Primer3 Output

No mispriming library specified

Using 1-based sequence positions

OLIGO start len tm gc% any 3' seq

LEFT PRIMER 68 20 60.24 55.00 7.00 2.00 TCGCTACTACCGATCGTTCC

RIGHT PRIMER 218 20 59.15 50.00 6.00 2.00 TGCAGGTTCACCTACGGATA

SEQUENCE SIZE: 227

INCLUDED REGION SIZE: 227

PRODUCT SIZE: 151, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 2.00

1 AATTCCCAGTAAGCACGAGTCATCAGCTCGTGTTGATTACGTCCCTGCCCTTTGTACACA

61 CCGCCCGTCGCTACTACCGATCGTTCCAGTTAATGAGCGCCTCGGATTGGTCCCGTAAGC

>>>>>>>>>>>>>>>>>>>>

121 GGATTCGCGTCTGCTCTCTGGCGTGCCGAGAAGATGTGCAAATTATCTGGAATAGAGGAA

181 GTAAAAGTCGTAACAAGGTATCCGTAGGTGAACCTGCAGAAGGATCA

<<<<<<<<<<<<<<<<<<<<

KEYS (in order of precedence):

>>>>>> left primer

<<<<<< right primer

ADDITIONAL OLIGOS

start len tm gc% any 3' seq

1 LEFT PRIMER 68 20 60.24 55.00 7.00 2.00 TCGCTACTACCGATCGTTCC

RIGHT PRIMER 218 21 60.01 52.38 6.00 2.00 TGCAGGTTCACCTACGGATAC

PRODUCT SIZE: 151, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 3.00

2 LEFT PRIMER 37 20 60.49 50.00 4.00 2.00 TTACGTCCCTGCCCTTTGTA

RIGHT PRIMER 218 20 59.15 50.00 6.00 2.00 TGCAGGTTCACCTACGGATA

PRODUCT SIZE: 182, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 2.00

3 LEFT PRIMER 68 20 60.24 55.00 7.00 2.00 TCGCTACTACCGATCGTTCC

RIGHT PRIMER 219 21 60.14 52.38 6.00 2.00 CTGCAGGTTCACCTACGGATA

PRODUCT SIZE: 152, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 2.00

4 LEFT PRIMER 3 20 59.44 50.00 3.00 1.00 TTCCCAGTAAGCACGAGTCA

RIGHT PRIMER 218 20 59.15 50.00 6.00 2.00 TGCAGGTTCACCTACGGATA

PRODUCT SIZE: 216, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 0.00

Statistics

con too in in no tm tm high high high

sid many tar excl bad GC too too any 3' poly end

ered Ns get reg GC% clamp low high compl compl X stab ok

Left 979 0 0 0 0 0 124 658 1 6 0 35 155

Right 1114 0 0 0 0 0 345 528 0 2 0 19 220

Pair Stats:

considered 330, unacceptable product size 322, ok 8

primer3 release 1.1.4

(primer3\_results.cgi release 0.4.0)