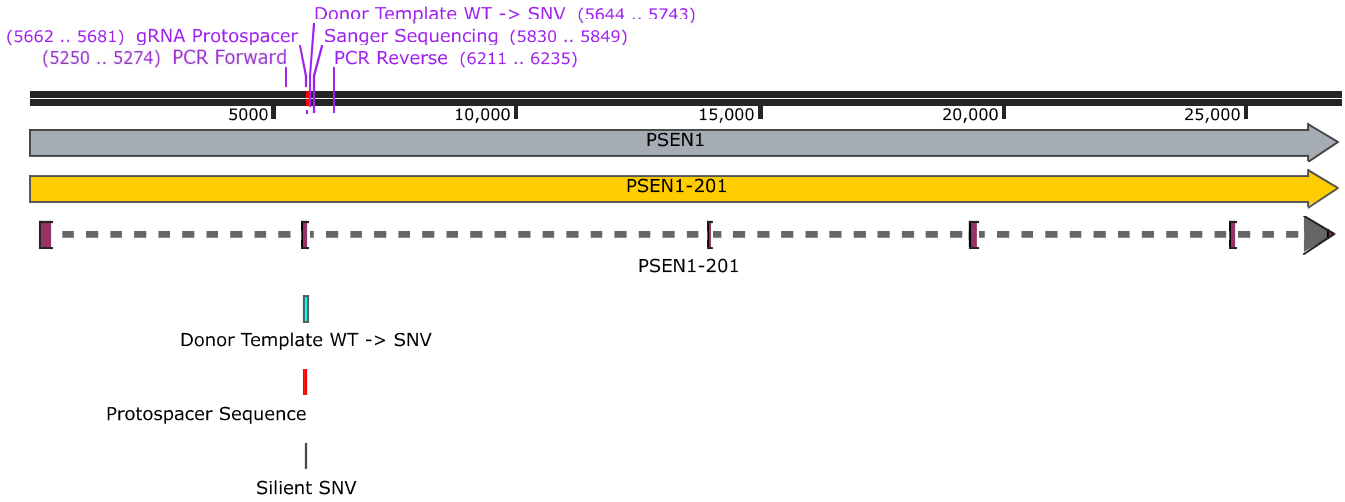

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PSEN1

PSEN1-201

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PSEN1

PSEN1-201

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PSEN1

PSEN1-201

185

E V F K T Y

ENSE00003979383

PSEN1-201

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PSEN1

PSEN1-201

190 195 200 205 210 215

N V A V D Y I T V A L L I W N F G V V G M I S I H W K G

ENSE00003979383

PSEN1-201

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PSEN1

PSEN1-201

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ENSE00003979383

PSEN1-201

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PSEN1

PSEN1-201

250 255

A W L I L A V I S V Y

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PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

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PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1-201

PSEN1-201

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PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

PCR Forward
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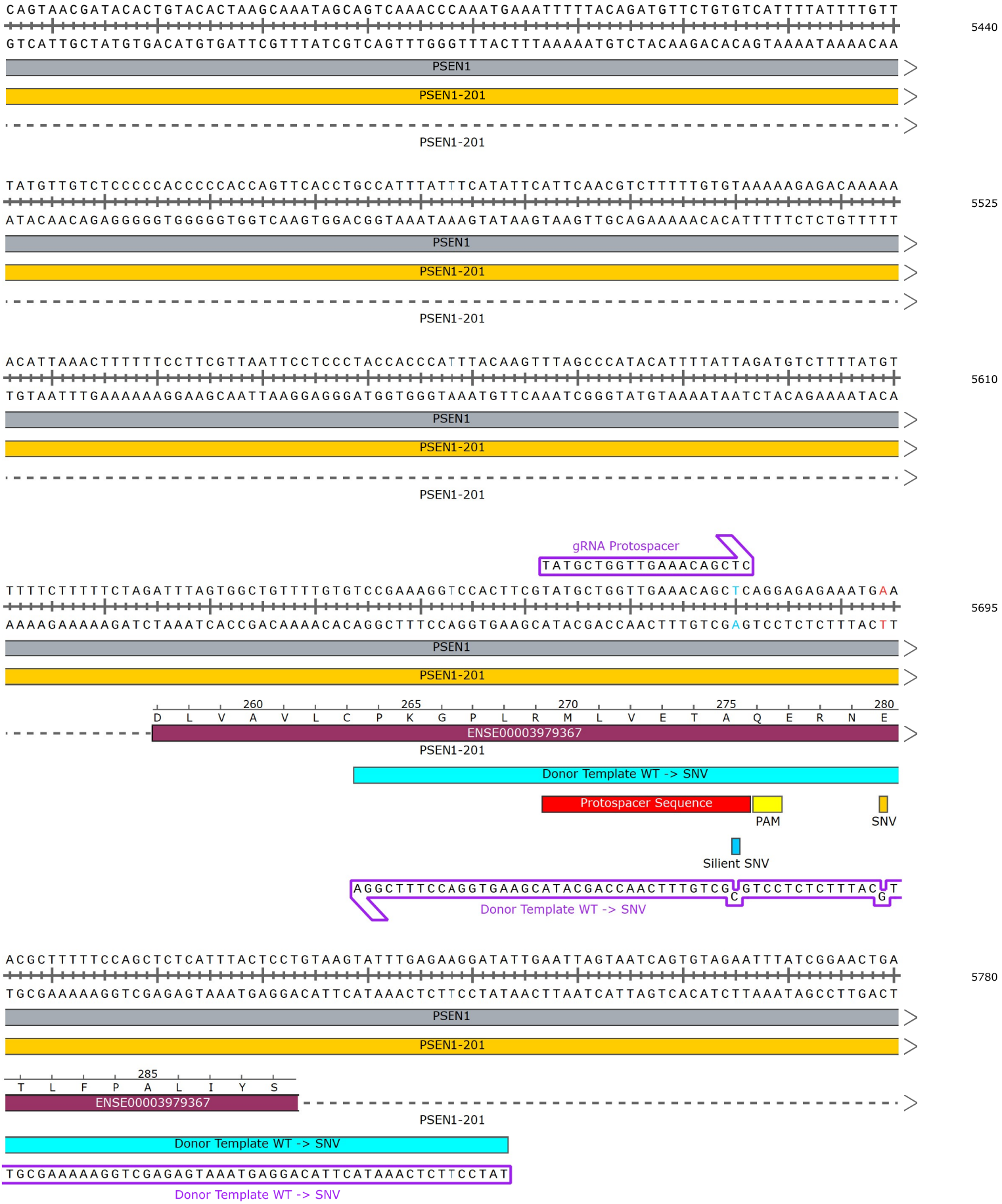
PSEN1

PSEN1-201

PSEN1-201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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

CCACCTTTCATTACCCCCAAACTTA

PCR Reverse

GAATCAATAGTTCTAGCAACTGAGGAGAGAAGTTGTAAGCTTGAAGGAAAGGTGATGAAGAAAAAATGCTTTCCTGTGTTTTCTT 6375
CTTAGTTATCAAGATCGTTGACTCCTCTCTTCAACATTCGAACTTCCTTTCCACTACTTCTTTTTTACGAAAGGACACAAAAGAA

PSEN1

PSEN1-201

PSEN1-201

GTTGTTGTTGTTGAGATAGGGTCTCACTCCCATCCAGGATGGAGTACAGTAGTGTGATCATGGCTCACTGCAGCCTCGACCTCCC 6460
CAACAACAACAACTCTATCCCAGAGTGAGGGTAGGTCCTACCTCATGTCATCACACTAGTACCGAGTGACGTCGGAGCTGGAGGG

PSEN1

PSEN1-201

PSEN1-201

AGGCTCAGGTGATCCACCCACCTCAGCCTCCCGAGTAGCTGTGACTACAGGCACGCACTACCAGGCCTGGCTAATTTTTTTGTGT 6545
TCCGAGTCCACTAGGTGGGTGGAGTCGGAGGGCTCATCGACACTGATGTCCGTGCGTGATGGTCCGGACCGATTAAAAAAACACA

PSEN1

PSEN1-201

PSEN1-201

TGTGTGTAGAGACTGGGTTTTGCCATGTGCCCAGGCTGGTCTTGAACTCCTCGGCTTAAGCGATCCTCCTGCCTTGACTTCACAA 6630
ACACACATCTCTGACCCAAAACGGTACACGGGTCCGACCAGAACTTGAGGAGCCGAATTCGCTAGGAGGACGGAACTGAAGTGTT

PSEN1

PSEN1-201

PSEN1-201

AGTGCTTGAGTTACAGGTGTGAGCTACCACGCCTGGCCATGTTTTCTTGTGTGAAGGATCTGTTTAGTTTTATATCTTTCTGTGG 6715
TCACGAACTCAATGTCCACACTCGATGGTGCGGACCGGTACAAAAGAACACACTTCCTAGACAAATCAAAATATAGAAAGACACC

PSEN1

PSEN1-201

PSEN1-201

CTCATATCTAATTTAGTTGACAGTACCTGTGGGTCACTAGGTAGACATTGCTAGCAGACGTTTAGAAATGAAATACTAGAGCTTG 6800
GAGTATAGATTAAATCAACTGTCATGGACACCCAGTGATCCATCTGTAACGATCGTCTGCAAATCTTTACTTTATGATCTCGAAC

PSEN1

PSEN1-201

PSEN1-201

GGAAAAAGTTGATATTTGAGATAGAGACTTGAAGAACATTAGCAGAGAGTTGGTAGTTAAGGTCTGTGAGCTGGTGAGCAATTCA 6885
CCTTTTTCAACTATAAACTCTATCTCTGAACTTCTTGTAATCGTCTCTCAACCATCAATTCCAGACACTCGACCACTCGTTAAGT

PSEN1

PSEN1-201

PSEN1-201

AATAAAAGCAGAAGAGAAGAGGAAGACAAGGGTCAAACTTTGTCAACTACTGTGTTTAGAGAATGAGACAAGAGAGGATACTACA 6970
TTATTTTCGTCTTCTCTTCTCCTTCTGTTCCCAGTTTGAAACAGTTGATGACACAAATCTCTTACTCTGTTCTCTCCTATGATGT

PSEN1

PSEN1-201

PSEN1-201

GGAAGTAGAGGAAAATAGTGGAAAATTGGGCAAGCCAGTATTTTTCACTTAAGAATATCATTACTGTTTTTTGATGTCAGCACAT 7055
CCTTCATCTCCTTTTATCACCTTTTAACCCGTTCGGTCATAAAAAGTGAATTCTTATAGTAATGACAAAAAACTACAGTCGTGTA

PSEN1

PSEN1-201

PSEN1-201

GAAATGGCTGCATAGTGTTCTCTTACGTAGATATTCAGTGGTGGGTATCCTCATTGATAGACATTTAGATCATTTCCATTTATTT 7140
CTTTACCGACGTATCACAAGAGAATGCATCTATAAGTCACCACCCATAGGAGTAACTATCTGTAAATCTAGTAAAGGTAAATAAA

PSEN1

PSEN1-201

PSEN1-201

TCTATCACAGACAGCACTTACAGAGTGCATCCATGAACTTATGAATATTATTATAAAATGTATTCTTACAGTAGAATTGCTAAGT 7225
AGATAGTGTCTGTCGTGAATGTCTCACGTAGGTACTTGAATACTTATAATAATATTTTACATAAGAATGTCATCTTAACGATTCA

PSEN1

PSEN1-201

PSEN1-201

CAAAGGATGTATTTAAATTTTGATAGTTTGCCATATTGCCTCCTAAAAAAGCTGTGCCTGTTTACATTCCCTTCAGTAATATGAA 7310
GTTTCCTACATAAATTTAAAACTATCAAACGGTATAACGGAGGATTTTTTCGACACGGACAAATGTAAGGGAAGTCATTATACTT

PSEN1

PSEN1-201

PSEN1-201

AGTATCAATTTCCTTACCCCTTTGGTGTTTTGGTTTGTTTTGTTTTGGAGACTGAGTCTCGCTCTGTCATGCAGGCTGGAGTGCA 7395
TCATAGTTAAAGGAATGGGGAAACCACAAAACCAAACAAAACAAAACCTCTGACTCAGAGCGAGACAGTACGTCCGACCTCACGT

PSEN1

PSEN1-201

PSEN1-201

GTGGTGCGATCTCGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCAGTTCTCCTGCCTCAGCCTCCGGAGTGGCTGGGATTAC 7480
CACCACGCTAGAGCCGAGTGACGTTGGAGGCGGAGGACCCAAGTTCGTCAAGAGGACGGAGTCGGAGGCCTCACCGACCCTAATG

PSEN1

PSEN1-201

PSEN1-201

AGGCGTGTGCCACCACACCCAGCTAATTTTTTGTATTTTTAGTGGAGACACGGTTTCACCATGTTGACCAGGCTGGTCTCGAACT 7565
TCCGCACACGGTGGTGTGGGTCGATTAAAAAACATAAAAATCACCTCTGTGCCAAAGTGGTACAACTGGTCCGACCAGAGCTTGA

PSEN1

PSEN1-201

PSEN1-201

CCTGACTTCAGGTGATCCGCCTGCCTAGGCCTCCCAAAATGCCAGGATTATAGCTGTGAGCCACCATGCCCGGCCACTGCTTTGT 7650
GGACTGAAGTCCACTAGGCGGACGGATCCGGAGGGTTTTACGGTCCTAATATCGACACTCGGTGGTACGGGCCGGTGACGAAACA

PSEN1

PSEN1-201

PSEN1-201

TAATGCTTGCCTGTGTCTGTGCATACATGCATGTGTGTGTGTCTGAGAGAGAAAGAGATCTAATAGGCAAAAAAATAACATCTTG 7735
ATTACGAACGGACACAGACACGTATGTACGTACACACACACAGACTCTCTCTTTCTCTAGATTATCCGTTTTTTTATTGTAGAAC

PSEN1

PSEN1-201

PSEN1-201

TTTTATTTTTTATTGTTTGTCTAATGCTTTGGGTGATTATTTGAACTTTTTTTCATGTGTTTCTTAGTTACAGATCTGAATTTAT 7820
AAAATAAAAAATAACAAACAGATTACGAAACCCACTAATAAACTTGAAAAAAAGTACACAAAGAATCAATGTCTAGACTTAAATA

PSEN1

PSEN1-201

PSEN1-201

TTTGTAACTGGCTTGGTATAATCTTTTTCATATTTGTGAAATTAATCTTTTTTGTGTGTGTGTGAGACAGTCTCTCTCTGTCACC 7905
AAACATTGACCGAACCATATTAGAAAAAGTATAAACACTTTAATTAGAAAAAACACACACACACTCTGTCAGAGAGAGACAGTGG

PSEN1

PSEN1-201

PSEN1-201

CAAGCTGGAGTACAGTGGCGCAATCTCAACTCACTGCAACCTCCATCTCCCAGGTTCAAGCAATTCTCCTCTCTCAGCCTCCCAA 7990
GTTCGACCTCATGTCACCGCGTTAGAGTTGAGTGACGTTGGAGGTAGAGGGTCCAAGTTCGTTAAGAGGAGAGAGTCGGAGGGTT

PSEN1

PSEN1-201

PSEN1-201

GTAGCTGGAATTACAGGCGCATGCCACCACGCCTGGCTGATTTTTGTATTTTTAGTAGAGACGGGATTTCACCACGTTGGCCAGG 8075
CATCGACCTTAATGTCCGCGTACGGTGGTGCGGACCGACTAAAAACATAAAAATCATCTCTGCCCTAAAGTGGTGCAACCGGTCC

PSEN1

PSEN1-201

PSEN1-201

CTGGTCTCAAGTGATCCAACTGCCTCAGACTCCCAAAGCATTAGTATTACAGGTGTGAGCCACTGCTCCCAGCCCTGTAAAATTA 8160
GACCAGAGTTCACTAGGTTGACGGAGTCTGAGGGTTTCGTAATCATAATGTCCACACTCGGTGACGAGGGTCGGGACATTTTAAT

PSEN1

PSEN1-201

PSEN1-201

ATCTTAATTATACAAGTAATTCATTATCCTTGAAAAAGGATAAACATTACAGATAAAAATAAATTTCACGGTAACTATCATCTCT 8245
TAGAATTAATATGTTCATTAAGTAATAGGAACTTTTTCCTATTTGTAATGTCTATTTTTATTTAAAGTGCCATTGATAGTAGAGA

PSEN1

PSEN1-201

PSEN1-201

AATCTTAATGCCTTATCAAGTACTTACCCCTGTTGTCAGTTTGTTGTATATCCTTGTAGATTTTTTTTGCCAATTTTTCTGTTGA 8330
TTAGAATTACGGAATAGTTCATGAATGGGGACAACAGTCAAACAACATATAGGAACATCTAAAAAAAACGGTTAAAAAGACAACT

PSEN1

PSEN1-201

PSEN1-201

GTTACTGGAAAAGCAGTTTCAAGAAGGAGAGAGGCTGGGCGTGGTGGCTAACACCTGTAATCCCAGCACTTTGGGAGGCCTAGGT 8415
CAATGACCTTTTCGTCAAAGTTCTTCCTCTCTCCGACCCGCACCACCGATTGTGGACATTAGGGTCGTGAAACCCTCCGGATCCA

PSEN1

PSEN1-201

PSEN1-201

GGGCGGATCACTTGAGGTCAGGAGTTTGAAACCAGCCTGGCCAACATGGTGAAACTCTGTCTTTACTAAAAATATAAAAATCAGC 8500
CCCGCCTAGTGAACTCCAGTCCTCAAACTTTGGTCGGACCGGTTGTACCACTTTGAGACAGAAATGATTTTTATATTTTTAGTCG

PSEN1

PSEN1-201

PSEN1-201

TGGGTGTGGTGGTGCACACTTGTAATCCCAGTTACTTGGGAGGCTGAGGTGGGAGGATCACTTGAACCCAGGAGGCGGAGGTTAC 8585
ACCCACACCACCACGTGTGAACATTAGGGTCAATGAACCCTCCGACTCCACCCTCCTAGTGAACTTGGGTCCTCCGCCTCCAATG

PSEN1

PSEN1-201

PSEN1-201

AGTGAGCCATGATCGTGCCACTGCACTCCAGCCTGAGTGACAGCAAGGCTTCATCCCCACCCTCCCAAAAAAAGAGAATATCTTT 8670
TCACTCGGTACTAGCACGGTGACGTGAGGTCGGACTCACTGTCGTTCCGAAGTAGGGGTGGGAGGGTTTTTTTCTCTTATAGAAA

PSEN1

PSEN1-201

PSEN1-201

TTGTTTGTTTGTTTGTTTGTTTGTTTGTTTGTGGCAGAGTCTTGCTGTGTCGCCCAGGCTGGAGTTCAGTGGGGCGATCTCGGCT 8755
AACAAACAAACAAACAAACAAACAAACAAACACCGTCTCAGAACGACACAGCGGGTCCGACCTCAAGTCACCCCGCTAGAGCCGA

PSEN1

PSEN1-201

PSEN1-201

CACTGCAAGCTCCGCCTCCTGGGTTCAGCCATTCTCCTGCCTCAGCCTCCCCAGCAGCTGGGACTACAGGCACACGCCGCCACGC 8840
GTGACGTTCGAGGCGGAGGACCCAAGTCGGTAAGAGGACGGAGTCGGAGGGGTCGTCGACCCTGATGTCCGTGTGCGGCGGTGCG

PSEN1

PSEN1-201

PSEN1-201

CCGGCTAATTTTTGTATTTTTAGTAGCAACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTTGTGATCCGCC 8925
GGCCGATTAAAAACATAAAAATCATCGTTGCCCCAAAGTGGTACAATCGGTCCTACCAGAGCTAGAGGACTGGAACACTAGGCGG

PSEN1

PSEN1-201

PSEN1-201

CGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGGCCGAGAATATCATTTTTTATAAAGAAGTCAAAG 9010
GCGGAGCCGGAGGGTTTCACGACCCTAATGTCCGCACTCGGTGGCGCGGACCGGCTCTTATAGTAAAAAATATTTCTTCAGTTTC

PSEN1

PSEN1-201

PSEN1-201

GTAATGAGGACTAAGTAAAACCATACAGTATTTGCTGTCTAAGATGTCATTAGTGACATTGAAGAGAGCAGTTTCAGTAGAGTGA 9095
CATTACTCCTGATTCATTTTGGTATGTCATAAACGACAGATTCTACAGTAATCACTGTAACTTCTCTCGTCAAAGTCATCTCACT

PSEN1

PSEN1-201

PSEN1-201

TAGAACCAGAAGCAGTACTCCAAAGGGAAGGTGCGTATGTGTGCATGCATGTCTCTGTGTTTTGCCAGTGCTGGCAGTGGAAGTG 9180
ATCTTGGTCTTCGTCATGAGGTTTCCCTTCCACGCATACACACGTACGTACAGAGACACAAAACGGTCACGACCGTCACCTTCAC

PSEN1

PSEN1-201

PSEN1-201

ATGGTGTAGGCAGAGAATGGGTGGTGAAGAAGGAGAGGTATAGTAAATGTCATGTACTACATCAAAGATTCCTGTCTCACAGGCA 9265
TACCACATCCGTCTCTTACCCACCACTTCTTCCTCTCCATATCATTTACAGTACATGATGTAGTTTCTAAGGACAGAGTGTCCGT

PSEN1

PSEN1-201

PSEN1-201

GAGCAGGTGGTGACCTGACAGGAGAACAGGTTTCAGGAAAGGTGTTTCAAGGAGAGGGAAGGTTCCATTTTATTTTATTTATTTA 9350
CTCGTCCACCACTGGACTGTCCTCTTGTCCAAAGTCCTTTCCACAAAGTTCCTCTCCCTTCCAAGGTAAAATAAAATAAATAAAT

PSEN1

PSEN1-201

PSEN1-201

TTTTTTTTGAAACAGAGTCTTGCTCTGTTGCTCGGGCTAGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCCCCGCCTCCCAA 9435
AAAAAAAACTTTGTCTCAGAACGAGACAACGAGCCCGATCTCACGTCACCACACTAGAACCGAGTGACGTTGGGGGCGGAGGGTT

PSEN1

PSEN1-201

PSEN1-201

GTTCAAGCAATGGTCCTGTCTCAGCCTCCGGAGTAGCTGGGATTATAGGCACCCACCACCACATCCGGCTAATGTTTGTATTTTT 9520
CAAGTTCGTTACCAGGACAGAGTCGGAGGCCTCATCGACCCTAATATCCGTGGGTGGTGGTGTAGGCCGATTACAAACATAAAAA

PSEN1

PSEN1-201

PSEN1-201

AGTAGAGTTGGGGTTTCGCCACATTGGCCAGGCTGGCCTTGAACTCCCCACCTCAAGTGATCCACCTGCCTCGGCCTCCCAAAGT 9605
TCATCTCAACCCCAAAGCGGTGTAACCGGTCCGACCGGAACTTGAGGGGTGGAGTTCACTAGGTGGACGGAGCCGGAGGGTTTCA

PSEN1

PSEN1-201

PSEN1-201

GCTGGGATTACAGACGTGAGCCACTGCACCCGACCTGTTTTATTTTATTTTTGAGGTAAGTCTTGCTCTGTTGCCCAGGCTGGAG 9690
CGACCCTAATGTCTGCACTCGGTGACGTGGGCTGGACAAAATAAAATAAAAACTCCATTCAGAACGAGACAACGGGTCCGACCTC

PSEN1

PSEN1-201

PSEN1-201

TGCAGTGGCGCAATCTCAGCTCACTGCAACCTCCATCTCCTGGGTTCAGGCAATTCTCCTGCCTCAGCCTCCCGAGTAGTTGAGA 9775
ACGTCACCGCGTTAGAGTCGAGTGACGTTGGAGGTAGAGGACCCAAGTCCGTTAAGAGGACGGAGTCGGAGGGCTCATCAACTCT

PSEN1

PSEN1-201

PSEN1-201

TTACAAGCATGCGCCACTATACCTGGCTAATTTTTTTTTTCCATATTTTTAGTTGAGCCACAGGTTGGGAGAAGGGAAAATACAT 9860
AATGTTCGTACGCGGTGATATGGACCGATTAAAAAAAAAAGGTATAAAAATCAACTCGGTGTCCAACCCTCTTCCCTTTTATGTA

PSEN1

PSEN1-201

PSEN1-201

TCTACTCAAAGTGAGTCCGTGGCAAAAGTGTGAGTACAGAGATGGGTGAGGAATTAGGACCAGACTTTCAGTCTGCAGCAACATT 9945
AGATGAGTTTCACTCAGGCACCGTTTTCACACTCATGTCTCTACCCACTCCTTAATCCTGGTCTGAAAGTCAGACGTCGTTGTAA

PSEN1

PSEN1-201

PSEN1-201

AAACATGTATGTTAATTTAATACTCAGAAAGAAGCATTTACTCTGTTTTAAAATATCTATCACATACTATATATATATATATATA 10,030
TTTGTACATACAATTAAATTATGAGTCTTTCTTCGTAAATGAGACAAAATTTTATAGATAGTGTATGATATATATATATATATAT

PSEN1

PSEN1-201

PSEN1-201

TATATATATATATATATATATATATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGTCTTGCTCTGTCACCCAGGCTG 10,115
ATATATATATATATATATATATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCTGTCAGAACGAGACAGTGGGTCCGAC

PSEN1

PSEN1-201

PSEN1-201

GAGTGCAGTAGCGTGATCTCGACTCACTGCAAGCTCCACCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTG 10,200
CTCACGTCATCGCACTAGAGCTGAGTGACGTTCGAGGTGGAGGGCCCAAGTGCGGTAAGAGGACGGAGTCGGAGGGCTCATCGAC

PSEN1

PSEN1-201

PSEN1-201

GGACTCTAGGCGCCCGCCACCATGCCTGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATTGTC 10,285
CCTGAGATCCGCGGGCGGTGGTACGGACCGATTAAAAAACATAAAAATCATCTCTGCCCCAAAGTGGCACAATCGGTCCTAACAG

PSEN1

PSEN1-201

PSEN1-201

TCGATCTCTTGACCTCGTAATCTGCCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCAGCCTATCA 10,370
AGCTAGAGAACTGGAGCATTAGACGGGAGGAGCCGGAGGGTTTCACGACCCTAATGTCCGCACTCGGTGGCACGGGTCGGATAGT

PSEN1

PSEN1-201

PSEN1-201

TATATAATATTTTTAAAACTCAACGTCTGTGCTCGCTTTAGCAGCACATAATAGTAAAATTGGAATGATACAGATGATTTGCATG 10,455
ATATATTATAAAAATTTTGAGTTGCAGACACGAGCGAAATCGTCGTGTATTATCATTTTAACCTTACTATGTCTACTAAACGTAC

PSEN1

PSEN1-201

PSEN1-201

TATTTTTTTAAAAGTTCTCAAGTCTATTTAATAACCACAGAATATGAGACATTCTGAGATGTTTTAGAAACAGTTCAACATATGT 10,540
ATAAAAAAATTTTCAAGAGTTCAGATAAATTATTGGTGTCTTATACTCTGTAAGACTCTACAAAATCTTTGTCAAGTTGTATACA

PSEN1

PSEN1-201

PSEN1-201

GGGAAAATAGGAGTATAAACCCTTACCTCCTGTGTAGATCAGGTAGGTTCAAGATTGCATCTGTTCTTTTGTAATACTAAATGTC 10,625
CCCTTTTATCCTCATATTTGGGAATGGAGGACACATCTAGTCCATCCAAGTTCTAACGTAGACAAGAAAACATTATGATTTACAG
PSEN1
PSEN1-201
PSEN1-201

TGGTGAAGATTTGAGGATTTTATATAAATCATTGAGTTTGAGAGGTTTTTTTGTTTTTGTTTTTGAGATGGAGTTTCACTCTTGT 10,710
ACCACTTCTAAACTCCTAAAATATATTTAGTAACTCAAACTCTCCAAAAAAACAAAAACAAAAACTCTACCTCAAAGTGAGAACA
PSEN1
PSEN1-201
PSEN1-201

TGCCCAGGCTGAAGTGCAATGGCACAATCTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCGATTCTCCTGCCTCGGCCTC 10,795
ACGGGTCCGACTTCACGTTACCGTGTTAGAGCCGAGTGACGTTGGAGGCGGAGGGTCCAAGTTCGCTAAGAGGACGGAGCCGGAG
PSEN1
PSEN1-201
PSEN1-201

CTGAGTAGCTGGGATTACAGACGCCTGCCACCACGCCCAGCTAATTTTTTGTATTTTTGTATTTTTAGTAGAGAGAGGGTTTCAC 10,880
GACTCATCGACCCTAATGTCTGCGGACGGTGGTGCGGGTCGATTAAAAAACATAAAAACATAAAAATCATCTCTCTCCCAAAGTG
PSEN1
PSEN1-201
PSEN1-201

CATGTTGGCCAGGCTGGTCTCAAACTTGTGACCTCAGGTGATCTACCCGCCTCACCCTCCCAAAGTGCTGGGATTACAGGCATGA 10,965
GTACAACCGGTCCGACCAGAGTTTGAACACTGGAGTCCACTAGATGGGCGGAGTGGGAGGGTTTCACGACCCTAATGTCCGTACT
PSEN1
PSEN1-201
PSEN1-201

GCCACCGCACCTGGCCTTCGTTTTGTTTTTTCAACAGAATGTAAGAATTTTTTCTTACATTTTTCTTACATTTTTAACAGAATGT 11,050
CGGTGGCGTGGACCGGAAGCAAAACAAAAAAGTTGTCTTACATTCTTAAAAAAGAATGTAAAAAGAATGTAAAAATTGTCTTACA
PSEN1
PSEN1-201
PSEN1-201

AAGAAAACCACAACGCAATGCCGATGAGTACTTTTTCCCTGAAGTGGATATAAGCATGAATATAAAAAGTTTTAAATCAGTCATC 11,135
TTCTTTTGGTGTTGCGTTACGGCTACTCATGAAAAAGGGACTTCACCTATATTCGTACTTATATTTTTCAAAATTTAGTCAGTAG
PSEN1
PSEN1-201
PSEN1-201

CTGGCTATTTGTTCTCTAAAAATCAATAAATAATTCTTTCATGCATTTTAATACTGTCTCCCAGTTAAGGGTATTCAGTTTGCAA 11,220
GACCGATAAACAAGAGATTTTTAGTTATTTATTAAGAAAGTACGTAAAATTATGACAGAGGGTCAATTCCCATAAGTCAAACGTT

PSEN1

PSEN1-201

PSEN1-201

AATGCTCTTACTGACAGGAAATGTATGAGCATTTTTGTTTTTTACTTCTGTCGTTTGACAGAAAAAATATACACCTACTCTTTGA 11,305
TTACGAGAATGACTGTCCTTTACATACTCGTAAAAACAAAAAATGAAGACAGCAAACTGTCTTTTTTATATGTGGATGAGAAACT

PSEN1

PSEN1-201

PSEN1-201

GCTAATTTATTCTTACCTAGTGGTCATTAGTAGAAGTGGTTCACTCTGGGAGCTTAACTAGAAGGGAAACTAACAATTCCTTGAG 11,390
CGATTAAATAAGAATGGATCACCAGTAATCATCTTCACCAAGTGAGACCCTCGAATTGATCTTCCCTTTGATTGTTAAGGAACTC

PSEN1

PSEN1-201

PSEN1-201

GTAGATCATTTTATCTAAAGCTTTTTGATTTCATATCAGTTGGGGGCGGGTATATTATGTTAATTTTTAAATCTGCATATTTTCC 11,475
CATCTAGTAAAATAGATTTCGAAAAACTAAAGTATAGTCAACCCCCGCCCATATAATACAATTAAAAATTTAGACGTATAAAAGG

PSEN1

PSEN1-201

PSEN1-201

AGCCAGGCATGACTATAATCCCAGGACTTTGGGAGGTAGAAGCAGGAGGATTGCTTGAGCCCAGGAATTCAAGACCACCCTAGAC 11,560
TCGGTCCGTACTGATATTAGGGTCCTGAAACCCTCCATCTTCGTCCTCCTAACGAACTCGGGTCCTTAAGTTCTGGTGGGATCTG

PSEN1

PSEN1-201

PSEN1-201

TACATTAAAAAACATATTTTTTTGTATTTATTTTTTATTTTATTTTTTTGAGACAGAGTTTCGCTCTCATTGCCCAGGCTGGAGT 11,645
ATGTAATTTTTTGTATAAAAAAACATAAATAAAAAATAAAATAAAAAAACTCTGTCTCAAAGCGAGAGTAACGGGTCCGACCTCA

PSEN1

PSEN1-201

PSEN1-201

GCAATGGCACGATCTCGGCTCACCACAGCCTCCGCCTCCTGGATTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTCGCCGGGAT 11,730
CGTTACCGTGCTAGAGCCGAGTGGTGTCGGAGGCGGAGGACCTAAGTTCGTTAAGAGGACGGAGTCGGAGGGCTCAGCGGCCCTA

PSEN1

PSEN1-201

PSEN1-201

TATAGACATGCACCACCACACCGGGCTAATTTTGTATTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAAC 11,815
ATATCTGTACGTGGTGGTGTGGCCCGATTAAAACATAAAAATCATCTCTGTCCCAAAGAGGTACAACCAGTCCGACCAGAACTTG

PSEN1

PSEN1-201

PSEN1-201

TCCTGACCTCAGGTGATCCACCCACCTCCGACTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCTGGCCTTTTTTTTT 11,900
AGGACTGGAGTCCACTAGGTGGGTGGAGGCTGAGGGTTTCACGACCCTAATGTCCACACTCGGTGGTACGGACCGGAAAAAAAAA

PSEN1

PSEN1-201

PSEN1-201

TTTTTTAATTTAAACGAAATCTGCTTATTTTCCTGTTGATGTAAGGTGTTTGTGTTAAGGTGAAATGAAAAGTGATTTTTAAAAA 11,985
AAAAAATTAAATTTGCTTTAGACGAATAAAAGGACAACTACATTCCACAAACACAATTCCACTTTACTTTTCACTAAAAATTTTT

PSEN1

PSEN1-201

PSEN1-201

AATATTATTTTAGGACTATTTAACAAATATACTATTTATGATAATTAACATGGGGTTAGCAAACTACTGCTTGAAGCCAAATATG 12,070
TTATAATAAAATCCTGATAAATTGTTTATATGATAAATACTATTAATTGTACCCCAATCGTTTGATGACGAACTTCGGTTTATAC

PSEN1

PSEN1-201

PSEN1-201

GCCCATGGCTTGTTTTTGTACAGCTTATAAGCTAAAAATGCTTTTTACATTTAAAAAAAAAAAAAAAGAACAAGGAAGAATATGT 12,155
CGGGTACCGAACAAAAACATGTCGAATATTCGATTTTTACGAAAAATGTAAATTTTTTTTTTTTTTTCTTGTTCCTTCTTATACA

PSEN1

PSEN1-201

PSEN1-201

GACACACAAAACCTGAAATGTTTACTCCCTGGCCATTTACAGAAAAAGTTAGCTGGACATTGATTTTCATGTTACTATTAACTGC 12,240
CTGTGTGTTTTGGACTTTACAAATGAGGGACCGGTAAATGTCTTTTTCAATCGACCTGTAACTAAAAGTACAATGATAATTGACG

PSEN1

PSEN1-201

PSEN1-201

TAAAACAAAGGAGCTTGTAGCTATATTTTTTCATACTTGCATAAAGAAAGAAAACCTAATAAATCGCTGGTGGCTTCATTTCCAA 12,325
ATTTTGTTTCCTCGAACATCGATATAAAAAAGTATGAACGTATTTCTTTCTTTTGGATTATTTAGCGACCACCGAAGTAAAGGTT

PSEN1

PSEN1-201

PSEN1-201

AAGGCTATGGAAATCCATAAACAGGCTGGGTGCAGTGGCTCATGCCTGTAATCCTAGCACTTTGGGAGGCTGAGGCGGGAGGATT 12,410
TTCCGATACCTTTAGGTATTTGTCCGACCCACGTCACCGAGTACGGACATTAGGATCGTGAAACCCTCCGACTCCGCCCTCCTAA

PSEN1

PSEN1-201

PSEN1-201

GCTTGAGCCCAGGAGTTTGAGTCTGGCCTGGGCAACGTAGTGAGACCCTGTTTTTAGAAAAAATGAAGATAAAAAACTAATCCAT 12,495
CGAACTCGGGTCCTCAAACTCAGACCGGACCCGTTGCATCACTCTGGGACAAAAATCTTTTTTACTTCTATTTTTTGATTAGGTA

PSEN1

PSEN1-201

PSEN1-201

AAACCTCATACTTGGTGGTTGCCCTTCAGTTTTTCTTCTTTAGATCTGGATTTAGTTAAACAGTGTATTGCCTGCCTGGTTTCTG 12,580
TTTGGAGTATGAACCACCAACGGGAAGTCAAAAAGAAGAAATCTAGACCTAAATCAATTTGTCACATAACGGACGGACCAAAGAC

PSEN1

PSEN1-201

PSEN1-201

TTAACTTTTGATCATTTGGTTGGGTTATCCTATAATGAAACTTGGTTGACCTCAGAAATAACAAGGTGGTCGTTCAGCTTCTTTG 12,665
AATTGAAAACTAGTAAACCAACCCAATAGGATATTACTTTGAACCAACTGGAGTCTTTATTGTTCCACCAGCAAGTCGAAGAAAC

PSEN1

PSEN1-201

PSEN1-201

ATTGTGTGTTTCTTTCATAAGTTCTTCAAGAAGCCTGAGTATTAGAAACATGGATAAAATTATTGTGATAAAAAGCCAGAGAGAC 12,750
TAACACACAAAGAAAGTATTCAAGAAGTTCTTCGGACTCATAATCTTTGTACCTATTTTAATAACACTATTTTTCGGTCTCTCTG

PSEN1

PSEN1-201

PSEN1-201

ATAAATGTCAAGTATCTTGTTTAAAATTACTGTGACCAGGCCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC 12,835
TATTTACAGTTCATAGAACAAATTTTAATGACACTGGTCCGGCCCGCACCACCGAGTGCGGACATTAGGGTCGTGAAACCCTCCG

PSEN1

PSEN1-201

PSEN1-201

TGAGGCGGGCGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACAGTGAAACCCCACCTCTACTAAAAAAAATACAAA 12,920
ACTCCGCCCGCCTAGTGCTCCAGTCCTCTAGCTCTGGTAGGACCGATTGTGTCACTTTGGGGTGGAGATGATTTTTTTTATGTTT

PSEN1

PSEN1-201

PSEN1-201

AAATTAGCCAGGCATGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCAGGAGACG 13,005
TTTAATCGGTCCGTACCACCGCCCGCGGACATCAGGGTCGATGAGCCCTCCGACTCCGTCCTCTTACCGCACTTGGGTCCTCTGC

PSEN1

PSEN1-201

PSEN1-201

GAGCTTGCAGTGAGCCGAGATCATGCCACTGTACTCCAGCCTGGGTGACAGAGCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAA 13,090
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PSEN1

PSEN1-201

PSEN1-201

AAAAATTACTGTGACCAGATTGGACTCAGCTTGCTGCTGGCATTTGGTTCCCACCATAACCTCATATGTCATGTGTTTGCTTATA 13,175
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PSEN1

PSEN1-201

PSEN1-201

TGTACTTTTGTGTTATTGTTGGTGTATCTTCAGGATAAGTTCCAAAATGTAATATTGCTGGGTTAAAGGATTAATGCACATGTAG 13,260
ACATGAAAACACAATAACAACCACATAGAAGTCCTATTCAAGGTTTTACATTATAACGACCCAATTTCCTAATTACGTGTACATC

PSEN1

PSEN1-201

PSEN1-201

TTTTATTAGATGTTACCAAATTTCCCTCCAGTGGGGATTATACCATTTTTCATTCCTGCCTGAAATATATGAGAGAAGCACCATT 13,345
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PSEN1

PSEN1-201

PSEN1-201

TTAAAGTTTTCACAATGTCTCTGAACTAAAATGTGGTAGAGATGCACATGTGTATATCTAGATCTAGATTGATATATTGATATAC 13,430
AATTTCAAAAGTGTTACAGAGACTTGATTTTACACCATCTCTACGTGTACACATATAGATCTAGATCTAACTATATAACTATATG

PSEN1

PSEN1-201

PSEN1-201

ATGTATTTTTGTAGAAGGGGCACAGAGGAGGCCTCTTGACTATCCCTATTATGTTTATTGCTTTTAACGTTTTTTCTCACGCCGG 13,515
TACATAAAAACATCTTCCCCGTGTCTCCTCCGGAGAACTGATAGGGATAATACAAATAACGAAAATTGCAAAAAAGAGTGCGGCC

PSEN1

PSEN1-201

PSEN1-201

GTTTAAAACATGGTTTAGCATTATTGAACATTCTAAAAATGAGACATAATATGAAGGAAATTTACTCTGTGCATCTTTTGAATTA 13,600
CAAATTTTGTACCAAATCGTAATAACTTGTAAGATTTTTACTCTGTATTATACTTCCTTTAAATGAGACACGTAGAAAACTTAAT

PSEN1

PSEN1-201

PSEN1-201

PSEN1-201

TAATCACCATCTGAGGCTTTTGTGAGCTCCAGTTTGTCCTGGAATTTAGAACATTCAACTAGTCCAGCTATTGTTTCAGTGGAAT 13,685
ATTAGTGGTAGACTCCGAAAACACTCGAGGTCAAACAGGACCTTAAATCTTGTAAGTTGATCAGGTCGATAACAAAGTCACCTTA

PSEN1

PSEN1-201

PSEN1-201

PSEN1-201

CTTGCTGGCCTGAACAGTTTTCCTTCTGGTTCCTTTTCAGGGACTAAAAATGATGAAGAGTTTTGTGATAGCAGGTGCAGTTTGA 13,770
GAACGACCGGACTTGTCAAAAGGAAGACCAAGGAAAAGTCCCTGATTTTTACTACTTCTCAAAACACTATCGTCCACGTCAAACT

PSEN1

PSEN1-201

PSEN1-201

PSEN1-201

GTACTACAGTAAACATTCAGTTTCAGAACTTCTTCTCTTACCTGCTAAAACCAAAGAGAACCTTTTTTTTATTTTTACTTCTGAT 13,855
CATGATGTCATTTGTAAGTCAAAGTCTTGAAGAAGAGAATGGACGATTTTGGTTTCTCTTGGAAAAAAAATAAAAATGAAGACTA

PSEN1

PSEN1-201

PSEN1-201

PSEN1-201

TGTTGAACAGTCTTAAGGCAGCATTAGGAAGACTGGCGATTTGTGTGGAGAAATGATGGCTTGTTGTTGTCTATGCATACTTTGT 13,940
ACAACTTGTCAGAATTCCGTCGTAATCCTTCTGACCGCTAAACACACCTCTTTACTACCGAACAACAACAGATACGTATGAAACA

PSEN1

PSEN1-201

PSEN1-201

PSEN1-201

GTGTCCAGTGCTTACCTGGAATTTTGTCTTTCCCAACAGCAACAATGGTGTGGTTGGTGAATATGGCAGAAGGAGACCCGGAAGC 14,025
CACAGGTCACGAATGGACCTTAAAACAGAAAGGGTTGTCGTTGTTACCACACCAACCACTTATACCGTCTTCCTCTGGGCCTTCG

PSEN1

PSEN1-201

290 295 300 305
S T M V W L V N M A E G D P E A

ENSE00003979370

PSEN1-201

TCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAGAAAGTAGGTAACTTTTATTAGATAATATCTTGATTTTTCAGGGTCAC 14,110
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PSEN1

PSEN1-201

310 315
Q R R V S K N S K Y N A E

ENSE00003979370

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

TGACTTAGGATGAGCTGGGTGCAGTGATGTGTGCCTGTAGTCCCAGCTACATGGCCAAGGCAAGAGGATCACTTGAGCTAAGGAG 14,705
ACTGAATCCTACTCGACCCACGTCACTACACACGGACATCAGGGTCGATGTACCGGTTCCGTTCTCCTAGTGAACTCGATTCCTC

PSEN1

PSEN1-201

PSEN1-201

TTCCGGATTACCCTGGGCAACTTATACCTTACCTCAAAAATAATAATAATAATGAATAATAATAATGACTTAGGATAAGAGAGTG 14,790
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

GAGTTGCTGTTTGTCAGGAAAGGGAGAGTTTATGTTTTATAAAGCCAGGAAATCTACAGAGTTAGCATTTAGGCAACTGCAAGGA 15,130
CTCAACGACAAACAGTCCTTTCCCTCTCAAATACAAAATATTTCGGTCCTTTAGATGTCTCAATCGTAAATCCGTTGACGTTCCT

PSEN1

PSEN1-201

PSEN1-201

AGATACTTTCAACCAGGAATTCCTATTTGGAACTCAGAGATGTGAGTCTTTATTATACAGTAAGCAAGGCAGCAGAACAAGGTCA 15,215
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PSEN1

PSEN1-201

PSEN1-201

TGTTAGACTCTCACGGGATCCTTAGGGTGTGACTTTGCTAGCCAGAAACCTCTGTGGCTGGTGGCACCTTTTCCTGAGATTTGCT 15,300
ACAATCTGAGAGTGCCCTAGGAATCCCACACTGAAACGATCGGTCTTTGGAGACACCGACCACCGTGGAAAAGGACTCTAAACGA

PSEN1

PSEN1-201

PSEN1-201

CAGGCCCACTGGGCTCATTCCACCTACTCAGCCTAGCTGGCTATGCTTGGCTTTCTCTACCAGCTGGACCCCATGCCTGCCAAAG 15,385
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PSEN1

PSEN1-201

PSEN1-201

GCAAGCCAGGCATGGAGCAGCGAGGAGTGCATGAGCAAGTGAGTGCAGGGTCCAGCCACTGCACACAGCCAGGCATGCTGGCTGC 15,470
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

ACTAGTAAACCTGATAGAAAAGTAAGAAATATACTGGAAAGAATTGCCACAAGCCTGGCTCTTGTGTTAACCTTGTGTTAACCTG 15,640
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

TCCTGAGTCTGGACTCCCCGAAGGGCCACATCTCTTCACTCCTCTCTTCTCTCCTTCTCGCCACCTGCAACGTGGCAAGTGGGGG 15,810
AGGACTCAGACCTGAGGGGCTTCCCGGTGTAGAGAAGTGAGGAGAGAAGAGAGGAAGAGCGGTGGACGTTGCACCGTTCACCCCC

PSEN1

PSEN1-201

PSEN1-201

GCACGTTTCAGCCCTGTTTGTCTTACGGTTCTTTCAATCCTGCCATTCAATGGGTCCCAAGTTCTTGTCCTGCATCCAGGAAGAA 15,895
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

CACTGTGGTCTGTGGAACTGGGAGCTTGGCCTCCAGGCTTCAGGCTTTCCCTGACTTGAGGTGGTGCTTCACCAGGGAACTTCCC 16,405
GTGACACCAGACACCTTGACCCTCGAACCGGAGGTCCGAAGTCCGAAAGGGACTGAACTCCACCACGAAGTGGTCCCTTGAAGGG

PSEN1

PSEN1-201

PSEN1-201

CTTTCCGCCTAGGAGCCTGTCTGCCTCCTGCTGCCATCAACCTGCTGTCTATAGCTCCCATGGCACCCAGGCTGTTCATGCCAAA 16,490
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PSEN1

PSEN1-201

PSEN1-201

GGGTGCCTGCAGGCCCACGGTAAGCTGCCTTCAGCCCCTCCTCAGTCTCCCTCCCATGCTTGTCAGCACCCAAAGTCCAGAGGGG 16,575
CCCACGGACGTCCGGGTGCCATTCGACGGAAGTCGGGGAGGAGTCAGAGGGAGGGTACGAACAGTCGTGGGTTTCAGGTCTCCCC

PSEN1

PSEN1-201

PSEN1-201

GCCAAGGTGGCAGGGGGCTGGCATGTCAGTGCTGCCCCAAGCGCCCGCACACCCGGCCAGGTCATGACAGCACCCAGCCTCAGCC 16,660
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PSEN1

PSEN1-201

PSEN1-201

ACAACTTTGCTCTGAAATCGGAGCCTGCAGACGCAAGGGGCTTCCTGGACCCCTGAGAGCACAGGGATGCCCAGGTCTACAGCCA 16,745
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PSEN1

PSEN1-201

PSEN1-201

CAGCTGGGAAGCTGCAGCTGTGGGAGTGCGGGACTTCTGCCCCACCAACTCAGAAGGGGGCAGGACTCCCGCCTGTTCCTGGCTC 16,830
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PSEN1

PSEN1-201

PSEN1-201

CTGCCAGCTCACAGAGCATGCTGCCCCAGCTGCACCTCCCCTGCTGCAGCTGCCATCTTTGCAGCAGCCACTCCAGATGGGCCGC 16,915
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

ACCTGTGTTAAGCTAAAGAAAATCAAATGATTGTCTGTGAGCATGTAGGTATATATGTATGTGAGTGAGTGATACAACAGAATTT 17,085
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PSEN1

PSEN1-201

PSEN1-201

CATTCATTTTACAGATGTTGACTGAGCACCTGACTATGTGCTAGGCCCTGGGGATATAGCACTGAACAAGATTTCCCCTGCCCTT 17,170
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PSEN1

PSEN1-201

PSEN1-201

GTGGAGCTTATAGTCTATTTGGAGAGATAGATGGTCAACAAATTATTACATAAATAATTCATACAGTTGTGATAGGTACTACAAA 17,255
CACCTCGAATATCAGATAAACCTCTCTATCTACCAGTTGTTTAATAATGTATTTATTAAGTATGTCAACACTATCCATGATGTTT

PSEN1

PSEN1-201

PSEN1-201

GAAGACGTATAAGTTGCTATGAAAGTTTATAATAGGGGAATTTTACGTATCCTGGAAAGTCAAGGGGTGCTTCCCTGAGGAAGTG 17,340
CTTCTGCATATTCAACGATACTTTCAAATATTATCCCCTTAAAATGCATAGGACCTTTCAGTTCCCCACGAAGGGACTCCTTCAC

PSEN1

PSEN1-201

PSEN1-201

GTAATAGGGGACGGCCCGCTGAAGGATGGAGGAAGAGCTTTCCAAGAGAGGGACAACATGAGCAAGGGCTTTGAAATGAGAAGGC 17,425
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

CTCTGTCAGAGCATTTCAGGATAAATTAGTCATAGATAATAATATAAAATTCATCAGTGGAAAAAAATGAGGCAGTTTTCCAAAG 17,850
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

AGACCTAATGCTTTATCTTCTCTATAGGAGGTGAATAAGTACCTCAAATTAAAACATCAAGTTATGGCACAATGAGCATGCTACT 18,105
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

GGTAGAAAAGGGACTGCTGTTTTCATTTATAAATCTTATTCTTATATTATTTCATAAACTCCAAACCAGAGAAGATTCAGGTTTT 18,275
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

CCTGAAGCTTACAAGCTTTACTTATTCATGGCAAATCTACTTCTGCTCTGAACATGTATTACTTTTATAAAAAATGAAGGAAGAA 18,445
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PSEN1

PSEN1-201

PSEN1-201

TAAAAGTACTTTGAACTTCACTTATATATTTTAATTATTTTTAATGTATGGAAGTTTTTTAAGACTATCATGCTCACCATTTTCA 18,530
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PSEN1

PSEN1-201

PSEN1-201

ATGAGATTGATAGTCATTATAATGAAATGACTGGCCCATAAAGACATTCACTCCCCGCTCCTTTCCCAATCCACCCTCCAGAATG 18,615
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PSEN1

PSEN1-201

PSEN1-201

AAGCCACTTTTATAATTTTGTCACCAAATCCAGGGATGAGTGCCAACAGTTAGGAAGCTTTCAGTTGCAAAAGATAAAAAGCCCA 18,700
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PSEN1

PSEN1-201

PSEN1-201

ACTCAGTTGCCTTAAACAAAGAAGAAATTTATTCTTTCACGTGACAGGAAGGCCTGAGGTGTAGGCATTTGAAATTTGTAGGGTT 18,785
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PSEN1

PSEN1-201

PSEN1-201

GGTTAATTTGGTGGCTCAGGGATGTTTTCAAGTAGCCCAACTTCCTACTCTACCATCACTAGTTTATAGGCTTGGTCTTCAGCCC 18,870
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PSEN1

PSEN1-201

PSEN1-201

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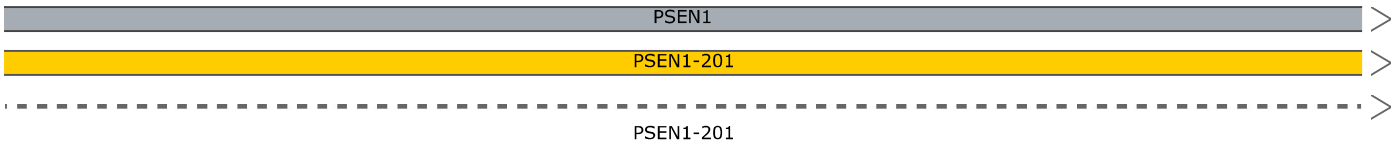

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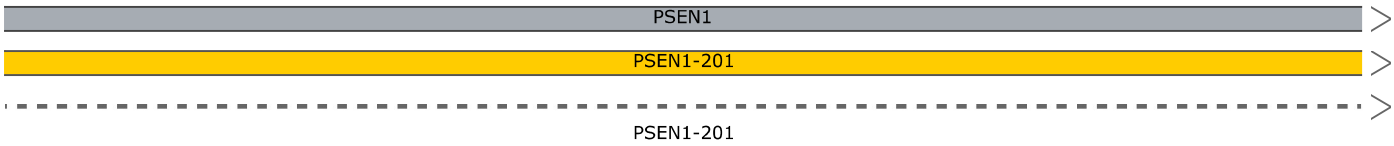

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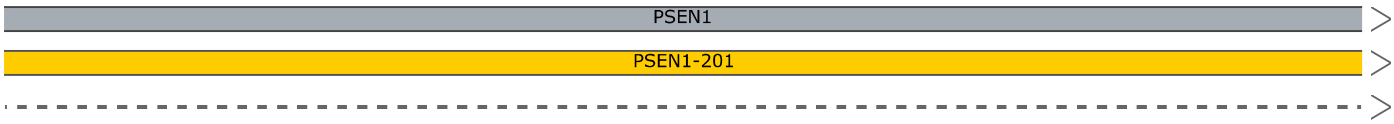

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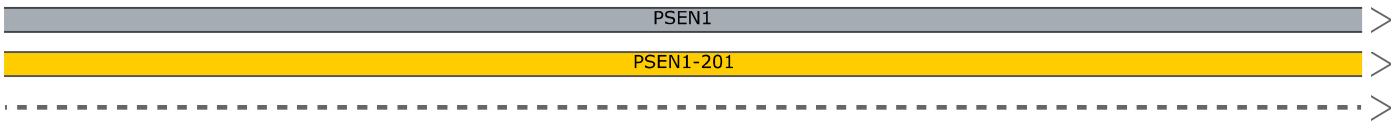

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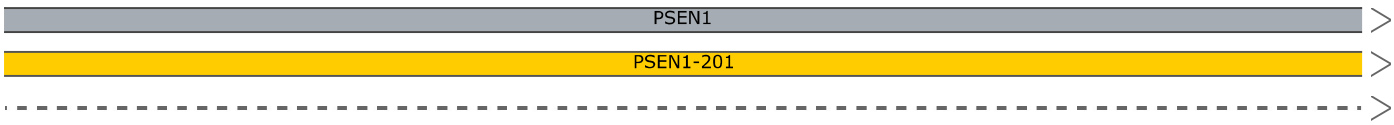

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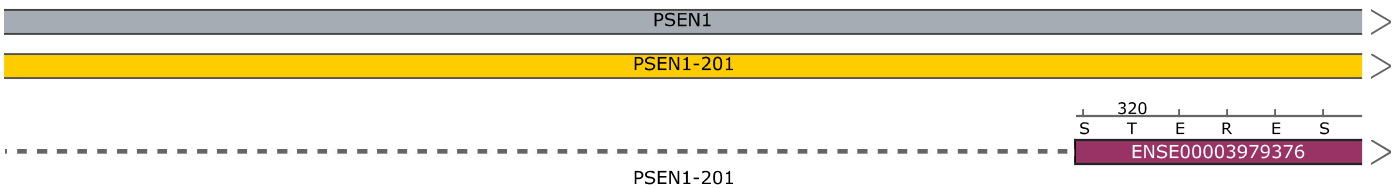

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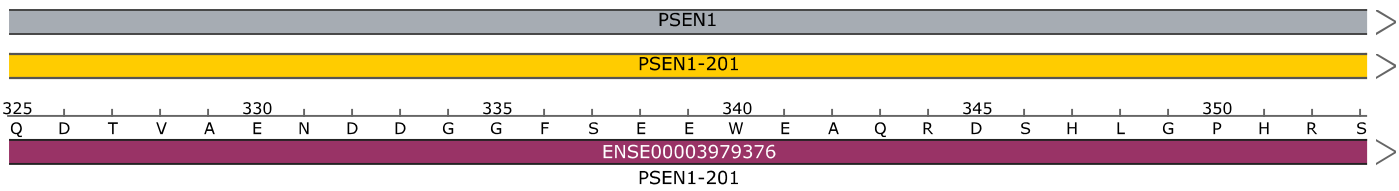

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PSEN1

PSEN1-201

355 360 365 370 375
T P E S R A A V Q E L S S S I L A G E D P E E

ENSE00003979376

PSEN1-201

CTATGTTGCAAAGTCATGGATTCCTTTAGGTAGCTACATTATCAACCTTTTTGAGAATAAAATGAATTGAGAGTGTTACAGTCTA 19,635
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PSEN1

PSEN1-201

PSEN1-201

ATTCTATATCACATGTAACTTTTATTTGGATATATCAGTAATAGTGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 19,720
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PSEN1

PSEN1-201

PSEN1-201

TTTGAGACAGAGTCTCGCTCTGTCGCCAGGTTGGAGTGCAATGGTGCGATCTTGGCTCACTGCAAGCTCCACCTCCCGGGTTCAA 19,805
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PSEN1

PSEN1-201

PSEN1-201

GTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGTGCGCCACCACGCCTGGATAATTTTTGTATTTTTAGTAGA 19,890
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

AAAAGATAGACAATAACAGGTGTTGGTGAGGATGCGAAGAAACTGGAATCCTCATACACTGCTGGTGGGAATGTAAAATAGTATA 21,505
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

CAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATCATACCATTGCACTCCAGCCTGG 22,100
GTCCTCCGACTCCGTCCTCTTAGTGAACTTGGACCCTCCACCTCCAACGTCACTCGACTCTAGTATGGTAACGTGAGGTCGGACC

PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

GCCAGTGTGGAATGTGATTTGGCAGTTTATTAAAAAGCTAAAAACCTAAACTTACATAGCCCAGCAATTGCACCCCCAGGAGTCT 23,545
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

380
R G V K L G
ENSE00003979377

PSEN1-201

ATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGT 24,820
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PSEN1

PSEN1-201

385 390 395 400 405 410
L G D F I F Y S V L V G K A S A T A S G D W N T T I A C
ENSE00003979377

PSEN1-201

TTCGTAGCCATATTAATTGTAAGTATACACTAATAAGAATGTGTCAGAGCTCTTAATGTCAAAACTTTGATTACACAGTCCCTTT 24,905
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PSEN1

PSEN1-201

415
F V A I L I
ENSE00003979377

PSEN1-201

AAGGCAGTTCTGTTTTAACCCCAGGTGGGTTAAATATTCCAGCTATCTGAGGAGCTTTTTGATAATTGGACCTCACCTTAGTAGT 24,990
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

GTGTAGTTTTTAAAATTCCCCAGGAAATTCTGGTATTTCTGTTTAGGAACCGCTGCCTCAAGCCTAGCAGCACAGATATGTAGGA 25,160
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PSEN1

PSEN1-201

PSEN1-201

AATTAGCTCTGTAAGGTTGGTCTTACAGGGATAAACAGATCCTTCCTTAGTCCCTGGACTTAATCACTGAGAGTTTGGTGGTGGT 25,245
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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

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PSEN1

PSEN1-201

PSEN1-201

GAGTCTCTGTCACCCAGGCTGGAGTGGTGCAATCTCGGCTCATTGCAACCTCTGCCTCCCAGATTTAAGTGATTCTCTGCCTCAG 25,500

CTCAGAGACAGTGGGTCCGACCTCACCACGTTAGAGCCGAGTAACGTTGGAGACGGAGGGTCTAAATTCACTAAGAGACGGAGTC

PSEN1

PSEN1-201

PSEN1-201

CCTCCCGAGTAGCTGGGATTACAGGTGCCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAAACAGGGTTTCACCATGT 25,585

GGAGGGCTCATCGACCCTAATGTCCACGGACGGTGGTGCGGGCCGATTAAAAACATAAAAATCATCTTTGTCCCAAAGTGGTACA

PSEN1

PSEN1-201

PSEN1-201

TGGCCAGGCTCCTCTTGAACTCCTGACCTCAAGTGATGTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC 25,670

ACCGGTCCGAGGAGAACTTGAGGACTGGAGTTCACTACACGGACGGAGCCGGAGGGTTTCACGACCCTAATGTCCGCACTCGGTG

PSEN1

PSEN1-201

PSEN1-201

CGCACCTGGCTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTCTTGCTCTGTCGCCCAAACTAGAGTGCAGTGACATTAGCTCA 25,755

GCGTGGACCGAAAAAAAAAAAAAAAAAAAAAACCTCTGTCTCAGAACGAGACAGCGGGTTTGATCTCACGTCACTGTAATCGAGT

PSEN1

PSEN1-201

PSEN1-201

CTGCAACTTCTGCCTCCTAGGTTCAAGCGATCCTCCTGTCTCAGCCTCCCAAGTAGCTGGAATTACATGTGTGCACCACCATGCC 25,840

GACGTTGAAGACGGAGGATCCAAGTTCGCTAGGAGGACAGAGTCGGAGGGTTCATCGACCTTAATGTACACACGTGGTGGTACGG

PSEN1

PSEN1-201

PSEN1-201

TGGCTAATTTTTGTATTTTTAGTGGAGATGAGGTTTTGCCACATTGCCCAGGCTGGTCTCAAACTTCTGACCTCAACTGATCTGC 25,925

ACCGATTAAAAACATAAAAATCACCTCTACTCCAAAACGGTGTAACGGGTCCGACCAGAGTTTGAAGACTGGAGTTGACTAGACG

PSEN1

PSEN1-201

PSEN1-201

CTGCCTCAGCCGCATAAAGTGCTGGGATTACAGGCATGAGCCACTGTGCCCAACCTGAAAACTATGATTTAAGTAAACAACCCAT 26,010

GACGGAGTCGGCGTATTTCACGACCCTAATGTCCGTACTCGGTGACACGGGTTGGACTTTTGATACTAAATTCATTTGTTGGGTA

PSEN1

PSEN1-201

PSEN1-201

AAAATATTTCTTGCTATTTTTACTAAAGATGTGTTATCTTGGCCGGGTGAAGACTTTCTAGTGTTTCCGTAACTAGGGTAAAAAA 26,095
TTTTATAAAGAACGATAAAAATGATTTCTACACAATAGAACCGGCCCACTTCTGAAAGATCACAAAGGCATTGATCCCATTTTTT

PSEN1

PSEN1-201

PSEN1-201

TGAACTCTATTATATGGCTTGTACATGTGTTTACAAGAAAGCAGTGTACTCCTCATAAATAAACTTTTAGTTTATTTTATTTTTT 26,180
ACTTGAGATAATATACCGAACATGTACACAAATGTTCTTTCGTCACATGAGGAGTATTTATTTGAAAATCAAATAAAATAAAAAA

PSEN1

PSEN1-201

PSEN1-201

AAACACTGCAGCCTCATCATGCTTCACGGAGGAGCCTGTGCGGGAAGAATGCTCCCACACAGCATAAAGAATGCTCCCGCACAGC 26,265
TTTGTGACGTCGGAGTAGTACGAAGTGCCTCCTCGGACACGCCCTTCTTACGAGGGTGTGTCGTATTTCTTACGAGGGCGTGTCG

PSEN1

PSEN1-201

PSEN1-201

ATAGAGAATGCCCCCGCACAGCATAGAGAAGCCCCCGCACAGCATAGAGAATGCCCCCGCACAGCATAGAGAAGCCCCCGCACAG 26,350
TATCTCTTACGGGGGCGTGTCGTATCTCTTCGGGGGCGTGTCGTATCTCTTACGGGGGCGTGTCGTATCTCTTCGGGGGCGTGTC

PSEN1

PSEN1-201

PSEN1-201

CATAGAGAATGCTCTTCACCTCTGGGTTTTTAACCAGCCAAACTAAAATCACAGAGGCCAACACATCATTTAAGATAGAAATTTC 26,435
GTATCTCTTACGAGAAGTGGAGACCCAAAAATTGGTCGGTTTGATTTTAGTGTCTCCGGTTGTGTAGTAAATTCTATCTTTAAAG

PSEN1

PSEN1-201

PSEN1-201

TGTATCTTTTAATTTTTTTCAAAGTAGTTTTACTTATTTTCAGATTCTATTTCTTTACTAGAATTAAGGGATAAAATAACAATGT 26,520
ACATAGAAAATTAAAAAAAGTTTCATCAAAATGAATAAAAGTCTAAGATAAAGAAATGATCTTAATTCCCTATTTTATTGTTACA

PSEN1

PSEN1-201

PSEN1-201

GTGCATAATGAACCCTATGAAACAAACAAAAGCTAGGTTTTTTTCATAGCTCTTCTTCCAGATTGAATGAACGTCTGTTCTAAAA 26,605
CACGTATTACTTGGGATACTTTGTTTGTTTTCGATCCAAAAAAAGTATCGAGAAGAAGGTCTAACTTACTTGCAGACAAGATTTT

PSEN1

PSEN1-201

PSEN1-201

TTTAACCCCAAAAGGAAAATATTCAGTTAACTATGTTAAAAACCAAGACTTGTGATTGAGTTTTGCCTGAAAATGCTTTCATAAT 26,690

AAATTGGGGTTTTCCTTTTATAAGTCAATTGATACAATTTTTGGTTCTGAACACTAACTCAAAACGGACTTTTACGAAAGTATTA

PSEN1

PSEN1-201

PSEN1-201

TATGTGTGAATGTGTGTCTTTCCCATCTTCTCCACAGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTG 26,775

ATACACACTTACACACAGAAAGGGTAGAAGAGGTGTCCCAAACACGGAATGTAATAATGAGGAACGGTAAAAGTTCTTTCGTAAC

PSEN1

PSEN1-201

420 425 430

G L C L T L L L L A I F K K A L

ENSE00002555450

PSEN1-201

CCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAGCCTTTTATGGACCAATTAG 26,860

GGTCGAGAAGGTTAGAGGTAGTGGAAACCCGAACAAAAGATGAAACGGTGTCTAATAGAACATGTCGGAAAATACCTGGTTAATC

PSEN1

PSEN1-201

435 440 445 450 455 460

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

ENSE00002555450

PSEN1-201

CATTCCATCAATTTTATATCTAGCATATTTGCGGTTAGAATCCCATGGATGT 3′

26,912

GTAAGGTAGTTAAAATATAGATCGTATAAACGCCAATCTTAGGGTACCTACA 5′

PSEN1

PSEN1-201

465

A F H Q F Y I *

ENSE00002555450

PSEN1-201

Feature	Location	Size	Type
✓ **PSEN1**	1 .. 26,912	26,912 bp	gene
/note = gene ENSG00000080815 Protein coding			
✓ **PSEN1-201**	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000324501			
PSEN1-202	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000357710			
PSEN1-204	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000394164			
PSEN1-205	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000406768 Retained intron			
PSEN1-207	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000553599			
PSEN1-209	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000554131			
PSEN1-215	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000556066 Retained intron			
PSEN1-218	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000556951			
PSEN1-220	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000557293			
PSEN1-223	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000559361 Nonsense mediated decay			
PSEN1-225	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000697912 Nonsense mediated decay			
PSEN1-226	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000697913 Retained intron			
PSEN1-229	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700265			
PSEN1-230	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700266 Nonsense mediated decay			
PSEN1-231	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700267			
PSEN1-232	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700268			
PSEN1-233	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700269			
PSEN1-235	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700271			
PSEN1-236	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700272 Nonsense mediated decay			
PSEN1-237	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700273			
PSEN1-238	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700302 Nonsense mediated decay			

Feature	Location	Size	Type
PSEN1-239	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700303 Nonsense mediated decay			
PSEN1-240	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700304 Nonsense mediated decay			
PSEN1-241	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700305 Nonsense mediated decay			
PSEN1-242	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700306			
PSEN1-243	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700307			
PSEN1-244	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700308 Nonsense mediated decay			
PSEN1-245	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700309 Nonsense mediated decay			
PSEN1-246	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700310 Nonsense mediated decay			
PSEN1-247	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700311 Nonsense mediated decay			
PSEN1-248	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700312			
PSEN1-249	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700313			
PSEN1-250	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700314 Nonsense mediated decay			
PSEN1-251	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700315 Nonsense mediated decay			
PSEN1-252	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700316 Nonsense mediated decay			
PSEN1-253	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700317			
PSEN1-254	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700318 Nonsense mediated decay			
PSEN1-255	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700319 Nonsense mediated decay			
PSEN1-256	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700320			
PSEN1-257	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700321			
PSEN1-258	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700322			
PSEN1-259	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700323			

Feature	Location	Size	Type
PSEN1-260	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700324			
PSEN1-262	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700375			
PSEN1-264	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700377 Nonsense mediated decay			
PSEN1-265	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700378			
PSEN1-266	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700379 protein_coding_CDS_not_defined			
PSEN1-268	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700389			
PSEN1-269	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700390 Retained intron			
PSEN1-271	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700404 Retained intron			
PSEN1-284	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700436 Nonsense mediated decay			
PSEN1-285	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700437			
PSEN1-287	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700468			
PSEN1-288	1 .. 26,912	26,912 bp	prim_transcript
/note = primary transcript ENST00000700469			
PSEN1-212	1 .. 26,883	26,883 bp	prim_transcript
/note = primary transcript ENST00000555386 Nonsense mediated decay			
PSEN1-222	1 .. 26,883	26,883 bp	prim_transcript
/note = primary transcript ENST00000557511			
PSEN1-208	1 .. 24,752	24,752 bp	prim_transcript
/note = primary transcript ENST00000553855 Nonsense mediated decay			
PSEN1-283	1 .. 21,017	21,017 bp	prim_transcript
/note = primary transcript ENST00000700435 protein_coding_CDS_not_defined			
PSEN1-286	1 .. 14,931	14,931 bp	prim_transcript
/note = primary transcript ENST00000700467 Retained intron			
PSEN1-234	1 .. 14,849	14,849 bp	prim_transcript
/note = primary transcript ENST00000700270 Retained intron			
PSEN1-282	1 .. 14,478	14,478 bp	prim_transcript
/note = primary transcript ENST00000700434 Retained intron			
PSEN1-281	1 .. 14,444	14,444 bp	prim_transcript
/note = primary transcript ENST00000700433 Retained intron			
PSEN1-280	1 .. 1173	1173 bp	prim_transcript
/note = primary transcript ENST00000700432 Retained intron			

Feature	Location	Size	Type
PSEN1-263	1 .. 726	726 bp	prim_transcript

/note = primary transcript ENST00000700376
Retained intron

PSEN1-267	1 .. 594	594 bp	prim_transcript

/note = primary transcript ENST00000700388
Retained intron

✓ **PSEN1-201**	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000326366
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-202	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000350342
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-204	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000377719
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-207	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000452477
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-209	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000451915
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-218	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000450551
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-220	238 .. 26,883	26,646 bp	CDS

6 segments = 736 bp

/codon_start = 1
/note = coding sequence ENSP00000451880
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWK,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKY
NAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNT
TIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI*
244 amino acids = 27.1 kDa

Feature	Location	Size			Type
PSEN1-222	238 .. 26,883	26,646 bp	■	→	CDS

▶ 5 segments = 682 bp

/codon_start = 1
/note = coding sequence ENSP00000451429
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIF
KKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI*
226 amino acids = 25.4 kDa

PSEN1-229	238 .. 26,883	26,646 bp	■	→	CDS

▶ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514901
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-231	238 .. 26,883	26,646 bp	■	→	CDS

▶ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514903
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-232	238 .. 26,883	26,646 bp	■	→	CDS

▶ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514904
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-233	238 .. 26,883	26,646 bp	■	→	CDS

▶ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514905
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-235	238 .. 26,883	26,646 bp	■	→	CDS

▶ 5 segments = 682 bp

/codon_start = 1
/note = coding sequence ENSP00000514906
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIF
KKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI*
226 amino acids = 25.4 kDa

PSEN1-237	238 .. 26,883	26,646 bp	■	→	CDS

▶ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514908
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

Feature	Location	Size	Type
PSEN1-242	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514933
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-243	238 .. 26,883	26,646 bp	CDS

5 segments = 757 bp

/codon_start = 1
/note = coding sequence ENSP00000514934
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,ATMVWLVNMAEGDPEAQRRV
SKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATAS
GDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI*
251 amino acids = 28.0 kDa

PSEN1-248	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514939
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-249	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514940
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-253	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514944
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-256	238 .. 26,883	26,646 bp	CDS

6 segments = 883 bp

/codon_start = 1
/note = coding sequence ENSP00000514947
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DVFYVFLFLDLVAVLCPKGPLR
MLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRA
AVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQP
FMDQLAFHQFYI*
293 amino acids = 32.8 kDa

PSEN1-257	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514948
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

Feature	Location	Size			Type
PSEN1-258	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514949
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-259	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514950
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-260	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514951
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-262	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514966
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-265	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514968
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-268	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514970
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

PSEN1-285	238 .. 26,883	26,646 bp	■	→	CDS

▸ 6 segments = 856 bp

/codon_start = 1
/note = coding sequence ENSP00000514988
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYL*
284 amino acids = 31.7 kDa

Feature	Location	Size	Type
PSEN1-287	238 .. 26,883	26,646 bp	CDS

5 segments = 757 bp

/codon_start = 1

/note = coding sequence ENSP00000515001

/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,ATMVWLVNMAEGDPEAQRRV
SKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATAS
GDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI*
251 amino acids = 28.0 kDa

PSEN1-288	238 .. 26,883	26,646 bp	CDS

6 segments = 856 bp

/codon_start = 1

/note = coding sequence ENSP00000515002

/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQE
RNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSI
LAGEDPEE,,RGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQ
FYI*
284 amino acids = 31.7 kDa

PSEN1-210	4106 .. 26,912	22,807 bp	prim_transcript

/note = primary transcript ENST00000554995
Retained intron

✓	**Donor Template WT -> SNV**	5644 .. 5743	100 bp	misc_feature
✓	**Protospacer Sequence**	5662 .. 5681	20 bp	misc_feature
✓	**Silient SNV**	5680 .. 5680	1 bp	misc_feature

/note = WT = T
SNV = G

✓	**PAM**	5682 .. 5684	3 bp	misc_feature
✓	**SNV**	5694 .. 5694	1 bp	misc_feature

/note = WT = A
SNV = C

PSEN1-270	13,681 .. 26,912	13,232 bp	prim_transcript

/note = primary transcript ENST00000700391
protein_coding_CDS_not_defined

PSEN1-213	13,747 .. 26,912	13,166 bp	prim_transcript

/note = primary transcript ENST00000555867
Retained intron

PSEN1-228	24,234 .. 26,912	2679 bp	prim_transcript

/note = primary transcript ENST00000697915
Retained intron

	Primer	Length	Binding Sites			Tm	Date Added
✓	**PCR Forward**	25-mer	5250 ..	5274	→	60°C	Jan 11, 2023
	/sequence = TTCTCCCTGTTTCTGCTCACTGTAG 48% GC / 7540.9 Da						
✓	**Donor Template WT -> SNV**	100-mer	5644 ..	5743	←	72°C	Jan 11, 2023
	/sequence = TATCCTTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAAAGCGTTGCATTTCTCTCCTGCGCTGTTTCAACCAGCATACGAAGTG 64% GC / 30,790.1 Da						
✓	**gRNA Protospacer**	20-mer	5662 ..	5681	→	55°C	Jan 11, 2023
	/sequence = TATGCTGGTTGAAACAGCTC 45% GC / 6132.1 Da						
✓	**Sanger Sequencing**	20-mer	5830 ..	5849	←	58°C	Jan 11, 2023
	/sequence = GAGTTCCAGGAATGCTGTGC 55% GC / 6173.1 Da						
✓	**PCR Reverse**	25-mer	6211 ..	6235	←	60°C	Jan 11, 2023
	/sequence = ATTCAAACCCCCATTACTTTCCACC 44% GC / 7440.9 Da						