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