

# CLUSTAL 2.1 multiple sequence alignment

KC470218.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470214.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470215.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470216.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470217.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470219.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470220.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470221.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470222.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470223.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470225.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470226.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470227.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470228.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470230.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470229.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470224.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KX514433.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KU298886.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
KC470213.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
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KC470218.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470214.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470215.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470216.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470217.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470219.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470220.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470221.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470222.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470223.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470225.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470226.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470227.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470228.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470230.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470229.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470224.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KX514433.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KU298886.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470213.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
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KC470218.1	ATTGCAAGACAGTATTGGAACCTTACAGAGGTATTTGAATTTGCATTCAAA
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# CLUSTAL 2.1 multiple sequence alignment

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

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KC470217.1      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470219.1      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470220.1      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470221.1      ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470222.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470223.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470225.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470226.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470227.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470228.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470230.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470229.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470224.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KX514433.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KU298886.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470213.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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KC470218.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470214.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470215.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470216.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470217.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470219.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470220.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470221.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470222.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470223.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470225.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470226.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470227.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470228.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470230.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470229.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KC470224.1      CTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTTATACAAT
KX514433.1      CTGTGTATGGAGACACATTGAAAACTAACTAACACTGGGTTATACAAT
KU298886.1      CTGTGTATGGAGACACATTGAAAACTAACTAACACTGGGTTATACAAT
KC470213.1      CTGTGTATGGAGACACATTGAAAACTAACTAACACTGGGTTATACAAT
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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

KC470221.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470222.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470223.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470225.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470226.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470227.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470228.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470230.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCATTTGAATCCAGCAGAAAA
KC470229.1	TTATTAATAAGGTGCCTGCGGTGCCAGAAACCATTTGAATCCAGCAGAAAA
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
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KC470221.1	ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470222.1	ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
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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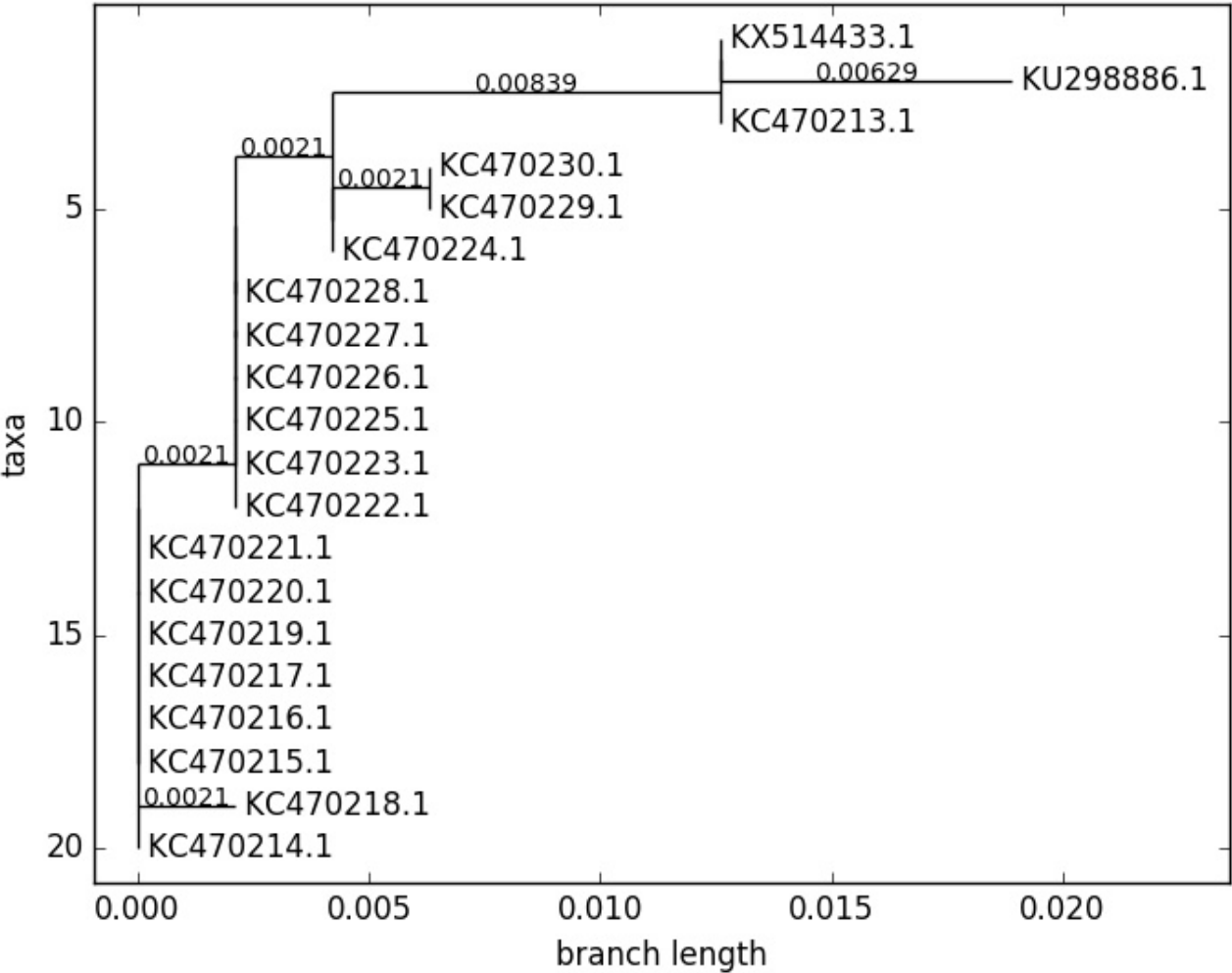
KC470218.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCAAGCACGACAGGAGAGACTC
KC470214.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470215.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470216.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470217.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470219.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470220.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470221.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470222.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470223.1	ATAGAGGCCAGTGCCATTTCGTGCTGCAACCGAGCACGACAGGAGAGACTC

CLUSTAL 2.1 multiple sequence alignment

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KC470225.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470226.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470227.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470228.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470230.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470229.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470224.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KX514433.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAAGACTC
KU298886.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAAGACTC
KC470213.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAAGACTC
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KC470218.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470214.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470215.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470216.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470217.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470219.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470220.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470221.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470222.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470223.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470225.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470226.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470227.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470228.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470230.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470229.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470224.1      CAACGACGCAGAGAAAACACAAGTATAA
KX514433.1      CAACGACGCAGAGAAAACACAAGTATAA
KU298886.1      CAACGACGCAGAGAAAACACAAGTATAA
KC470213.1      CAACGACGCAGAGAAAACACAAGTATAA
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Multiple Sequence Alignment tree



## Consensus sequence

ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCTGTGCACGGAAGTGAACACTTCACTGCAAGAC  
ATAGAAATAACCTGTGTATATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTCAAAGATTTATTTGT  
AGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAAATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATT  
ATTCAGACTCTGTGTATGGAGACACATTAGAAAACTAACTAACACTGGGTATACAATTTATTAATAAGGTGCCTGCGG  
TGCCAGAAACCGTTGAATCCAGCAGAAAACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACTA