

# >Short palindrome Aligment of 2 sequences

Score = 485.0, Identities = 101/107 (94%),  
Positives = 101/107 (94%), Gaps = 4/107 (3%)

Short palindromes F

Short palindrome R (reversed) 12643 T 12643

Short palindrome F 12852 CAGGGTTAAATCATTAGAATAATAAATACTTAATAAGCTTTTTTCTATTATTAATGT 1279.  
A GGGTTAAAT ATTAGAATAATAAATACTTAATAAGCTTTTTTCTATTATTAATGT

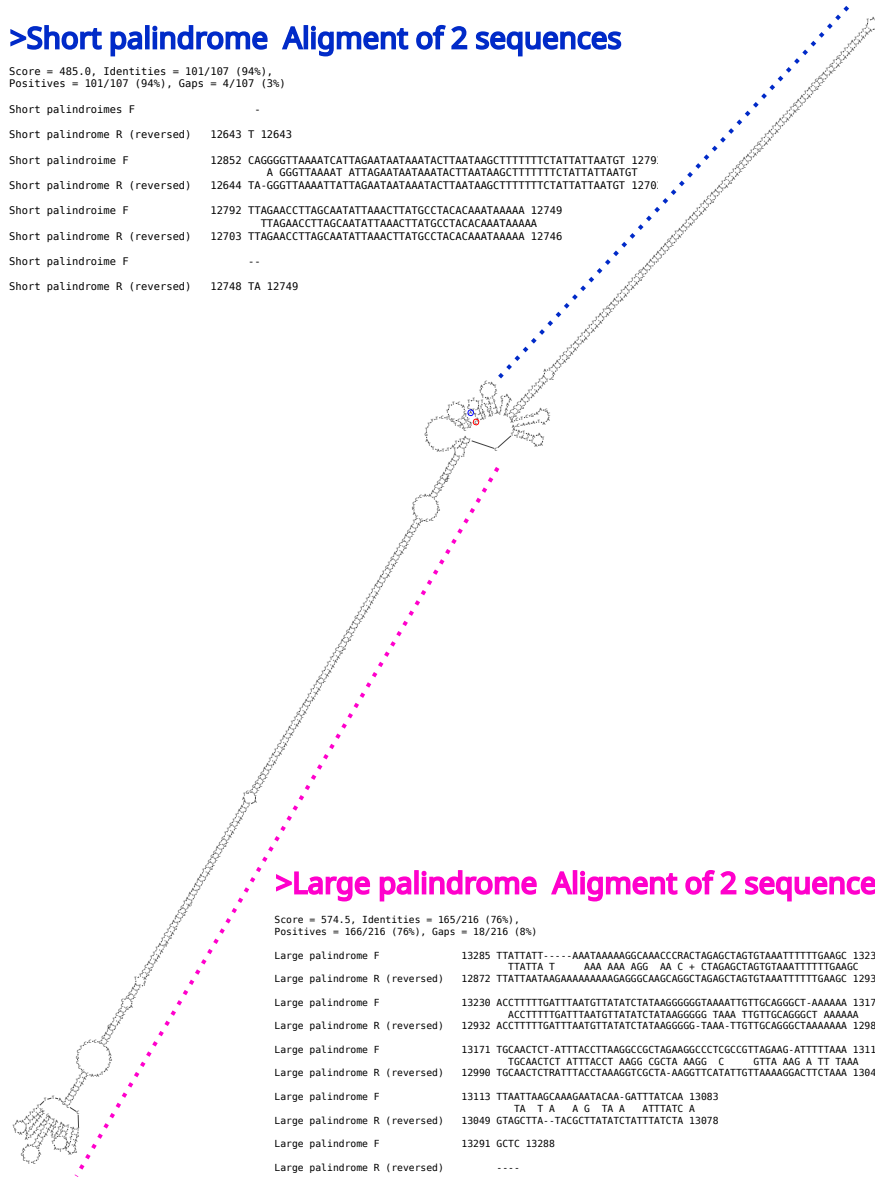
Short palindrome R (reversed) 12644 TA-GGGTTAAATTTAGAATAATAAATACTTAATAAGCTTTTTTCTATTATTAATGT 1270.

Short palindrome F 12792 TTAGAACCTTAGCAATATTAACTTATGCCTACACAAATAAAAA 12749  
TTAGAACCTTAGCAATATTAACTTATGCCTACACAAATAAAAA

Short palindrome R (reversed) 12703 TTAGAACCTTAGCAATATTAACTTATGCCTACACAAATAAAAA 12746

Short palindrome F --

Short palindrome R (reversed) 12748 TA 12749



# >Large palindrome Aligment of 2 sequences

Score = 574.5, Identities = 165/216 (76%),  
Positives = 166/216 (76%), Gaps = 16/216 (8%)

Large palindrome F 13285 TTATTATT-----AAATAAAAAGGCCAACCCRACTAGAGCTAGTGTAAATTTTTTGAAGC 1323  
TTATTA T AAA AAA AGG AA C + CTAGAGCTAGTGTAAATTTTTTGAAGC

Large palindrome R (reversed) 12872 TTATTAATAAGAAAAAAGAGGGCAAGCAGGCTAGAGCTAGTGTAAATTTTTTGAAGC 1293

Large palindrome F 13230 ACCCTTTTGATTAAATGTATATCTATAAGGGGGGTAAATTTGTCAGGGCT-AAAAA 1317.  
ACCTTTTGATTAAATGTATATCTATAAGGGGGT TAAA TTGTCAGGGCT AAAAA

Large palindrome R (reversed) 12932 ACCCTTTTGATTAAATGTATATCTATAAGGGGGT-TAAA-TTGTCAGGGCTAAAAA 1298

Large palindrome F 13171 TGCAACTCT-ATTTACCTTAAGGCGGCTAGAGGCCCTCGCGCTAGAG-ATTTTAAA 1311.  
TGCAACTCT ATTTACCT AAGG CGTA AAGG C GTTA AAG A TT TAAA

Large palindrome R (reversed) 12990 TGCAACTCTATTTACCTTAAGGTCGCTA-AAGGTCATATTGTAAAAGGACTCTTAA 1304

Large palindrome F 13113 TTAATTAAGCAAGAATACAA-GATTTATCAA 13083  
TA A A G TA A ATTTATC A

Large palindrome R (reversed) 13049 GTAGCTTA--TACGCTTATCTATTTATCTA 13078

Large palindrome F 13291 GCTC 13288

Large palindrome R (reversed) ----