

pIndigoBAC-5 Sequencing Primers

Cat. Nos. BFP0701 and BRP0801

DISCONTINUED

Related Products: The following products are also available:

- pIndigoBAC-5 (*Bam*H I-Cloning Ready)
- pIndigoBAC-5 (*Hind* III-Cloning Ready)
- SequiTherm EXCEL™ II DNA Sequencing Kits

pIndigoBAC-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⁺])) +
([41 (#G+C) - 500] / length) method)

where [Na⁺] = 0.1 M

pIndigoBAC-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 ($(81.5 + 16.6(\log [\text{Na}^+])) +$
 $([41(\#G+C) - 500] / \text{length})$ method)

where $[\text{Na}^+] = 0.1 \text{ M}$

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

Orientation for BAC End-Sequencing: The following is the nucleotide sequence of pIndigoBAC-5 (bases 230-489) from the pIndigoBAC-5 Forward Sequencing Primer (230-256) to the pIndigoBAC-5 Reverse Sequencing Primer (489-464) encompassing the T7 RNA polymerase promoter (311-330), the *Bam*H I site (353-358) and the *Hind* III site (383-388).

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230 GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC
280 ACGACGTTGT AAAACGACGG CCAGTGAATT GTAATACGAC TCACTATAGG
330 GCGAATTCGA GCTCGGTACC CGGGGATCCT CTAGAGTCGA CCTGCAGGCA
380 TGCAAAGCTTG AGTATTCTAT AGTCTCACCT AAATAGCTTG GCGTAATCAT
430 GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC
480 AACATACGAG

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