

Alignment: Local DNA homologies.
Parameters: Both strands. Method: FastScan - Max Score

Mol 1 K123000 registry (1-330) Mol 2 K123000 real (1-330)
Number of sequences to align: 2
Settings: Similarity significance value cutoff: >= 60%

Homology Block: Percent Matches 82 Score 110 Length 330

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K123000 regi 1 atggccggccctcatatccaagtgactaccgcgatggggagatacgcgaactcgacgtc
K123000 real 1 .....t..g..t..t.....t..a..t.....g..g.....t

K123000 regi 61 gcagcctccgggttcctgatggaagcccttcgcgacgccaatcgcgagggcgtcgaggcg
K123000 real 61 .....t.....t.....g..g..t.....t..c.....t..t..g.....

K123000 regi 121 atgtgcggcggatgctgctcctgcgcgacctgccacgtctacatcgacgctgctccgcc
K123000 real 121 .....t.....t.....t..t.....t.....t.....t.....g.....a....

K123000 regi 181 gggaccctgccgcccgtctcctccgacgaggagatgctgctttccggcctggtctcgacc
K123000 real 181 ..t.....g..tag....t..a..a.....g.....t..t...

K123000 regi 241 ccgggacggtcgcggtctcctgccaaattccggtcacggccgaactggatggccttaag
K123000 real 241 ..g..c..c..t..t..g..t.....g..c.....a..c..a.....c.....g..a

K123000 regi 301 ctcacgatcccgccggactccaccggttaa
K123000 real 301 ..g..c.....tag.....
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