

# CLUSTAL 2.1 multiple sequence Alignment

MF288709.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCAGATCT
MF288708.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCAGATCT
MF288713.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288710.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288712.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATTT
MF288711.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATTT
MF288714.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288716.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288715.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288717.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288727.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288726.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288724.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288721.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288720.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288719.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288718.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288725.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288723.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288722.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT

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MF288709.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288708.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288713.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288710.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288712.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288711.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288714.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288716.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288715.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288717.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288727.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288726.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288724.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288721.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288720.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288719.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288718.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288725.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288723.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288722.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT

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MF288709.1	ATTGCAAGACAGTATTGGAACCTTACAGAGGTATTTGAATTTGCATTTAAA
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# CLUSTAL 2.1 multiple sequence Alignment

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MF288708.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288713.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288710.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288712.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288711.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288714.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288716.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288715.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288717.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288727.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288726.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288724.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288721.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288720.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288719.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288718.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288725.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288723.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288722.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
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MF288709.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288708.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288713.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288710.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288712.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288711.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288714.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288716.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288715.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288717.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288727.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288726.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288724.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288721.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288720.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288719.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288718.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288725.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288723.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288722.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
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MF288709.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288708.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288713.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288710.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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# CLUSTAL 2.1 multiple sequence Alignment

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MF288712.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288711.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288714.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288716.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCGGACT
MF288715.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCGGACT
MF288717.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288727.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288726.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288724.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288721.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288720.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288719.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288718.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288725.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288723.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288722.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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MF288709.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288708.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288713.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288710.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288712.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288711.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288714.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288716.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288715.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288717.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288727.1      CTGTGTATGGAGACACATTGGAGAACTAACTAACACTGGGTTATACAAT
MF288726.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288724.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288721.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288720.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288719.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288718.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288725.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288723.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288722.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
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MF288709.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288708.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288713.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288710.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288712.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288711.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288714.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
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# CLUSTAL 2.1 multiple sequence Alignment

MF288716.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288715.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288717.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288727.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288726.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288724.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288721.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288720.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288719.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288718.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288725.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288723.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA  
MF288722.1 TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA

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MF288709.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288708.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288713.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288710.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288712.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288711.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288714.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288716.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288715.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288717.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288727.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288726.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288724.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288721.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288720.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288719.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288718.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288725.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288723.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288722.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT

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MF288709.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288708.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288713.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288710.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288712.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288711.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288714.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288716.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288715.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288717.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC

# CLUSTAL 2.1 multiple sequence Alignment

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MF288727.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288726.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288724.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288721.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288720.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288719.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288718.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288725.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288723.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288722.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
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MF288709.1      CAACGACGCAGAGAAACACAAGTATAA
MF288708.1      CAACGACGCAGAGAAACACAAGTATAA
MF288713.1      CAACGACGCAGAGAAACACAAGTATAA
MF288710.1      CAACGACGCAGAGAAACACAAGTATAA
MF288712.1      CAACGACGCAGAGAAACACAAGTATAA
MF288711.1      CAACGACGCAGAGAAACACAAGTATAA
MF288714.1      CAACGACGCAGAGAAACACAAGTATAA
MF288716.1      CAACGACGCAGAGAAACACAAGTATAA
MF288715.1      CAACGACGCAGAGAAACACAAGTATAA
MF288717.1      CAACGACGCAGAGAAACACAAGTATAA
MF288727.1      CAACGACGCAGAGAAACACAAGTATAA
MF288726.1      CAACGACGCAGAGAAACACAAGTATAA
MF288724.1      CAACGACGCAGAGAAACACAAGTATAA
MF288721.1      CAACGACGCAGAGAAACACAAGTATAA
MF288720.1      CAACGACGCAGAGAAACACAAGTATAA
MF288719.1      CAACGACGCAGAGAAACACAAGTATAA
MF288718.1      CAACGACGCAGAGAAACACAAGTATAA
MF288725.1      CAACGACGCAGAGAAACACAAGTATAA
MF288723.1      CAACGACGCAGAGAAACACAAGTATAA
MF288722.1      CAACGACGCAGAGAAACACAAGTATAA
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### Consensus sequence

>/chido/chido\_E6 Consensus threshold=0.7

ATGGCGCGCTTTGAGGATCCAACACGGCGACCTACAAGCTACCTGATCTGTGCACGGAA  
CTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTATATTGCAAGACAGTATTGGAA  
CTTACAGAGGTATTTGAATTTGCATTTAAAGATTTATTTGTGGTGTATAGAGACAGTATA  
CCGCATGCTGCATGCCATAAATGTATAGATTTTTTATTCTAGAATTAGAGAATTAAGACAT  
TATTCAGACTCTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTATACAAT  
TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAACTTAGACAC  
CTTAATGAAAAACGACGATTXCACAACATAGCTGGGCACTATAGAGGCCAGTGCCATTCG  
TGCTGCAACCGAGCACGACAGGAAXGACTCCAACGACGCAGAGAAACACAAGTATAA