

A

&gt;EGFPm\_art2

ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAG  
 CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC  
 GATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC  
 CCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAG  
 CCGTACCCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAA  
 GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC  
 GcGCCGAGGTGAAGTTCGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG  
 GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC  
 ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGG  
 TGAAC TTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGGTGGGTAATA  
 AATCAGATAACAGG TAGCATCATTAGAGCCAGAGCTCTGTCTC A GCTCCTGTTAT  
 CTTCTTTATTCCCAGCTGGCCGACCACTACCAGCAGAACACCCCCATCGGCGAC  
 GGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCA  
 AAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCG  
 CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAA

B

Acceptor (AG) sites. Threshold 0.000 (100%).  
 1 P: 210 W: 4.10 Seq: tacggcgtgcAGtgcttcagcc  
 2 P: 306 W: 0.23 Seq: atcttcttcaAGgacgacggca  
**3 P: 615 W: 12.60 Seq: tttattccccAGctggccgacc**  
 Donor (GT) sites. Threshold 0.079 (100%).  
 1 P: 4 W: 10.02 Seq: -----atgGTgagcaagggc  
 2 P: 67 W: 3.30 Seq: ggacggcgacGTaaacggccac  
 3 P: 337 W: 5.96 Seq: ccgcgccgagGTgaagttcgag  
 4 P: 361 W: 1.90 Seq: cgacaccctgGTgaaccgcatc  
 5 P: 490 W: 6.94 Seq: cggcatcaagGTgaacttcaag  
**6 P: 535 W: 11.28 Seq: cagcgtgcagGTgggtaataaa**  
 7 P: 539 W: 1.34 Seq: gtgcaggtggGTaataaatcag  
 8 P: 558 W: 8.20 Seq: cagataacagGTagcatcatta  
 9 P: 798 W: 4.10 Seq: agctgtacaaGTaa-----

C

Created Mon Mar 1 12:19:48 2021

