

## pCC1™ / pEpiFOS™-5 Sequencing Primers

Cat. Nos. F5FP010 and F5RP011

### **pCC1 / pEpiFOS-5 Forward Sequencing Primer**

**5' - GGATGTGCTGCAAGGCGATTAAGTTGG - 3'**

#### **Product Specifications**

**Storage:** Store at -20°C.

**Concentration:** 1 nmol @ 50 µM ..... 20 µl

in TE Buffer (10 mM Tris-HCl [pH 7.5], 1 mM EDTA).

**Length:** 27 nucleotides

**G+C content:** 14

**Molecular Weight:** 8,409 daltons

#### **Temperatures of Dissociation & Melting:**

$T_d$ : 79°C (nearest neighbor method)

$T_m$ : 78°C (% G+C method)

$T_m$ : 82°C ([2 (A+T) + 4 (G+C)] method)

$T_m$ : 68°C ((81.5 + 16.6 (log [Na<sup>+</sup>])) +  
([41 (#G+C) - 500] / length) method)  
where [Na<sup>+</sup>] = 0.1 M

**pCC1 / pEpiFOS-5 Reverse Sequencing Primer**

**5' - CTCGTATGTTGTGTGGAATTGTGAGC - 3'**

**Product Specifications**

**Storage:** Store at -20°C.

**Concentration:** 1 nmol @ 50 µM ..... 20 µl

in TE Buffer (10 mM Tris-HCl [pH 7.5], 1 mM EDTA).

**Length:** 26 nucleotides

**G+C content:** 12

**Molecular Weight:** 8,038 daltons

**Temperatures of Dissociation & Melting:**

$T_d$ : 71°C (nearest neighbor method)

$T_m$ : 75°C (% G+C method)

$T_m$ : 76°C ([2 (A+T) + 4 (G+C)] method)

$T_m$ : 65°C ((81.5 + 16.6 (log [Na<sup>+</sup>])) +  
([41 (#G+C) - 500] / length) method)  
where [Na<sup>+</sup>] = 0.1 M

**Quality Control:** The primers are function-tested in a DNA cycle sequencing reaction using the SequiTherm EXCEL™ II DNA Sequencing Kit and the pCC1 or pEpiFOS-5 vector as template.

**Related Products:** The following products are also available:

- CopyControl™ Fosmid Library Production Kits
- EpiFOS™ Fosmid Library Production Kit
- SequiTherm EXCEL™ II DNA Sequencing Kits

**Orientation for Fosmid End-Sequencing:** The following is the nucleotide sequence of pCC1FOS and pEpiFOS-5 (bases 230-501) from the pCC1/pEpiFOS Forward Sequencing Primer (230-256) to the pCC1/pEpiFOS Reverse Sequencing Primer (501-476) encompassing the T7 RNA polymerase promoter (311-330) and the *Eco*72 I site (359-364).

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230 GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC
280 ACGACGTTGT AAAACGACGG CCAGTGAATT GTAATACGAC TCACTATAGG
330 GCGAATTCGA GCTCGGTACC CGGGGATCCC ACGTGGGATC CTCTAGAGTC
380 GACCTGCAGG CATGCAAGCT TGAGTATTCT ATAGTGTAC CTAATAGCT
430 TGGCGTAATC ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC
480 ACAATTCAC ACAACATACG AG

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