Primer3 Output

No mispriming library specified

No hyb oligo mishyb library specified

Using 1-based sequence positions

OLIGO start len tm gc% any 3' seq

LEFT PRIMER 385 20 59.99 50.00 2.00 0.00 AAACGGCTACCACATCCAAG

RIGHT PRIMER 632 20 60.07 55.00 4.00 1.00 GACCCGAGATCCAACTACGA

HYB OLIGO 520 20 59.89 50.00 7.00 3.00 TAACGAGGATCCATTGGAGG

SEQUENCE SIZE: 1770

INCLUDED REGION SIZE: 1770

PRODUCT SIZE: 248, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 2.00

1 AGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTACAAACCTTCACATGGT

61 GAAACTGCGAATGGCTCATTAAATCAGTTATGGTTCCTTAGATCGTACAATCCTACTTGG

121 ATAACTGTGGCAATTCTAGAGCTAATACATGCTACACAGCTCCGACCGTACGGGAAGAGC

181 GCTTTTGTTAGTACAAAACCAATCCGGGCTCCGGTCCGGTCCACTTGGTGACTCTGAACA

241 ACTTTGTGCTGATCGCACGGCCTCGTGCCGGCGACGTATCTTTCAAATGTCTGCCCTATC

301 AACTGTCGATGGTACGTGATATGCCTACCATGGTTTTCACGGGTAACGGGGAATCAGGGT

361 TCGATTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCG

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421 CAAATTACCCACTCCTGACACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTT

481 CGAGGCCCCGTAATTGGAATGAGTACACTTTAAATCCTTTAACGAGGATCCATTGGAGGG

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541 CAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTTG

601 CAGTTAAAAAGCTCGTAGTTGGATCTCGGGTCCAGGCTTGCGGTCCGCCTCGCGGCGGTT

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

661 ACTGCTCGTCCTGACCTACCTCCCGGTGTGTCCCTTGGTGCTCTTGATTGAGTGTCTCGG

721 GCGGCCGGAACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCGTGTCGCCTGAAT

781 AATGGTGCATGGAATGATGGAATAGGACCTCGGTTCTATTTTGTTGGTTTTCGGAACTCG

841 AGGTAATGATTAAGAGGGACTGACGGGGGCATTCGTATTGCGGTGTTAGAGGTGAAATTC

901 TTGGATCGCCGCAAGACGAACTACAGCGAAAGCATTTGCCAAGCATGTTTTCATTAATCA

961 AGAACGAAAGTCAGAGGTTCGAAGACGATCAGATACCGTCGTAGTTCTGACCATAAACGA

1021 TGCCAACTGGCGATCCGCCGGAGTTGCTTCAATGACTCGGCGGGCAGCCTCCGGGAAACC

1081 AAAGTTTTTGGGTTCCGGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGG

1141 AAGGGCACCACCAGGAGTGGAGCCTGTGGCTTAATTTGACTCAACACGGGAAAACTCACC

1201 CGGCCCGGACACTGCAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCGGTGGGTGGTG

1261 GTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGATAACGAACGAG

1321 ACTCTAGCCTGCTAAATAGTTCGAGGATCCTCTTATGCGTCCTCGCCAACTTCTTAGAGG

1381 GACAAGTGGCGTTTAGCCACACGAGATTGAGCAATAACAGGTCTGTGATGCCCTTAGATG

1441 TTCGGGGCCGCACACGCGCTACACTGAATGCATCAGCGTGCGTCTACTCTTGCCCGAGAG

1501 GGCTGGGAAACCCGTTGAACCGCATTCGTGCTAGGGATTGGGGCTTGTAATTCTTCCCCA

1561 TGAACGAGGAATTCCCAGTAAGCACGAGTCATCAGCTCGTGTTGATTACGTCCCTGCCCT

1621 TTGTACACACCGCCCGTCGCTACTACCGATCGTTCCAGTTAATGAGCGCCTCGGATTGGT

1681 CCCGTAAGCGGATTCGCGTCTGCTCTCTGGCGTGCCGAGAAGATGTGCAAATTATCTGGA

1741 ATAGAGGAAGTAAAAGTCGTAACAAGGTAT