# Pseudoalteromonas atlantica T6C  Genome Compared to Forward and Reverse Sequencing Reactions of the Agarase Clone from the University of Calgary.

Yellow highlights are primer sites.
Green is the start codon of Agarase.
Red is the stop codon of Agarase.

The T6C lines are from the genome of *Pseudoalteromonas atlantica* T6C.

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T6C    CAATTACTTAGTTTTAGTTTAAAACCTTAGGCTCTGCTCAGCCTTGTGTATCCGCACATA

AgaFor ------------------------------------------------------------

T6C    CCCAAGGTTGAGCACCCTATTTAATAACGGAAACAACAACATGAAATACCCACAATTCAT
                                :   : :::: :::::::::::::::::::::::
AgaFor ------------------------NNATNCGGAACA-CAACATGAAATACCCACAATTCAT

T6C    TACAAAGGTCGCCTTTAGGGCAAGCGCGATTGCGCTAGCTATTACCCTAACCGGCTGTAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor TACAAAGGTCGCCTTTAGGGCAAGCGCGATTGCGCTAGCTATTACCCTAACCGGCTGTAG

T6C    TCATGATCAACATGAAATTGCTCAGGCTCAGGGTGTTCCACAAGACCTTGCTGGAAACGG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor TCATGATCAACATGAAATTGCTCAGGCTCAGGGTGTTCCACAAGACCTTGCTGGAAACGG

T6C    TAGCCCACTAGGCAGTGCAGAGGACGCGTTTACCAACGAGCAAAAAATCGTCTCACTGAT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor TAGCCCACTAGGCAGTGCAGAGGACGCGTTTACCAACGAGCAAAAAATCGTCTCACTGAT

T6C    TGACTTTGATAACCAAGAGCAACTTAACTGGCTGCAGCAAAGTGATACCTCATTCGCGCA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor TGACTTTGATAACCAAGAGCAACTTAACTGGCTGCAGCAAAGTGATACCTCATTCGCGCA

T6C    GATCACCAGCAGCGAGAGCTTAATTGACAAGCAATTAGCGGTGGAGTTTGCGAAAACCGG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor GATCACCAGCAGCGAGAGCTTAATTGACAAGCAATTAGCGGTGGAGTTTGCGAAAACCGG

T6C    TAATATTTCCACGTTGCGCGTAGAGCCACCGAAGCCTTGGGATCTTAGGGAGTACGAAAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor TAATATTTCCACGTTGCGCGTAGAGCCACCGAAGCCTTGGGATCTTAGGGAGTACGAAAA

T6C    CTACAACATTGCCTTTGATGTGCAAAACACCAGCCCAGATTCAGTTCATTTGTACTTGTC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor CTACAACATTGCCTTTGATGTGCAAAACACCAGCCCAGATTCAGTTCATTTGTACTTGTC

T6C    TTTGGAAAATGTAAACGGACAAATCCAGAGTCACTCAATTTCTCTGGCTCCGAATTACAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor TTTGGAAAATGTAAACGGACAAATCCAGAGTCACTCAATTTCTCTGGCTCCGAATTACAA
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T6C    AGGCACGGTGTATTTTCCCCTCGATGGTATTGAAGCAGAAACCGACAGCGGCATGTGGGG
       :::::::::::::::::::::::::::::::::::::::::::: ::::::::::::::
AgaFor AGGCACGGTGTATTTTCCCCTCGATGGTATTGAAGCAGAAACCGATAGCGGCATGTGGGG

T6C    AGATGTGCCTCATTGGCAAACCCAAGACGACTTAATGGTGTGGCGTTCTTGGCGCAAAGC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor AGATGTGCCTCATTGGCAAACCCAAGACGACTTAATGGTGTGGCGTTCTTGGCGCAAAGC

T6C    AGAGCAAGACTATAGCCAACTCACCGCGCTTAATTTCTTCACTATTGGAATATTGGAAAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor AGAGCAAGACTATAGCCAACTCACCGCGCTTAATTTCTTCACTATTGGAATATTGGAAAA

T6C    CAAATCTGTGATTTTGGATGATGTGCGTCTGCGCGCGAATCCAGCTCACGACCCGAACGT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor CAAATCTGTGATTTTGGATGATGTGCGTCTGCGCGCGAATCCAGCTCACGACCCGAACGT

T6C    ATCGGTCGGATTAATCGATAAATACGGGCAAAACGCCAAACAAAGCACCCCCTTAGATGT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor ATCGGTCGGATTAATCGATAAATACGGGCAAAACGCCAAACAAAGCACCCCCTTAGATGT

T6C    GCATTCAGATGCCCAACTAAAACAACAAGCCGATGAAGAACTGGCCAAGCTAGCCAAATC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaFor GCATTCAGATGCCCAACTAAAACAACAAGCCGATGAAGAACTGGCCAAGCTAGCCAAATC

T6C    ATCGGGTATGCCAGACCGTTCTCGTTTTGGTGGTTATACCAAAGCCCCAAAACGTGAAGC
       :::::::::::::::::::::::::::::::::::::::::::::::: ::::::::
AgaFor ATCGGGTATGCCAGACCGTTCTCGTTTTGGTGGTTATACCAAAGCCCCAAA-CGTGAAGC

T6C    AACCGGCTTTTTTAGAACGGAAAAGGTCGATGGTAAGTGGTGGATGGTCGACCCTGATGG
       :::::::::::: :::::::::::::: ::::::::::::::::::::::::::::::::
AgaFor AACCGGCTTTTT-AGAACGGAAAAGGNCGATGGTAAGTGGTGGATGGTCGACCCTGATGG

T6C    CTATCTGTTTTTCTCACACGGGCCAGCTAACGTGCGTATGGCAAACATGAGTACGTTAAC
       :::::::::::: ::::: ::::::::::::  :::::::::::::::::::::::::: :
AgaFor CTATCTGTTTT-CTCACNCGGGCCAGCTAT-GTGCGTATGGCAAACATGAGTACGTNA--

T6C    CGGAATAGACTACGACCAACCGAGTATTCGCGTGCGCACCAGTGATGAAATTACCCCAGA
       :  : ::::::::::::      :::: :: :  :  :: :   ::::::
AgaFor CNNANTAGACTACGACN---NNAGTANTCNCNNGNNCANCNNNGATGAA-----------

T6C    AGATTCCATGGGAATTGTATCTGTTCCTGACAGCGCAAAAGAAAAACGCTATGTCATTTC

AgaFor ------------------------------------------------------------

T6C    AAAGGCGCGCAACGATATGTTTCAGTGGTTACCAAGCTATGATGATGAGCTCTCTGAGCA

AgaRev ------------------------------------------------------------

T6C    CTATAGCTATCGCCGCTCTACCCACAAAGGGCCTATTCCTTACGGCGAGACCTACAGCTT

AgaRev ------------------------------------------------------------
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T6C     TTACCGCGCTAATTTAGAACGTAGATACGGTGATGACGACCTACGCGCAGGTGAAGGTGA

AgaRev ------------------------------------------------------------

T6C     AAAAGCAGGCGAAAATCAAGGCAGCGATCCTTCCTACGTAAAAAAATGGCATGACGTCAC
                                                            :::::: :
AgaRev -----------------------------------------------------GACGTCNC

T6C     CGCACAGCGTATGCATGACTGGGGGTTTACCTCTTTTGGTAACTGGGTAGACCCAGCGTT
         :::::: ::: :::::::::::: ::   ::::::  :::    ::::: :::::::::
AgaRev  NGCACAGNGTANGCATGACTGGGGNTT--ACTCTTT--GTAN--NGGTAGNCCCAGCGTT

T6C     TTATCAATCAGAGCAAGTGCCTTATTTCGCCAATGGTTGGATCATCGGCGATTACCAAAC
        :::::: ::::::::::     ::::    :      ::::::::::::::   : :::
AgaRev  TTATCA-TCAGAGCAAGTNNN--ATTTNNNAANNN---GGATCATCGGCGAT--ACNAAC

T6C     ACTGTCGGGTCACACTAATCATTGGGGCTTGATGCCAGATCCTTTTGATCCCGTATTTGC
        :::: :::::::::::::::::::: :::::::::::::::::::::    :::: ::
AgaRev  ACTGCCGGGTCACACTAATCATTGGG-CTTGATGCCAGATCCTTTTGATNNN-TATT-GC

T6C     ACAGCGAGCAAAGGTCACTATCGATGCTATTGCCGAAAATATTCAAGCGTCACCTTGGTG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  ACAGCGAGCAAAGGTCACTATCGATGCTATTGCCGAAAATATTCAAGCGTCACCTTGGTG

T6C     TGCGGGTATTTTTATTGATAATGAGAAGAGCTGGGGAGAGCGTGAAGGCACAGTGTCACA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  TGCGGGTATTTTTATTGATAATGAGAAGAGCTGGGGAGAGCGTGAAGGCACAGTGTCACA

T6C     ACGCTATGGGGTGATCCTTGATGCACTATCAAAAAATATTGAGAAGAGCCCTGCAAAAAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  ACGCTATGGGGTGATCCTTGATGCACTATCAAAAAATATTGAGAAGAGCCCTGCAAAAAC

T6C     GGCCTTTGCAGCCCATTTGCAGCAAAAATACCAGACGATCGATGCATTGAATTCTGCATG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  GGCCTTTGCAGCCCATTTGCAGCAAAAATACCAGACGATCGATGCATTGAATTCTGCATG

T6C     GTCATCACACTTCGATAGTTGGCAAATGTTTGAAGATGACGCCAGCGTCAGCACGCACAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  GTCATCACACTTCGATAGTTGGCAAATGTTTGAAGATGACGCCAGCGTCAGCACGCACAC

T6C     CGATGCCCAAATTGCTGATTTGTCAAAAATGCTCGAGATGCTGGGTGAGCAGTACTTTAA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  CGATGCCCAAATTGCTGATTTGTCAAAAATGCTCGAGATGCTGGGTGAGCAGTACTTTAA

T6C     AGTGGTACACAATACCTTAGAAGCGGCGCTGCCAGAGCACTTGTACATGGGCGCGCGCAT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  AGTGGTACACAATACCTTAGAAGCGGCGCTGCCAGAGCACTTGTACATGGGCGCGCGCAT


T6C     GGCCAACTGGGGCATGCCTGATGAAATCATTACTGCCTCTTTGAAATACTCTGACGTACT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  GGCCAACTGGGGCATGCCTGATGAAATCATTACTGCCTCTTTGAAATACTCTGACGTACT
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T6C     GAGCTTCAATATTTATGAGGAAGGGGTGCAAGAAGACTATTGGAAGTTCCTTGAAGAAGT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  GAGCTTCAATATTTATGAGGAAGGGGTGCAAGAAGACTATTGGAAGTTCCTTGAAGAAGT

T6C     CGACTTACCCGTAGTGATTGGTGAGTTTCATATTGGCAGCACGACAGATTCAGGCATGTA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  CGACTTACCCGTAGTGATTGGTGAGTTTCATATTGGCAGCACGACAGATTCAGGCATGTA

T6C     CAACCCGGGTATTGTGCACAGCGCAAACCAGCAAGACAGAGCCCAAATGTACAAAGATTA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  CAACCCGGGTATTGTGCACAGCGCAAACCAGCAAGACAGAGCCCAAATGTACAAAGATTA

T6C     CATGCAAAGCGTGTTAGACAAGCCGTATATGGTCGGGGCCCATTGGTTTCAATACATAGA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  CATGCAAAGCGTGTTAGACAAGCCGTATATGGTCGGGGCCCATTGGTTTCAATACATAGA

T6C     TGAGCCCATATCGGGGCGTGCATTTGACGGCGAAAACGCCAATATCGGCTTTGTAACGGT
        :::::::::::::::::::::::::::::::::::::::::::: ::::::::::::::
AgaRev  TGAGCCCATATCGGGGCGTGCATTTGACGGCGAAAACGCCAATACCGGCTTTGTAACGGT

T6C     AACGGATATCCCATATCCGCATATGATCCAAGCGGTCAAAGAGGTGACATCCACCATGTA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  AACGGATATCCCATATCCGCATATGATCCAAGCGGTCAAAGAGGTGACATCCACCATGTA

T6C     CCAAAAACGCTTAGCCGACTAATACAGGCTTAGTGATAACAAAAAACGCCCGATAACGTC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AgaRev  CCAAAAACGCTTAGCCGACTAATACAGGCTTAGTGATAACAAAAAACGCCCGATAACGTC

T6C     GGGCGTTTTGCGTTTGTAAACGACTATTCTCCTTGCACGTTAACTACCACTCGACCGCGA
        ::::::::::::: :      ::  :
AgaRev  GGGCGTTTTGCGNTNNNN--CGNNTNN--------------------------------
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