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Program: needle
Rundate: Wed 12 Apr 2017 21:11:51
Commandline: needle
-auto
-stdout
-asequence emboss_needle-I20170412-211150-0698-90736739-pg.asequence
-bsequence emboss_needle-I20170412-211150-0698-90736739-pg.bsequence
-datafile EDNAFULL
-gapopen 10.0
-gapextend 0.5
-endopen 10.0
-endextend 0.5
-aformat3 pair
-snucleotide1
-snucleotide2
Align_format: pair
Report_file: stdout

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#
Aligned_sequences: 2
1: EMBOSS_001
2: EMBOSS_001
Matrix: EDNAFULL
Gap_penalty: 10.0
Extend_penalty: 0.5
#
Length: 316
Identity: 134/316 (42.4%)
Similarity: 134/316 (42.4%)
Gaps: 146/316 (46.2%)
Score: 187.0

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EMBOSS_001 1 ATGGATCTCGG-----AATTCCAGGC--TATGAGATCT 31
EMBOSS_001 1 ATGG---CGGTAGACGAGTGGGTAAATAACT-CAGGCCGTAGGCG---- 41
EMBOSS_001 32 TC--GATCGTCCAATAG-----TCCACCACATG---AA---TCCCATG 66
EMBOSS_001 42 -CAAGATCG--CAA-AGGAGATGTTGC-CCAAAGGGGTAACGGTCCGATG 86
EMBOSS_001 67 ATTG-----CCGACGACATTGTGCACAGCAAC--GATGACAT 101
EMBOSS_001 87 CTGGATCTGCAAGCAGCCCG-----GTGCCAACCAACTGGACCACAT 128
EMBOSS_001 102 ----CCTCAATCCTGAGTACCTTATCCTCGTTTCTCATGAGACTCACAAT 147
EMBOSS_001 129 CAAGCCACGGTCC-AAGTACC-----CAGA 152
EMBOSS_001 148 GCTATTCACTATGGCGA-CGCT--AATCATCTTCCTAG----- 182
EMBOSS_001 153 GCTGATC---TGG-GACCGCTCCAA-CATCGTCCCAGCGCACGACTT 196
EMBOSS_001 183 --AACA--TTGGTTGATCG-----TCGTCCCGGTG-----A 209

EMBOSS_001 197 GCAACAACCTT-GAAGAGCGACGGGGATGGACCCGGGGACTGGGATTCCA 245

EMBOSS_001 210 TACAAAGCTCTGGTAA 225

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EMBOSS_001 246 TTCCGAGGTATGGTGA 261

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