CLUSTAL 2.1 multiple sequence alignment

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KC470218.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470214.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470215.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470216.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470217.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470219.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470220.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470221.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470222.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470223.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470225.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470226.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470227.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470228.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470230.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470229.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470224.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KX514433.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KU298886.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470213.1          ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
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KC470218.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470214.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470215.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470216.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470217.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470219.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470220.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470221.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470222.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470223.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470225.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470226.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470227.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470228.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470230.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470229.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470224.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KX514433.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KU298886.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470213.1          GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
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KC470218.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
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KC470214.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470215.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470216.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470217.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470219.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470220.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470221.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470222.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470223.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470225.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470226.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470227.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470228.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470230.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470229.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470224.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KX514433.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTTAAA
KU298886.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTTAAA
KC470213.1                    ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTTAAA
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KC470218.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470214.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470215.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470216.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470217.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470219.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470220.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470221.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470222.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470223.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470225.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470226.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470227.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470228.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470230.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470229.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470224.1                    GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KX514433.1                    GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KU298886.1                    GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470213.1                    GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
                              ********** **************************************** 


KC470218.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470214.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470215.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470216.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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CLUSTAL 2.1 multiple sequence alignment

KC470217.1                      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470219.1                      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470220.1                      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470221.1                      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470222.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470223.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470225.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470226.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470227.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470228.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470230.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470229.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470224.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KX514433.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KU298886.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470213.1                      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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KC470218.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470214.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470215.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470216.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470217.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470219.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470220.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470221.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470222.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470223.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470225.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470226.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470227.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470228.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470230.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470229.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470224.1                      CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KX514433.1                      CTGTGTATGGAGACACATTGGAAAAACTAACTAACACTGGGTTATACAAT
KU298886.1                      CTGTGTATGGAGACACATTGGAAAAACTAACTAACACTGGGTTATACAAT
KC470213.1                      CTGTGTATGGAGACACATTGGAAAAACTAACTAACACTGGGTTATACAAT
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KC470218.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470214.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470215.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470216.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470217.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470219.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470220.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
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CLUSTAL 2.1 multiple sequence alignment

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KC470221.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470222.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470223.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470225.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470226.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470227.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470228.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470230.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCATTGAATCCAGCAGAAAA
KC470229.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCATTGAATCCAGCAGAAAA
KC470224.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KX514433.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KU298886.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470213.1                      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
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KC470218.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470214.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470215.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470216.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470217.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470219.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470220.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470221.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
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KC470223.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470225.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470226.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470227.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470228.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470230.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KC470229.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KC470224.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KX514433.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KU298886.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAACNNNGCTGGGCACT
KC470213.1                      ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
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KC470218.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCAAGCACGACAGGAGAGACTC
KC470214.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470215.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470216.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470217.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470219.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470220.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470221.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470222.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470223.1                      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
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CLUSTAL 2.1 multiple sequence alignment
KC470225.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470226.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470227.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470228.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470230.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470229.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470224.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KX514433.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
KU298886.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
KC470213.1                        ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
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KC470218.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470214.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470215.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470216.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470217.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470219.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470220.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470221.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470222.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470223.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470225.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470226.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470227.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470228.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470230.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470229.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470224.1                        CAACGACGCAGAGAAACACAAGTATAA
KX514433.1                        CAACGACGCAGAGAAACACAAGTATAA
KU298886.1                        CAACGACGCAGAGAAACACAAGTATAA
KC470213.1                        CAACGACGCAGAGAAACACAAGTATAA
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Multiple Sequence Alignment tree
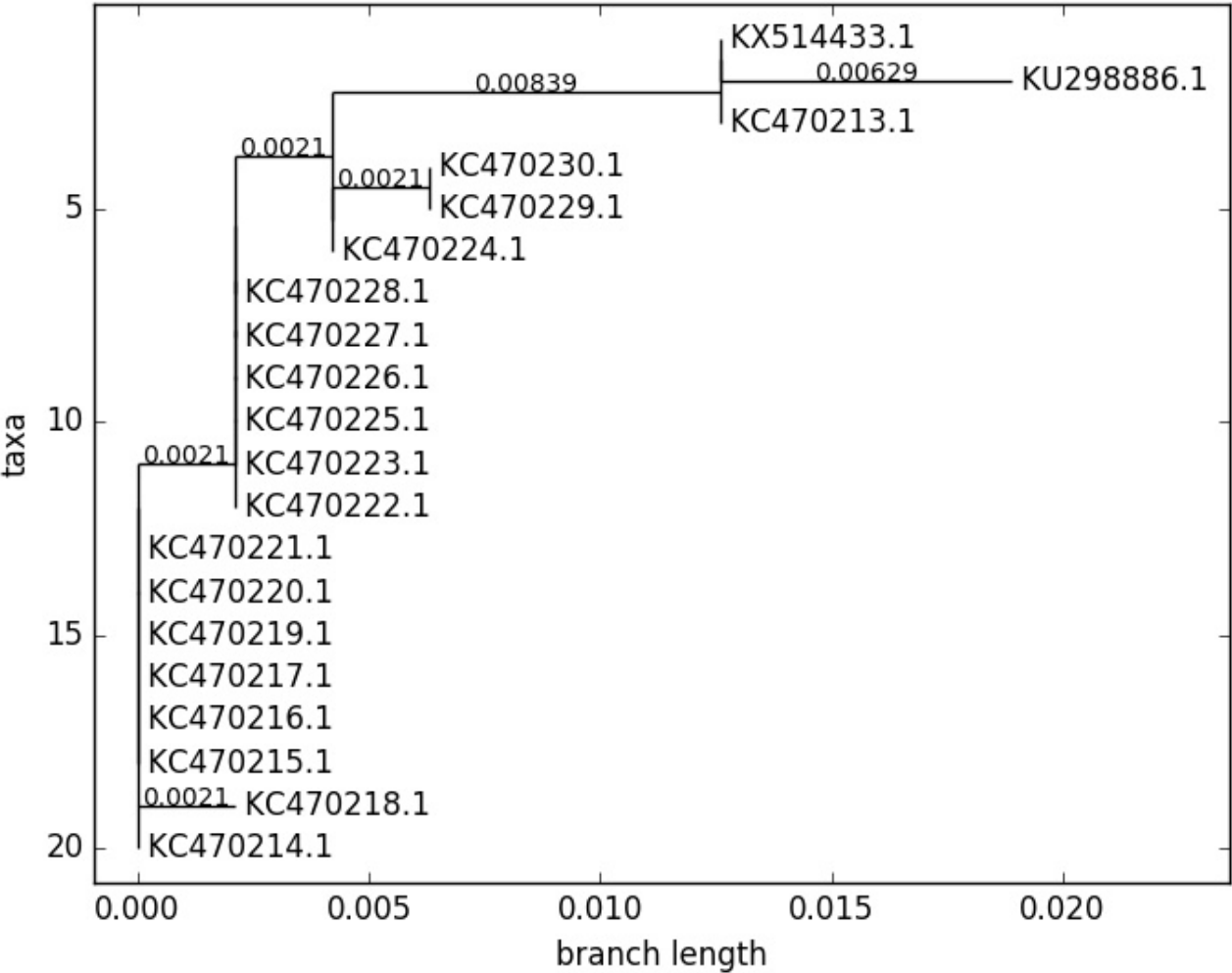
Consensus sequence

ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCTGTGCACGGAACTGAACACTTCACTGCAAGAC
ATAGAAATAACCTGTGTATATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAAGATTTATTTGT
AGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAAATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATT
ATTCAGACTCTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAATTTATTAATAAGGTGCCTGCGG
TGCCAGAAACCGTTGAATCCAGCAGAAAAACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACTA