

CLUSTAL 2.1 multiple sequence alignment

KC470224.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470223.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470225.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470214.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470215.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470216.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470217.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470218.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470219.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470220.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470221.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470222.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470228.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470227.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470226.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470230.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470229.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KU298886.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470213.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470212.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
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KC470224.1	TCAAAATGAAATTCCGGTTGACCTTTTATGTCACGAGCAATTAAGCGACT
KC470223.1	TCAAAATGAAATTCCGGTTGACCTTTTATGTCACGAGCAATTAAGCGACT
KC470225.1	TCAAAATGACATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470214.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470215.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470216.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470217.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470218.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470219.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470220.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470221.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470222.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470228.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470227.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470226.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470230.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470229.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KU298886.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470213.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470212.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT

KC470224.1	CAGAGGAAGAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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CLUSTAL 2.1 multiple sequence alignment

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KC470223.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470225.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470214.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470215.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470216.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470217.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470218.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470219.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470220.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470221.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470222.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470228.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470227.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470226.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470230.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470229.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KU298886.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470213.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470212.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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KC470223.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470225.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470214.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470215.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470216.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470217.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470218.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470219.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470220.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470221.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470222.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470228.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470227.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470226.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470230.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470229.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KU298886.1      GCCCGACGAGCTGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
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KC470212.1      GCCCGACGAGCTGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
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KC470224.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
KC470223.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
KC470225.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
KC470214.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
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CLUSTAL 2.1 multiple sequence alignment

KC470215.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470216.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470217.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470218.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470219.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470220.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470221.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470222.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470228.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470227.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470226.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470230.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470229.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KU298886.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470213.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470212.1	GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC

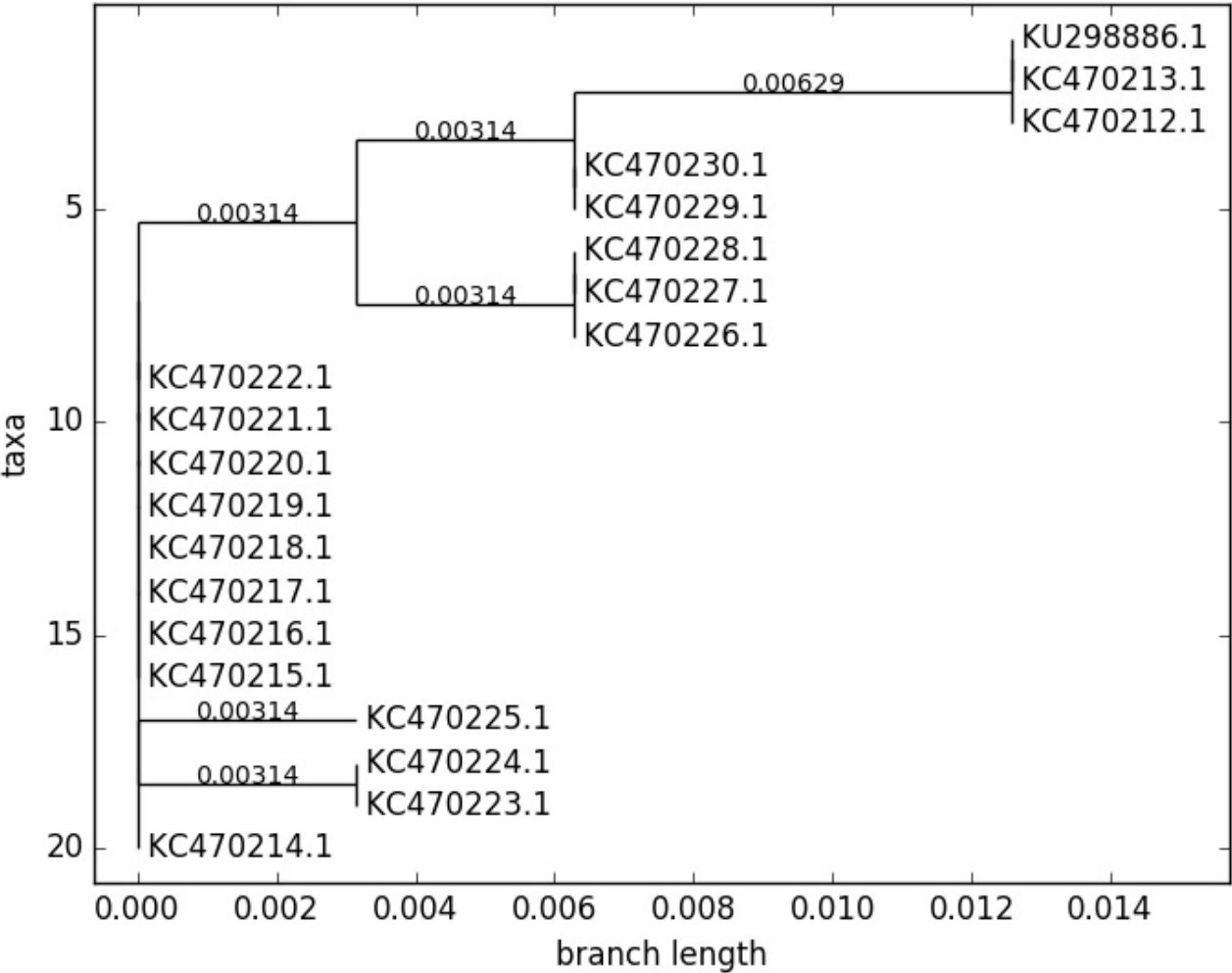
KC470224.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470223.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470225.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470214.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470215.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470216.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470217.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470218.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470219.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470220.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470221.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470222.1	GAGCATTCCAGCAGCTGTTTCTGAGCACCCCTGTCCTTTGTGTGTCCGTGG
KC470228.1	GAGCATTCCAGCAGCTGTTTCTGAAAACCCTGTCCTTTGTGTGTCCGTGG
KC470227.1	GAGCATTCCAGCAGCTGTTTCTGAAAACCCTGTCCTTTGTGTGTCCGTGG
KC470226.1	GAGCATTCCAGCAGCTGTTTCTGAAAACCCTGTCCTTTGTGTGTCCGTGG
KC470230.1	GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KC470229.1	GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KU298886.1	GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KC470213.1	GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KC470212.1	GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG

KC470224.1	TGTGCATCCCAGCAGTAA
KC470223.1	TGTGCATCCCAGCAGTAA
KC470225.1	TGTGCATCCCAGCAGTAA
KC470214.1	TGTGCATCCCAGCAGTAA
KC470215.1	TGTGCATCCCAGCAGTAA
KC470216.1	TGTGCATCCCAGCAGTAA
KC470217.1	TGTGCATCCCAGCAGTAA

CLUSTAL 2.1 multiple sequence alignment

KC470218.1	TGTGCATCCCAGCAGTAA
KC470219.1	TGTGCATCCCAGCAGTAA
KC470220.1	TGTGCATCCCAGCAGTAA
KC470221.1	TGTGCATCCCAGCAGTAA
KC470222.1	TGTGCATCCCAGCAGTAA
KC470228.1	TGTGCATCCCAGCAGTAA
KC470227.1	TGTGCATCCCAGCAGTAA
KC470226.1	TGTGCATCCCAGCAGTAA
KC470230.1	TGTGCATCCCAGCAGTAA
KC470229.1	TGTGCATCCCAGCAGTAA
KU298886.1	TGTGCATCCCAGCAGTAA
KC470213.1	TGTGCATCCCAGCAGTAA
KC470212.1	TGTGCATCCCAGCAGTAA

Multiple Sequence Alignment tree



Consensus sequence

ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCCTCAAAATGAAATTCCGGTTGACCTTCTATGT
CACGAGCAATTAAGCGACTCAGAGGAAGAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCAGCCCGACGAGC
CGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAAGTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAG