACTCCGTCAAAAGGTTTCTTTTGTGTTTTGAACGAGTTTTTTCGTTTACATTAATATCATATAAGACCGATATCGTTTCATCAA

18,020

PSEN1

PSEN1-201

PSEN1-201

AGTTGTGAATATTATTTGCATAGTGAGAATATAAAGCTGAATTTAATATAAGGTTATGGCACTGGGAAGACAGGAAGAGTTACAT
TCAACACTTATAATAAACGTATCACTCTTATATTTTCGACTTAAATTATATTTCCAATACCGTGACCCTTCTGTCTTCTCAATGTA

18,105

PSEN1

PSEN1-201

PSEN1-201

TTGCGTGCACTAAAGGATGAGACCTAATGCTTTATCTTCTCTATAGGAGGTGAATAAGTACCTCAAATTAACATCAAGTTATG
AACGCACGTGATTTCTACTCTGGATTACGAAATAGAAGAGATATCCTCCACTTATTCATGGAGTTTAATTTTTGTAGTTCAATAC

18,190

PSEN1

PSEN1-201

PSEN1-201

GCACAATGAGCATGCTACTTATAATTAATTATGGAGGTAATAACCAAAAGGGATGGCTAAAAGAGTTTAAGGTAGGAATGAGTAT
CGTGTTACTCGTACGATGAATATTAATTAATACCTCCATTTATGGTTTTCCCTACCGATTTTCTCAAATTCATCCTTACTCATA

18,275

PSEN1

PSEN1-201

PSEN1-201

CAGAAGTGAGGAGGGGAGGGGGTAGAAAAAGGGACTGCTGTTTTTCATTTATAAATCTTATTCTTATATTATTTTCATAAACTCCAAAC
GTCTTCACTCCTCCCTCCCCCATCTTTTCCCTGACGACAAAAAGTAAATATTTAGAAATAAGAATATAATAAAGTATTTGAGGTTTG

18,360

PSEN1

PSEN1-201

PSEN1-201

CAGAGAAGATTCAGGTTTTTGGAGATCTGGATAATAAAAAAGAATACAAAACCTATCAATACAAAATTGTGAGGGCTCTCCAGAGG
GTCTCTTCTAAGTCCAAAAACCTCTAGACCTATTATTTTTCTTATGTTTTGATAGTTATGTTTTAACACTCCCGAGAGGGTCTCC

18,445

PSEN1

PSEN1-201

PSEN1-201

AAGCCATGCAAGGAAGGGCCCTGAAGCTTACAAGCTTTACTTATTCATGGCAAATCTACTTCTGCTCTGAACATGTATTACTTTT
TTCCGGTACGTTCCCTCCCGGACTTCGAATGTTGCAAATGAATAAGTACCGTTTAGATGAAGACGAGACTTGTACATAATGAAAA

18,530

PSEN1

PSEN1-201

PSEN1-201

ATAAAAAATGAAGGAAGAATAAAAGTACTTTGAACTTCACTTATATATTTTAATTATTTTTAATGTATGGAAGTTTTTTAAGACT
TATTTTTTACTTCCCTTCTTATTTTCATGAACTTGAAGTGAATATATAAAATTAATAAAAAATTACATACCTTCAAAAAATTCTGA

18,615

PSEN1

PSEN1-201

PSEN1-201

ATCATGCTCACCATTTTTCAATGAGATTGATAGTCATTATAATGAAATGACTGGCCATAAAGACATTCACTCCCCGCTCCTTTCC
TAGTACGAGTGGTAAAAGTTACTCTAACTATCAGTAATATTACTTTACTGACCGGGTATTTCTGTAAGTGAGGGGCGAGGAAAAGG

18,700

PSEN1

PSEN1-201

PSEN1-201

CAATCCACCCTCCAGAATGAAGCCACTTTTTATAATTTTGTACCAAATCCAGGGATGAGTGCCAACAGTTAGGAAGCTTTTCAGTT
GTTAGGTGGGAGGTCTTACTTCGGTGAAAATATTAACAGTGGTTTAGGTCCCTACTCACGGTTGTCAATCCTTCGAAAAGTCAA

18,785

PSEN1

PSEN1-201

PSEN1-201

GCAAAAGATAAAAAGCCCAACTCAGTTGCCTTAAACAAAGAAGAAATTTATTCTTTCACGTGACAGGAAGGCCTGAGGTGTAGGC
CGTTTTCTATTTTTCGGGTTGAGTCAACGGAATTTGTTTCTTCTTAAATAAGAAAGTGCACTGTCTTCCGGACTCCACATCCG

18,870

PSEN1

PSEN1-201

PSEN1-201

ATTTGAAATTTGTAGGGTTGGTTAATTTGGTGGGCTCAGGGATGTTTTCAAGTAGCCCAACTTCCTACTCTACCATCACTAGTTTA
TAAACTTTAAACATCCCAACCAATTA AACCCACCGAGTCCCTACAAAAGTTCATCGGGTTGAAGGATGAGATGGTAGTGATCAAAT

18,955

PSEN1

PSEN1-201

PSEN1-201

TAGGCTTGGTCTTCAGCCCACTGCTCTTCGTGGTCATGACAGCTGTAGTTCTAGGCATCATGTCTAGATAAGGCAACATTCAGGG
ATCCGAACCAGAAAGTCGGGTGACGAGAAGCACCAGTACTGTGACATCAAGATCCGTAGTACAGATCTATTCCGTTGTAAGTCCC

19,040

PSEN1

PSEN1-201

PSEN1-201

GTAGAAGGGGACTGTTTTATTTTTCTTTAGTCTCTCTTAAAGAGTGAGAAAAATTTCCAGGAATCCCGGTGGACTTTGCTTC
CATCTTCCCCTGACAAATAAAAAAGGAAATCAGAGAGAATTTCTCACTCTTTTTAAAAGGGTCCTTAGGGCCACCTGAAACGAAG

19,125

PSEN1

PSEN1-201

PSEN1-201

ACCACTCATAGGTTTCATACCAAGTTACAACCCACAACTTAGAGCTTTTGTAGGAAGAGGCTTGGTGGGATTACCGTGCTTGG
TGGTGAGTATCCAAGTATGGTTCAATGTTGGGGTGTGGAAATCTCGAAAACAATCCTTCTCCGAACCACCTAATGGCACGAACC

19,210

PSEN1

PSEN1-201

PSEN1-201

CTTGGCTTGGTCAGGATTCACCACCAGAGTCATGTGGGAGGGGGTGGGAACCCAAACAATTCAGGATTCTGCCCTCAGGAAATAA
GAACCGAACCAGTCCTAAGTGGTGGTCTCAGTACACCCTCCCCACCCTTGGGTTTGTAAAGTCCTAAGACGGGAGTCCTTTATT

19,295

PSEN1

PSEN1-201

PSEN1-201

AGGAGAAAATAGCTGTTGGATAAACTACCAGCAGGCACTGCTACAGCCCATGCTTTGTGGTTTTAAGGGCCAGCTAGTTACAATGA
TCCTCTTTTATCGACAACCTATTTGATGGTCGTCCGTGACGATGTGCGGTACGAAAACACCAAATTCCTCGGTCGATCAATGTTACT

19,380

PSEN1

PSEN1-201

PSEN1-201

CAGCTAGTFACTGTTTCCATGTAATTTCTTAAAGGTATTAATTTTCTAAATATTAGAGCTGTAACCTTCCACTTTCTCTTGAA
GTCGATCAATGACAAAGGTACATTAAGAATTTCCATAATTTAAAAGATTTATAATCTCGACATTGAAGGTGAAAGAGAACTT

19,465

PSEN1

PSEN1-201

PSEN1-201

GGCACAGAAAGGGAGTCACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAGTGAGGAATGGGAAGCCCAGAGGGACAGTC
CCGTGTCTTTCCCTCAGTGTTCTGTGACAACGTCTCTTACTACTACCGCCCAAGTCACTCCTTACCCCTTCGGGTCTCCCTGTCAAG

19,550

PSEN1

PSEN1-201

S T E R E S Q D T V A E N D D G G F S E E W E A Q R D S

ENSE00003979376

PSEN1-201

ATCTAGGGCCTCATCGCTCTACACCTGAGTCACGAGCTGCTGTCCAGGAACCTTCCAGCAGTATCCTCGCTGGTGAAGACCCAGA
TAGATCCCGGAGTAGCGAGATGTGGACTCAGTGCTCGACGACAGGTCCCTTGAAAGGTCGTCATAGGAGCGACCACTTCTGGGTCT

19,635

PSEN1

PSEN1-201

H L G P H R S T P E S R A A V Q E L S S S I L A G E D P E

ENSE00003979376

PSEN1-201

GGAAAGTATGTGCATTTCTCTATGTTGCAAAGTCATGGATTCTTTAGGTAGCTACATTATCAACCTTTTTGAGAATAAAATGAA
CCTTTCATACACGTAAAGAGATACAACGTTTCAGTACCTAAGGAAATCCATCGATGTAATAGTTGGAAAAACTCTTATTTTACTT

19,720

PSEN1

PSEN1-201

E
ENSE...

PSEN1-201

TTGAGAGTGTTACAGTCTAATTCTATATCACATGTAACCTTTATTTGGATATATCAGTAATAGTGCTTTTTTTTTTTTTTTTTTTT
AACTCTCACAAATGTCAGATTAAGATATAGTGACATTGAAAATAAACCTATATAGTCATTATCACGAAAAAAAAAAAAAAAAAAAA

19,805

PSEN1

PSEN1-201

PSEN1-201

TTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCGCTCTGTGCCAGGTTGGAGTGCAATGGTGCATCTTGGCTCACTGCAAG
AAAAAAAAAAAAAAAAAAAAAAAAAACTCTGTCTCAGAGCGAGACAGCGGTCCAACCTCACGTTACCACGCTAGAACCAGTGACGTTT

19,890

PSEN1

PSEN1-201

PSEN1-201

CTCCACCTCCC666TTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGTGCGCCACCACGCCTGGATAA
GAGGTGGAGGGCCCAAGTTCACTAAGAGGACGGAGTCGGAGGGTTCATCGACCCTGATGTCCGCACGCGGTGGTGC66ACCTATT

19,975

PSEN1

PSEN1-201

PSEN1-201

TTTTTGTATTTTAGTAGAGATGGGGTTTTACCATCTTGGGCGAGGCTGGTCTTGAACCTCCTGACATCATGATCTGCCTGCCTTAG
AAAAACATAAAATCATCTCTACCCCAAAGTGGTAGAACCCGTCGACCAGAACTTGAGGACTGTAGTACTAGACGGACGGAATC

20,060

PSEN1

PSEN1-201

PSEN1-201

CCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTACCTGGCCTCCCTTCAGACTTTTTAAGTTGGCATTTTACAGCCTGAC
GGAGGGTTTTACGACCCTAATGTCCGCACTCGGTGACATGGACCGGAGGGAAGTCTGAAAAATTCAACCGTAAAAATGTCGGACTG

20,145

PSEN1

PSEN1-201

PSEN1-201

CTTTTGGCATTATTTTTATAAAGTAAAAGATTTGTTTTTTAATTGTTCCAGTAAGCCTTCATGGCCGTAATACATTTGTCTACA
GAAAAACCGTAAATAAAAATATTTTCATTTTCTAAACAATAAATAAACAAGGTCATTCGGAAGTACCGGCATTATGTAAACAGATGT

20,230

PSEN1

PSEN1-201

PSEN1-201

AAAATTTTATTAATATGTCTCACTCTGCTGTAGAGAGATCTGTGGATTTGCATGATACAACCTTGTACATTATTATTCTTTTTGT
TTTTAAAATAATTATACAGAGTGAGACGACATCTCTCTAGACACCTAAACGTAATGTTGGAACATGTAATAATAAGGAAAAACA

20,315

PSEN1

PSEN1-201

PSEN1-201

TGACAAGTGCTATATTTTTATTTTAAAGAAAAATCAAAGGGATTTAGGATATTGGCAGAAATGCAAGTATTTCTTCAGTGTCTAAGA
ACTGTTACAGATATAAAAATAAAAATTTCTTTTAGTTTTCCCTAAATCCTATAACCGTCTTTACGTTTCATAAAGAAGTCACAGATTCT

20,400

PSEN1

PSEN1-201

PSEN1-201

TGTGTTGCCACTTGATGGATTTAAGTTAACACTTAGGGCTTCTTAGGAACATTATCAGCCACTAAAGCCCTTTGGTTAGGGCTCA
ACACAACGGTGAACTACCTAAATTCAATTGTGAATCCCGAAGAATCCTTGTAATAGTCGGTGATTTGCGGAAACCAATCCCGAGT

20,485

PSEN1

PSEN1-201

PSEN1-201

GTCATCTCTTCAGTTAGTCTTAGAGATGTGGTTCATTGAATAAGACTTTAGCATATTTTTCCAACCAAGTTATTTTTGGTTGTCTT
CAGTAGAGAAGTCAATCAGAATCTCTACACCAAGTAACTTATTCTGAAATCGTATAAAAAGGTTGGTTCAATAAAAAACCAACAGAA

20,570

PSEN1

PSEN1-201

PSEN1-201

GTTTTTGCAAGAGTGAACTTGATTAAAACATTACAACAAGAATATTAAGTAGTTTTAAGGAAACAAACACCTAGGTTCCCTTAGC
CAAAAACGTTCTCACTTTGAACTAATTTTGTAAATGTTGTTCTTATAATTCATCAAAATTCCTTTGTTTGTGGATCCAAGGAATCG

20,655

PSEN1

PSEN1-201

PSEN1-201

ATCTTTAATCATTAGTCACTAATTATTATGACCTTGACATATCCATCAGTTTGAGGAGAACAACCTTTTTACACCTTGTCTCAGTT
TAGAAAATTAGTAATCAGTGATTAATAATACTGGAACCTGTATAGGTAGTCAAACCTCTCTTGTGAAAAATGTGGAACAGGAGTCAA

20,740

PSEN1

PSEN1-201

PSEN1-201

TTTTAACTGAGTCAGAACTTTCACTGGGCATGTTTCATGACTTTACTGCTTGGCTGAGTTTTCCAGATATCAAAGCCCAGCTGCAG
AAAATTGACTCAGTCTTGAAAAGTGACCCGTACAAGTACTGAAATGACGAACCGACTCAAAAAGGTCTATAGTTTTCGGGTCGACGTC

20,825

PSEN1

PSEN1-201

PSEN1-201

CCTGTGACTTTACACTCCTGGAAAAGTAGACGTATCTGCCTGCTCTTACAGCAGGCTTTAGCTTGCCTTTGCTGGGACTTTGTT
GGACACTGAAAAGTGTGAGGACCTTTTCATCTGCATAGACGGACGAGAATGTCGTCCGAAATCGAACGGAAACGACCTGAAACAA

20,910

PSEN1

PSEN1-201

PSEN1-201

CTGCCCTCAGTTACCACAGTAATTAGGTTGCCTCTTCTACTTTCTCTTTTCTCACAGGCACCAGGAGCCAGAGGAAATAACATA
GACGGGAGTCAATGGTGTCAATTAATCCAACGGAGAAGATGAAAGGAGAAAAGAGTGTCCGTGGTCTCTCGGTCTCCTTTATTGTAT

20,995

PSEN1

PSEN1-201

PSEN1-201

ATAGTTGTTGACCAGAGCAGCAGCATAATTCTTTCATGACTGCCTTTTCTAATTTGACGATTCCCTCTCCTGAGAGGGCTCTTTG
TATCAACAACCTGGTCTCGTCTCGTATTAAAGAAAGTACTGACGGAAAAGATTAAACTGCTAAGGGAGAGGACTCTCCCGAGAAAC

21,080

PSEN1

PSEN1-201

PSEN1-201

TGTCCTCCTCCTCTTCGTCTCCAACTTTTAAAAAAAAAAAAAGTGAAACTATCAAGTATTGCTCCTGCTAACTTCAGATCAGTATT
ACAGGAGGAGGAGAAGCAGAGGTTGAAAATTTTTTTTTTTTCACTTTGATAGTTCATAACGAGGACGATTGAAGTCTAGTCATAA

21,165

PSEN1

PSEN1-201

PSEN1-201

TTCTTTCTCTGAAGCCAATGCAAAGTAATAACGGACGTGCTTCATCATCTTAGCATTTCAGCACACGTGTCACCATCTCTGATGGT
AAGAAAGAGACTTCGGTTACGTTTCATTATTGCCTGCACGAAGTAGTAGAATCGTAAGTCGTGTGCACAGTGGTAGAGACTACCA

21,250

PSEN1

PSEN1-201

PSEN1-201

GTGAGCATGTTAAACCAGACTTGTGGGTACTTACCAAAAGGTTTCAGTTGACACTATAGGTCAGTTGCTAAAAGGCACAAATGTCT
CACTCGTACAATTTGGTCTGAACACCCATGAATGGTTTTCCAAGTCAACTGTGATATCCAGTCAACGATTTTCCGTGTTTACAGA

21,335

PSEN1

PSEN1-201

PSEN1-201

TCTAAAGCAATCTGTTAAAAGTCAACATTTAACATTTAATTAGAAAAGTCAAGGATCTGAATGTTTAGTTCTCCCAAGAAA
AGATTTTCGTTAGACAATTTTTCAGTTGTAATTTGTAATTAATCTTTTGACTAGTTTCCCTAGACTTACAAATCAAGAGGGTTCTTT

21,420

PSEN1

PSEN1-201

PSEN1-201

ATGTAAAAATGATCTGTAAACACATAAAAAAGATACTCAGCATCATTAGCCATCAAGGAAATGCAAATCAAACCCTTCATACTC
TACATTTTTACTAGACATTTGTGTATTTTTCTATGAGTCGTAGTAATCGGTAGTTCTTTACGTTTAGTTTTGGTGAAGTATGAG

21,505

PSEN1

PSEN1-201

PSEN1-201

ACTAGATTGGCTATAATAAAAAAGATAGACAATAACAGGTGTTGGTGAGGATGCGAAGAAACTGGAATCCTCATACTGCTGGT
TGATCTAACCGATATTATTTTTCTATCTGTTATTGTCCACAACCACTCCTACGCTTCTTTGACCTTAGGAGTATGTGACGACCA

21,590

PSEN1

PSEN1-201

PSEN1-201

GGGAATGTAAAATAGTATAGTGATTTTGGAAAACAGTTCGGTAGTTCTTTGAAAAGATTAAATATGACCCGGTAATTCTACTCCTA
CCCTTACATTTTATCATATCACTAAAACCTTTTTGTCAAGCCATCAAGAAACTTTCTAATTTATACTGGGCCATTAAGATGAGGAT

21,675

PSEN1

PSEN1-201

PSEN1-201

GGTATATACTCAAGAGAATTTTAAAACATATGTCAACACAAAGACACATATACAATGGTCATAGTAATATTGTTTCATAACAGGTA
CCATATATGAGTTCTCTTAAAATTTTGTATACAGTTGTGTTTCTGTGTATATGTTACCAGTATCATTATAACAAGTATTGTCCAT

21,760

PSEN1

PSEN1-201

PSEN1-201

AAAACAGAAACAACCCACATGTCTATTAAGTATAAGTGGATAATAAATGTGGTATATTCATACAATGGAATATTACTTGGTTAT
TTTTGTCTTTGTTGGGTGTACAGATAATTGACTATTACCTATTATTACCATATAAGTATGTTACCTTATAATGAACCAATA

21,845

PSEN1

PSEN1-201

PSEN1-201

AAAAAGAAACAATCTATCATTAGTACACTTAGGATGAGCTTGTACTGGCATGTTGGCTGTGGGAAGTATATCTTGAAATTCACT
TTTTTCTTTGTTAGATAGTAATCATGTGAATCCTACTCGAACAAATGACCGTACAACCGACACCCCTTCATATAGAACTTTAAGTGA

21,930

PSEN1

PSEN1-201

PSEN1-201

AAAAGACCAACTATTGCTGGGCGCAGTGGCTCAAGCACCTGTAATCCCAGCACTTTGGAAGGCCAAGGCAGGCGGACCACCTGAG
TTTTCTGGTTGATAACGACCCGCGTCACCGAGTTCGTGGACATTAGGGTCGTGAAACCTTCCGGTTCGGTCCGCTGGTGGACTC

22,015

PSEN1

PSEN1-201

PSEN1-201

ATCAGGAGTTTCGAGACCAGCCCAACCAACATGGAGAAACCCACCTCTACTAAAAATACAAAATTAGCCCATTTGTTGGTGGCACAT
TAGTCCTCAAGCTCTGGTCGGGTTGGTTGTACCTCTTTGGGGTGGAGATGATTTTTATGTTTTAATCGGGTAACACCACCGTGTA

22,100

PSEN1

PSEN1-201

PSEN1-201

GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATCATA
CGGACATCAGGGTCGATGAGTCTCCGACTCCGTCTTCTTAGTGAACCTTGGACCTCCACCTCCAACGTCACCTCGACTCTAGTAT

22,185

PSEN1

PSEN1-201

PSEN1-201

CCATTGCACTCCAGCCTGGGCAACAAGAGCGAAACTCCATCTCAAAAAAAAAAAAAAAAAAGACCAACTACCTTCACAATAAATAA
GGTAACGTGAGGTCGGACCCGTTGTTCTCGCTTTGAGGTAGAGTTTTTTTTTTTTTTTTTCTGGTTGATGGAAGTGTTATTTATT

22,270

PSEN1

PSEN1-201

PSEN1-201

AAATGTCTTACATTTCTAATTAATAATTTTTGTTTCAGTTTTATTATTTCAGCTTTAAAAAGGAAGGGAATTCTGACATGTTACAACA
TTTACAGAATGTAAAGATTAATTTTAAAAACAAGTCAAAAATAATAAGTCGAAATTTTTCTTCCCTTAAGACTGTACAATGTTGT

22,355

PSEN1

PSEN1-201

PSEN1-201

TGAATAAATCTTGAGTACTTTGTGCTAAGTGAAATAAGCTAGTTACAAAAAGAAAAATACTGTATGATTCCACTTACATCAGAGT
ACTTATTTAGAACTCATGAAACACGATTCACCTTTATTCGATCAATGTTTTCTTTTTATGACATACTAAGGTGAATGTAGTCTCA

22,440

PSEN1

PSEN1-201

PSEN1-201

AGTCAGAAAAGTAGACTGGTGGTTGCCAGGGGTTAAGGGGAGGGGAAATGAAGGGTCGTTTAAATGGGTGTAGAGTTTCAGTTTTAC
TCAGTCTTTTCATCTGACCACCAACGGTCCCAATTCCCTCCCTTTACTTCCCAGCAAATTACCCACATCTCAAAGTCAAATG

22,525

PSEN1

PSEN1-201

PSEN1-201

AAGATGAAAAGAGTTCTGTGGATGGACGATGGTAATGGTAGCACAATGATACGATTATACCTAGTGTCTTTGAACGGTGAACCTTA
TTCTACTTTTCTCAAGACACCTACCTGCTACCATTACCATCGTGTTACTATGCTAATATGGATCACAGAAACTTGCCACTTGAAT

22,610

PSEN1

PSEN1-201

PSEN1-201

AAAAGGGTTAAGATGTTAACTTGATGGGTATCTTACCACAGTTAAATTTTTATTATTTTTTTATTTTTTTGAGACAATTTTCGCTC
TTTTCCCAATTCTACAATTTGAACTACCCATAGAATGGTGTCAATTTAAAAATAATAAAAAATAAAAAACTCTGTTAAAGCGAG

22,695

PSEN1

PSEN1-201

PSEN1-201

GTTGCCTAGGGTGGAGTGCAGTGCTGGGATCTCAGCTCACTGCAACTCTGCCTCCCAGGTTCAAGCGATACTCCTGCCTCAGCCT
CAACGGATCCCACCTCACGTACGACCCCTAGAGTCGAGTGACGTTGAGACGGAGGGTCCAAGTTCGCTATGAGGACGGAGTCGGA

22,780

PSEN1

PSEN1-201

PSEN1-201

CCCGAGTAGCTGGGACTACAGGCACACATCACCATACCCGGCTAATTTTTATATTTTTTAGTAGAGACAAGGTTTCACCATGTTGG
GGGCTCATCGACCCTGATGTCCGTGTGTAGTGGTATGGGCCGATTAATAATAATAATAATCATCTCTGTTCCAAAGTGGTACAACC

22,865

PSEN1

PSEN1-201

PSEN1-201

CCAGGCTGGTCTTGAACCTCCTGACCTCAAGTGATCTGCCACCTCAGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTGT
GGTCCGACCAGAACTTGAGGACTGGAGTTCCTAGACGGGTGGAGTCCGAGGGTCTCACGACCCTAATGTCCACACTCGGTGACA

22,950

PSEN1

PSEN1-201

PSEN1-201

GCCC GGCCAAAAAATTTTTTTTAAATACCGTTAAGAAGTGGAAAATAAGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCA
CGGGCCGGTTTTTTTTAAAAAATTTATGGCAATTCTTCACCTTTTATTCCGGTCCACACCACCGAGTGTGGACATTAGGGTCGT

23,035

PSEN1

PSEN1-201

PSEN1-201

CTTTGGGAGACCAAGGTTGGTGGATCACCTGAGGTTTGGAGTTTGGAGACCAGCCTGGCCAACATGGTAAAAACCTCATATCTACTA
GAAACCTCTGGTTCCAACCACCTAGTGGACTCCAACCTCAAACCTCTGGTCGGACCGGTTGTACCATTTTGGAGTATAGATGAT

23,120

PSEN1

PSEN1-201

PSEN1-201

AAAATACAAAATTAGCCGGGCGTGGTGGCGCATGTCTGTAATCCCAGCTATTCGAGAGGCTGCGGCAGGATAATTGCTTGAAATC
TTTTATGTTTAATCGGCCCGCACACCACCGCTACAGACATTAGGGTCGATAAGCTCTCCGACGCCGTCTTATTAACGAACTTTAG

23,205

PSEN1

PSEN1-201

PSEN1-201

GGGAGGTGGAGGTTTTCAGTGAGCCGAGATCACTTAAAAAAAAAAGGAAAAAAGCTACCAGCTGAGAGAAAAATATATGCAAATC
CCCTCCACCTCCAAAGTCACTCGGCTCTAGTGAATTTTTTTTTTCTTTTATTTCGATGGTCGACTCTCTTTTATATACGTTTAG

23,290

PSEN1

PSEN1-201

PSEN1-201

ATATTGAAGTCCTGTTAAAGGACTTGTATTTAGGATATATAAAGGATGCTTACAACCTAATACGAAGACGATAGCCCAAATTTAA
TATAACTTCAGGACAATTTCTGAACATAAATCCTATATATTTCTACGAATGTTGAATTATGCTTCTGCTATCGGGTTTAAATT

23,375

PSEN1

PSEN1-201

PSEN1-201

GATAGGGAAATGCTTTGACTAGACATTCTACAAAAGAGATATATAATGGCTAAAAAGCACATGAAAAGATGCTCAACATCATT
CTATCCCTTTACGAAACTGATCTGTAAGATGGTTTTCTCTATATATTACCGATTTTTCTGTACTTTTTCTACGAGTTGTAGTAAT

23,460

PSEN1

PSEN1-201

PSEN1-201

ATCAGAGTGGCTAGAATGAAAAAGGCTAACAATACCAAGAGCTGGTGGAGGATGTGAAAAACTGGAACCTCAATTGTTGCTGGT
TAGTCTCACCGATCTTACTTTTTCCGATTGTTATGGTTCTCGACCACTCCTACACTTTTTTGACCTTGAGAGTTAACAACGACCA

23,545

PSEN1

PSEN1-201

PSEN1-201

GGAAATTCAGACTGGTACAGCCAGTGTGGAATGTGATTTGGCAGTTTATTAAAAAGCTAAAAACCTAAACTTACATAGCCCAGCA
CCTTTAAGTCTGACCATGTCGGTCACACCTTACACTAAACCGTCAAATAATTTTTCGATTTTTGGATTTGAATGTATCGGGTCGT

23,630

PSEN1

PSEN1-201

PSEN1-201

ATTGCACCCCCAGGAGTCTACCCAATGGAAATGAAAAACAGTCCGTCCCCACAGAGACATGGACATAAATGTTTCATAGCAGCATT
TAACGTGGGGGTCCTCAGATGGGTTACCTTTACTTTTTGTGTCAGGCAGGGGTGTCTCTGTACCTGTATTTACAAGTATCGTTCGTAAT

23,715

PSEN1

PSEN1-201

PSEN1-201

TTCAGAATAGCCCCAAATTGAAAAACAATCCAGATGTCCATCAACTGGTAAATGGATAAGCAAACCATATAATGGAAAACCATTCA
AAGTCTTATCGGGGTTAACTTTTGTAGGTCTACAGGTAGTTGACCATTTACCTATTCGTTTGGTATATTACCTTTTGGTAAAGT

23,800

PSEN1

PSEN1-201

PSEN1-201

GCTTCCAATAACTTCCAAGAACTGTAGACACATGCAGTATCATGGTTAAACCTCAAAAAACATTATATTAAGTAAAAATAGGCGAG
CGAAGGTTATTGAAGGTTCTTTGACATCTGTGTACGTCATAGTACCAATTTGGAGTTTTTGTAAATATAATTCATTTTATCCGCTC

23,885

PSEN1

PSEN1-201

PSEN1-201

GCATGTATTGTATGAGTCATATGAAATGTCTAGAAAAGGCAAATTTATTGAGATAGAAAAGCAGATCACTGGTTGCTTAAGGCCTA
CGTACATAACATACTCAGTATACTTTACAGATCTTTTCCGTTTAAATAACTCTATCTTTCGTCTAGTGACCAACGAATTCGGAT

23,970

PSEN1

PSEN1-201

PSEN1-201

GGGTAGGAGTGGGGATTAAGTAACTGTAAACGGGTACAAGGTACTGACTGGGGCAATGGACATGTGGATTGTGATGATAGTTAAATTG
CCCATCCTCACCCCTAATTGACATTTGCCCATGTTCCATGGACTGACCCCGTTACCTGTACACCTAACACTACTATCAATTTAAC

24,055

PSEN1

PSEN1-201

PSEN1-201

TACAGCTCTCTCTATATATAGTTGTACAGCTCTATTAATTTCCACAATCATTGAATCATGTCTTCCAGTTTTATGAGGTAAATC
ATGTGCGAGAGAGATATATATCAACATGTGCGAGATAATTAAGGTTGTTAGTAAGTACTTAGTACAGAAGGTCAAAAATACTCCATTTAG

24,140

PSEN1

PSEN1-201

PSEN1-201

ATAGTCCAATGAAGCTTTTTTAAAAATAAGATGATAGGCCATGTGTGGTGGCTCACGTCTGTAATCCCAGCACTTTGGGAGGCCA
TATCAGGTTACTTCGAAAAAATTTTTATTCTACTATCCGGTACACACCAGTGCAGACATTAGGGTCGTGAAACCCTCCGGT

24,225

PSEN1

PSEN1-201

PSEN1-201

AGGTGGGTGGATCATGAGGTCAGGAGTTCGAGACCAGCCTGACCAACATGGTGAAACCCTGTCTCCATCAAAAAATAAAAAATTA
TCCACCCACCTAGTACTCCAGTCCTCAAGCTCTGGTCGGACTGGTTGTACCACTTTGGGACAGAGGTAGTTTTTTATTTTTTTAAT

24,310

PSEN1

PSEN1-201

PSEN1-201

GCCAGGCATGGTGGCATGCGCCTGTAATCCCACCTACTCAGGAGGCTGAGACAGGAAAGTCGCTTGAACCTGGGCGGCAGAGTCT
CGGTCCGTACCACCGTACGCGGACATTAGGGTGGATGAGTCCTCCGACTCTGTCTTTTCAGCGAACTTGGACCCGCCGTCTCAGA

24,395

PSEN1

PSEN1-201

PSEN1-201

GCAGTGAGCCGAGATCATGCTGCTGTAATCCCACCTACTCAGGAGGCTGAGACAGGAAAGTCGCTTGAACCTGGGCGGCAGAGTCT
CGTCACTCGGCTCTAGTACGACGACATGAGGTCGGACCCGGTGTCTCGTTTTGAGGTAGAGTTTTTTTTTTTTTTATAATTAATT

24,480

PSEN1

PSEN1-201

PSEN1-201

TATGATAAAATGATGCCTATCTCAGAATTCTTGTAAGGATTTCTTAGTACAAGTGCTGGGTATAAACTATATATTCAATAGATGA
ATACTATTTTACTACGGATAGAGTCTTAAGAACATTCCTAAAGAATCATGTTTCACGACCCATATTTGATATATAAGTTATCTACT

24,565

PSEN1

PSEN1-201

PSEN1-201

CGATTATTACTTATTATTGTTATTGATAAATAACAGCAGCATCTACAGTTAAGACTCCAGAGTCAGTCACATAGAATCTGGAAC
GCTAATAATGAATAAATAACAATAACTATTTATTGTCGTCGTAGATGTCAATTCTGAGGTCTCAGTCAGTGTATCTTAGACCTTGA

24,650

PSEN1

PSEN1-201

PSEN1-201

CCTATTGTAGAAAACAAAAAGAAAGAAAACACAGCTGAAGCCTAATTTTGTATATCATTACTGACTTCTCTCATTTCATTGTG
GGATAACATCTTTTGGTTTTTTCTTTCTTTTGTGTCGACTTCGGATTAACATATAGTAAATGACTGAAGAGAGTAAGTAACAC

24,735

PSEN1

PSEN1-201

PSEN1-201

GGGTTGAGTAGGGCAGTGATATTTTTGAATTGTGAAATCATAGCAAAGAGTGACCAACTTTTTAATATTTGTAACCTTTCTTTT
CCCAACTCATCCCGTCACTATAAAAACTTAACACTTTAGTATCGTTTCTCACTGGTTGAAAAATTATAAACATTGGAAAGGAAAA

24,820

PSEN1

PSEN1-201

PSEN1-201

TAGGGGGAGTAAAACCTTGGATTGGGAGATTTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTG
ATCCCCCTCATTTTGAACCTAACCCCTCTAAAGTAAAAGATGTGCACAAGACCAACCATTTTCGGAGTCGTTGTGCGGTACCTCTGAC

24,905

PSEN1

PSEN1-201

R G V K L G L G D F I F Y S V L V G K A S A T A S G D W
ENSE00003979377

PSEN1-201

GAACACAACCATAGCCTGTTTTCGTAGCCATATTAATTGTAAGTATACACTAATAAGAATGTGTCAGAGCTCTTAATGTCAAAACT
CTTGTTGGTATCGGACAAAGCATCGGTATAATTAACATTCATATGTGATTATTCTTACACAGTCTCGAGAATTACAGTTTTGA

24,990

PSEN1

PSEN1-201

405 410 415
N T T I A C F V A I L I

ENSE00003979377

PSEN1-201

TTGATTACACAGTCCCTTTAAGGCAGTTCTGTTTTAACCCAGGTGGGTTAAATATTCCAGCTATCTGAGGAGCTTTTTGATAAT
AACTAATGTGTCAGGGAAATTCCGTCAAGACAAAATTGGGGTCCACCCAATTTATAAGGTCGATAGACTCCTCGAAAACTATTA

25,075

PSEN1

PSEN1-201

PSEN1-201

TGGACCTCACCTTAGTAGTTCTCTACCCTGGCCACACATTAGAATCACTTGGGAGCTTTTAAAACCTGTAAGCTCTGCCCTGAGAT
ACCTGGAGTGGAATCATCAAGAGATGGGACCGGTGTGTAATCTTAGTGAACCTCGAAAATTTTGACATTGAGACGGGACTCTA

25,160

PSEN1

PSEN1-201

PSEN1-201

ATTCTTACTCAATTTAATTGTGTAGTTTTTAAAATTTCCCAGGAAATTTCTGGTATTTCTGTTTAGGAACCGCTGCCTCAAGCCTA
TAAGAATGAGTTAAATTAACACATCAAAAATTTAAGGGTCTTTAAGACCATAAAGACAAAATCCTTGGCGACGGAGTTTCGGAT

25,245

PSEN1

PSEN1-201

PSEN1-201

GCAGCACAGATATGTAGGAAATTAGCTCTGTAAGGTTGGTCTTACAGGGATAAACAGATCCTTCCTTAGTCCCTGGACTTAATCA
CGTCGTGTCTATACATCCTTTAATCGAGACATTTCAACCAGAATGTCCCTATTTGTCTAGGAAGGAATCAGGGACCTGAATTAGT

25,330

PSEN1

PSEN1-201

PSEN1-201

CTGAGAGTTTGGTGGTGGTTTTGCATTTAATGACACAACCTGTAGCATGCAGTGTACTTAAAGACAGCAAGCATCTAGTGAGAGG
GACTCTCAAACCACCACAAAACGTAATTAATGACTGTGTTGGACATCGTACGTCACAATGAATTTCTGTGCTCGTTGCTAGATCACTCTCC

25,415

PSEN1

PSEN1-201

PSEN1-201

AGCTGGTGCCATGCATGACCCACATAGATCTTGCTGATAGTGCTACAGCATGAACCCTGAAGCTTTCAAACTATGATTTTTTTT
TCGACCACGGTACGTACTGGGGTGTATCTAGAACGACTATCACGATGTCGTA CTGGGACTTCGAAAGTTTTGATACTAAAAAAA

25,500

PSEN1

PSEN1-201

PSEN1-201

TTTTTTTTTTTTTTGAGACGGAGTCTCTGTCAACCAGGCTGGAGTGGTGCAATCTCGGCTCATTGCAACCTCTGCCTCCCAGATTT
AAAAAAAAAAAAAACTCTGCCTCAGAGACAGTGGGTCCGACCTCACCACGTTAGAGCCGAGTAACGTTGGAGACGGAGGGTCTAAA

25,585

PSEN1

PSEN1-201

PSEN1-201

AAGTGATTCTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGCCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAG
TTCAC TAAGAGACGGAGTCGGAGGGCTCATCGACCCTAATGTCCACGGACGGTGGTGCGGGCCGATTAAAAACATAAAAAATCATC

25,670

PSEN1

PSEN1-201

PSEN1-201

AAACAGGGTTTACCATGTTGGCCAGGCTCCTCTTGAACCTCCTGACCTCAAGTGATGTGCCTGCCTCGGCCTCCCAAAGTGCTGG
TTTGTCCCAAAGTGGTACAACCGGTCCGAGGAGAACTTGAGGACTGGAGTTCACTACACGGACGGAGCCGGAGGGTTTACGACC

25,755

PSEN1

PSEN1-201

PSEN1-201

GATTACAGGCGTGAGCCACCGCACCTGGCTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTCTTGCTCTGTGCCCCAACTAGA
CTAATGTCCGCACTCGGTGGCGTGGACCGAAAAAAAAAAAAAAAAAAAAAACCCTCTGTCTCAGAACGAGACAGCGGGTTTGATCT

25,840

PSEN1

PSEN1-201

PSEN1-201

GTGCAGTGACATTAGCTCACTGCAACTTCTGCCTCCTAGGTTCAAGCGATCCTCCTGTCTCAGCCTCCCAAGTAGCTGGAATTAC
CACGTCACTGTAATCGAGTGACGTTGAAGACGGAGGATCCAAGTTCGCTAGGAGGACAGAGTCGGAGGGTTCATCGACCTTAATG

25,925

PSEN1

PSEN1-201

PSEN1-201

ATGTGTGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTGGAGATGAGGTTTTGCCACATTGCCAGGCTGGTCTCAAACCTT
TACACACGTGGTGGTACGGACCGATTAAAAACATAAAAAATCACCTCTACTCCAAAACGGTGTAAACGGGTCCGACCAGAGTTTGAA

26,010

PSEN1

PSEN1-201

PSEN1-201

CTGACCTCAACTGATCTGCCTGCCTCAGCCGCATAAAGTGCTGGGATTACAGGCATGAGCCACTGTGCCAACCTGAAAACTATG
GACTGGAGTTGACTAGACGGACGGAGTCGGCGTATTTTACAGACCTAATGTCCGTA CTCTCGGTGACACGGGTTGGACTTTTGATAC

26,095

PSEN1

PSEN1-201

PSEN1-201

ATTTAAGTAAACAACCCATAAAATATTTTCTTGCTATTTTTACTAAAGATGTGTTATCTTGGCCGGGTGAAGACTTTCTAGTGTTT
TAAATTCATTTGTTGGGTATTTTATAAAGAACGATAAAAAATGATTTCTACACAATAGAACC GGCCCACTTCTGAAAGATCACAAA

26,180

PSEN1

PSEN1-201

PSEN1-201

CCGTAAGTAGGGTAAAAAATGAACTCTATTATATGGCTTGTACATGTGTTTACAAGAAAGCAGTGTA CTCTCATAAAATAAACTT
GGCATTGATCCCATTTTTTACTTGAGATAATATACCGAACATGTACACAAATGTTCTTTTCGTACATGAGGAGTATTTATTTGAA

26,265

PSEN1

PSEN1-201

PSEN1-201

TTAGTTTATTTTATTTTTTAAACACTGCAGCCTCATCATGCTTCACGGAGGAGCCTGTGCGGGAAGAATGCTCCACACAGCATA
AATCAAATAAAATAAAAAATTTGTGACGTCGGAGTAGTACGAAGTGCCTCCTCGGACACGCCCTTCTTACGAGGGTGTGTCGTAT

26,350

PSEN1

PSEN1-201

PSEN1-201

AAGAATGCTCCCGCACAGCATAGAGAATGCCCCGCACAGCATAGAGAAGCCCCCGCACAGCATAGAGAATGCCCCGCACAGCA
TTCTTACGAGGGCGTGTGTCGTATCTCTTACGGGGGCGTGTGTCGTATCTCTTCGGGGGCGTGTGTCGTATCTCTTACGGGGGCGTGTGTCGT

26,435

PSEN1

PSEN1-201

PSEN1-201

TAGAGAAGCCCCGCACAGCATAGAGAATGCTCTTCACCTCTGGGTTTTTAACCAGCCAAACTAAAATCACAGAGGCCAACACAT
ATCTCTTCGGGGGCGTGTGTCGTATCTCTTACGAGAAGTGGAGACCCAAAAATTTGGTTCGGTTTGTATTTAGTGTCTCCGGTTGTGTA

26,520

PSEN1

PSEN1-201

PSEN1-201

CATTTAAGATAGAAATTTCTGTATCTTTTAATTTTTTCAAAGTAGTTTTACTTATTTTTCAGATTCTATTTCTTTACTAGAATTA
GTAAATTCATCTTTAAAGACATAGAAAATTAATAAAGTTTCATCAAAATGAATAAAAGTCTAAGATAAAGAAATGATCTTAAT

26,605

PSEN1

PSEN1-201

PSEN1-201

AGGGATAAAATAACAATGTGTGCATAATGAACCCCTATGAAACAAACAAAAGCTAGGTTTTTTTCATAGCTCTTCTTCCAGATTGA
TCCCTATTTTATTGTTACACACGTATTACTTGGGATACTTTGTTTGTTCGATCCAAAAAAGTATCGAGAAGAAGGTCTAACT

26,690

PSEN1

PSEN1-201

PSEN1-201

ATGAACGTCTGTTCTAAAATTTAACCCCAAAGGAAAATATTCAGTTAACTATGTTAAAAACCAAGACTTGTGATTGAGTTTTGC
TACTTGCAGACAAGATTTTAAATTGGGGTTTTCTTTTATAAGTCAATTGATACAATTTTGGTTCTGAACACTAACTCAAAACG

26,775

PSEN1

PSEN1-201

PSEN1-201

CTGAAAATGCTTTTCATAATTATGTGTGAATGTGTGTCTTTCCCATCTTCTCCACAGGGTTTTGTGCCTTACATTATTACTCCTTGC
GACTTTTACGAAAGTATTAATACACACTTACACACAGAAAGGGTAGAAGAGGTGTCCCAAACACGGAATGTAATAATGAGGAACG

26,860

PSEN1

PSEN1-201

PSEN1-201

G L C 420 L T L L L 425 A
ENSE00002555450

CATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTCCTACTTTGCCACAGATTATCTTGTACAG
GTAAAAGTTCTTTCGTAACGGTTCGAGAAGGTTAGAGGTTAGTGGAAACCCGAACAAAAGATGAAACGGTGTCTAATAGAACATGTC

26,945

PSEN1

PSEN1-201

PSEN1-201

I F K K A L P A L P I S I T F G L V F Y F A T D Y L V Q

ENSE00002555450

PSEN1-201

CCTTTTATGGACCAATTAGCATTCCATCAATTTTATATCTAGCATATTTGCGGTTAGAATCCCATGGATGTTTCTTCTTTGACTA
GGAAAATACCTGGTTAATCGTAAGGTAGTTAAAATATAGATCGTATAAACGCCAATCTTAGGGTACCTACAAAGAAGAACTGAT

27,030

PSEN1

PSEN1-201

455 P F M D Q 460 L A F H Q 465 F Y I *
ENSE00002555450
PSEN1-201

TAACAAAATCTGGGGAGGACAAAGGTGATTTTCTGTGTCCACATC
ATTGTTTATAGACCCCTCCTGTTTCCACTAAAAGGACACAGGTGTAG











































3'

27,076

5'

PSEN1
















PSEN1-201

















Feature	Location	Size			Type
✓ PSEN1	1 .. 27,076	27,076 bp			gene
/note	= gene ENSG00000080815 Protein coding				
✓ PSEN1-201	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000324501				
PSEN1-202	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000357710				
PSEN1-204	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000394164				
PSEN1-205	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000406768 Retained intron				
PSEN1-207	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000553599				
PSEN1-209	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000554131				
PSEN1-215	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000556066 Retained intron				
PSEN1-218	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000556951				
PSEN1-220	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000557293				
PSEN1-223	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000559361 Nonsense mediated decay				
PSEN1-225	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000697912 Nonsense mediated decay				
PSEN1-226	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000697913 Retained intron				
PSEN1-229	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700265				
PSEN1-230	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700266 Nonsense mediated decay				
PSEN1-231	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700267				
PSEN1-232	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700268				
PSEN1-233	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700269				
PSEN1-235	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700271				
PSEN1-236	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700272 Nonsense mediated decay				
PSEN1-237	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700273				
PSEN1-238	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700302 Nonsense mediated decay				

















Feature	Location	Size			Type
PSEN1-239	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700303 Nonsense mediated decay				
PSEN1-240	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700304 Nonsense mediated decay				
PSEN1-241	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700305 Nonsense mediated decay				
PSEN1-242	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700306				
PSEN1-243	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700307				
PSEN1-244	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700308 Nonsense mediated decay				
PSEN1-245	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700309 Nonsense mediated decay				
PSEN1-246	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700310 Nonsense mediated decay				
PSEN1-247	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700311 Nonsense mediated decay				
PSEN1-248	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700312				
PSEN1-249	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700313				
PSEN1-250	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700314 Nonsense mediated decay				
PSEN1-251	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700315 Nonsense mediated decay				
PSEN1-252	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700316 Nonsense mediated decay				
PSEN1-253	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700317				
PSEN1-254	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700318 Nonsense mediated decay				
PSEN1-255	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700319 Nonsense mediated decay				
PSEN1-256	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700320				
PSEN1-257	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700321				
PSEN1-258	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700322				
PSEN1-259	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700323				

Feature	Location	Size			Type
PSEN1-260	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700324				
PSEN1-262	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700375				
PSEN1-264	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700377 Nonsense mediated decay				
PSEN1-265	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700378				
PSEN1-266	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700379 protein_coding_CDS_not_defined				
PSEN1-268	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700389				
PSEN1-269	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700390 Retained intron				
PSEN1-271	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700404 Retained intron				
PSEN1-284	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700436 Nonsense mediated decay				
PSEN1-285	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700437				
PSEN1-287	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700468				
PSEN1-288	1 .. 27,076	27,076 bp			prim_transcript
/note	= primary transcript ENST00000700469				
PSEN1-212	1 .. 26,987	26,987 bp			prim_transcript
/note	= primary transcript ENST00000555386 Nonsense mediated decay				
PSEN1-222	1 .. 26,987	26,987 bp			prim_transcript
/note	= primary transcript ENST00000557511				
PSEN1-208	1 .. 24,856	24,856 bp			prim_transcript
/note	= primary transcript ENST00000553855 Nonsense mediated decay				
PSEN1-283	1 .. 21,121	21,121 bp			prim_transcript
/note	= primary transcript ENST00000700435 protein_coding_CDS_not_defined				
PSEN1-286	1 .. 15,035	15,035 bp			prim_transcript
/note	= primary transcript ENST00000700467 Retained intron				
PSEN1-234	1 .. 14,953	14,953 bp			prim_transcript
/note	= primary transcript ENST00000700270 Retained intron				
PSEN1-282	1 .. 14,582	14,582 bp			prim_transcript
/note	= primary transcript ENST00000700434 Retained intron				
PSEN1-281	1 .. 14,548	14,548 bp			prim_transcript
/note	= primary transcript ENST00000700433 Retained intron				
PSEN1-280	1 .. 1277	1277 bp			prim_transcript
/note	= primary transcript ENST00000700432 Retained intron				

Feature	Location	Size	Type
PSEN1-263	1 .. 830	830 bp	prim_transcript
/note	= primary transcript ENST00000700376 Retained intron		
PSEN1-267	1 .. 698	698 bp	prim_transcript
/note	= primary transcript ENST00000700388 Retained intron		
PSEN1-201	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000326366		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-202	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000350342		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-204	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000377719		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-207	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000452477		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-209	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000451915		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-218	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000450551		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-220	342 .. 26,987	26,646 bp	CDS
▶ 6 segments	= 736 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000451880		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWK,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQFYI* 244 amino acids = 27.1 kDa		

Feature	Location	Size			Type
PSEN1-222	342 .. 26,987	26,646 bp			CDS
▶ 5 segments = 682 bp					
/codon_start = 1					
/note = coding sequence ENSP00000451429					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQFYI*					
226 amino acids = 25.4 kDa					
PSEN1-229	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514901					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-231	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514903					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-232	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514904					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-233	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514905					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-235	342 .. 26,987	26,646 bp			CDS
▶ 5 segments = 682 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514906					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQFYI*					
226 amino acids = 25.4 kDa					
PSEN1-237	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514908					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLV FYFATDYL VQP FMDQLAFHQ					
284* amino acids = 31.7 kDa					

Feature	Location	Size			Type
PSEN1-242	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514933					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-243	342 .. 26,987	26,646 bp			CDS
▶ 5 segments = 757 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514934					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,ATMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQFYI*					
251 amino acids = 28.0 kDa					
PSEN1-248	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514939					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-249	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514940					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-253	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514944					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ					
284* amino acids = 31.7 kDa					
PSEN1-256	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 883 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514947					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DV F YVFLDLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ					
299 amino acids = 32.8 kDa					
PSEN1-257	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514948					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ					
284* amino acids = 31.7 kDa					

Feature	Location	Size			Type
PSEN1-258	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514949				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-259	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514950				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-260	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514951				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-262	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514966				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-265	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514968				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-268	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514970				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-285	342 .. 26,987	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514988				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa				

Feature	Location	Size			Type
PSEN1-287	342 .. 26,987	26,646 bp		→	CDS
▶ 5 segments = 757 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000515001				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,ATMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGPHRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFATDYLVQPFMDQLAFHQFYI* 251 amino acids = 28.0 kDa				
PSEN1-288	342 .. 26,987	26,646 bp		→	CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000515002				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGPHRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFATDYLVQPFMDQLAFHQ 284 amino acids = 31.7 kDa				
PSEN1-210	4210 .. 27,076	22,867 bp		→	prim_transcript
/note	= primary transcript ENST00000554995 Retained intron				
✓ Protospacer Sequence	5766 .. 5785	20 bp		⇌	misc_feature
✓ Silent SNV	5784 .. 5784	1 bp		⇌	misc_feature
/note	= WT = T SNV = G				
✓ PAM	5786 .. 5788	3 bp		⇌	misc_feature
✓ SNV	5798 .. 5798	1 bp		⇌	misc_feature
/note	= REV = A SNV = C				
PSEN1-270	13,785 .. 27,076	13,292 bp		→	prim_transcript
/note	= primary transcript ENST00000700391 protein_coding_CDS_not_defined				
PSEN1-213	13,851 .. 27,076	13,226 bp		→	prim_transcript
/note	= primary transcript ENST00000555867 Retained intron				
PSEN1-228	24,338 .. 27,076	2739 bp		→	prim_transcript
/note	= primary transcript ENST00000697915 Retained intron				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	5354 .. 5378	60°C	Jan 11, 2023
/sequence = TTCTCCCTGTTTCTGCTCACTGTAG 48% GC / 7540.9 Da				
✓ Donor Template SNV -> REV	100-mer	5748 .. 5847	73°C	Jan 11, 2023
/sequence = TATCCTTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTG 62% GC / 8571.1 Da				
✓ gRNA Protospacer	20-mer	5766 .. 5783	53°C	Jan 11, 2023
/sequence = TATGCTGGTTGAAACAGCGC 50% GC / 6157.1 Da				
✓ Sanger Sequencing	20-mer	5934 .. 5953	58°C	Jan 11, 2023
/sequence = GAGTTCCAGGAATGCTGTGC 55% GC / 6173.1 Da				
✓ PCR Reverse	25-mer	6315 .. 6339	60°C	Jan 11, 2023
/sequence = ATTCAAACCCCCATTA CTTTCCACC 44% GC / 7440.9 Da				