

Score Expect Identities Gaps Strand Frame
1312 bits(710) 0.0() 714/716(99%) 0/716(0%) Plus/Plus

Features:

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Query 1 AGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAACGCTCGGAAACGGACGCTAATAC 60
|
Sbjct 101 AGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAACGCTCGGAAACGGACGCTAATAC 160

Query 61 CGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCCTGCGCTATCAGATGAGCCT 120
|
Sbjct 161 CGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCCTGCGCTATCAGATGAGCCT 220

Query 121 AGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTACCAAGGCGACGATCCGTAACGGTC 180
|
Sbjct 221 AGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTACCAAGGCGACGATCCGTAACGGTC 280

Query 181 TGAGAGGATGATCAGTCACACTGGAAGTGGAGACACGGTCCAGACTCTACGGGAGGCGAGC 240
|
Sbjct 281 TGAGAGGATGATCAGTCACACTGGAAGTGGAGACACGGTCCAGACTCTACGGGAGGCGAGC 340

Query 241 AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAA 300
|
Sbjct 341 AGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAA 400

Query 301 GGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAGTTACCTAATACGTAATT 360
|
Sbjct 401 GGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAGTTACCTAATACGTAAGT 460

Query 361 GTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATA 420
|
Sbjct 461 GTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATA 520

Query 421 CAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGGTAGGTGGTTCGTTA 480
|
Sbjct 521 CAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGGTAGGTGGTTCGTTA 580

Query 481 AGTTGGATGTGAAATCCCCGGCTCAACCTGGGAACTGCATTCAAAGTGTGCGAGCTAGA 540
|
Sbjct 581 AGTTGGATGTGAAATCCCCGGCTCAACCTGGGAACTGCATTCAAAGTGTGCGAGCTAGA 640

Query 541 GTATGGTAGAGGGTGGTGGAATTTCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGA 600
|
Sbjct 641 GTATGGTAGAGGGTGGTGGAATTTCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGA 700

Query 601 ACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGG 660
|
Sbjct 701 ACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGG 760

Query 661 GAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCC 716
|
Sbjct 761 GAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCC 816
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