## IκBα Dominant-Negative Vector Set Information



Map of pCMV-I $\kappa$ B $\alpha$  and pCMV-I $\kappa$ B $\alpha$ M Vectors. All restriction sites shown are unique.

## Description

The IkBa Dominant-Negative Vector Set consists of two vectors, pCMV-IkBa and pCMV-IkBaM. These vectors are convenient tools for examining NFkB regulation by manipulating its inhibitor, IkBa. In uninduced cells, IkBa binds NFkB and inhibits its activation by preventing NFkB from translocating to the nucleus. However, upon activation of NFkB by agents likeTNF, IkBa can be phosphorylated, thus leading to the disassociation of IkBa from NFkB. pCMV-IkBaM contains two mutations that prevent this phosphorylation step; therefore, cells expressing IkBaM block the NFkB pathway (1–3). The IkBa gene and IkBaM gene differ by serine to alanine mutations at residues 32 and 36 (1). Both proteins are expressed at high levels from the constitutive CMV promoter.

The SV40 polyadenylation sequence directs proper processing of the 3' end of the mRNAs. The vector backbone contains an SV40 origin for replication in mammalian cells expressing the SV40T antigen. A neomycin-resistance cassette (Neo')—consisting of the SV40 early promoter, the Tn5 neomycin/kanamycin resistance gene, and polyadenylation signals from the Herpes simplex virus thymidine kinase (HSVTK) gene—allows kanamycin selection in *E. coli* and neomycin selection in eukaryotic cells. The vector backbone also provides a pUC origin of replication for propagation in *E. coli* and an f1 origin for single-stranded DNA production.



Clon**tech** 

United States/Canada 800.662.2566 Asia Pacific +1.650.919.7300 Europe +33.(0)1.3904.6880 Japan +81.(0)77.543.6116

Clontech Laboratories, Inc. ATakara Bio Company 1290 Terra Bella Ave. Mountain View, CA 94043 Technical Support (US) E-mail: tech@clontech.com www.clontech.com

## Use

pCMV-I $\kappa$ B $\alpha$  can be used to screen drug candidates for their effects on NF $\kappa$ B pathway or to study the involvement of upstream kinases which precede I $\kappa$ B $\alpha$  degradation. I $\kappa$ B $\alpha$  overexpression eliminates any low-level stimulation produced from the culture medium, and ensures that any NF $\kappa$ B stimulation measured is due to the agent you are testing. pCMV-I $\kappa$ B $\alpha$ M can be used to "knock down" expression of endogenous I $\kappa$ B $\alpha$  or block NF $\kappa$ B signaling in a particular cell line.

In conjunction with one of our NF $\kappa$ B *cis*-acting reporter vectors, such as pNF $\kappa$ B-SEAP, pNF $\kappa$ B-Luc, or pNF $\kappa$ B-d2EGFP (Cat. Nos. 631905, 631904, and 631803, resp.), you can measure the activation of NF $\kappa$ B in your system by measuring the expression of the reporter gene (4). For more information about our Signal Transduction Vectors, visit our web site at www.clontech. com

Both vectors can be transfected into mammalian cells using any standard method. Stable transformants can be selected using G418 (5).

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Note:The following list of features is based on the pCMV-I $\kappa$ B $\alpha$  Vector. pCMV-I $\kappa$ B $\alpha$ M differs from pCMV-I $\kappa$ B $\alpha$  by two mutations at residues 32 & 36 of I $\kappa$ B $\alpha$ . Due to different subcloning parameters, the pCMV-I $\kappa$ B $\alpha$ M Vector is 30 bp smaller than pCMV-I $\kappa$ B $\alpha$ .

Location of features\*

- Human cytomegalovirus (CMV) immediate early promoter: 1–589 Enhancer region: 59–465; TATA box: 554–560 Transcription start point: 583 C→G mutation to remove Sac I site: 569
- $I \kappa B \alpha$  gene: Start codon (ATG): 613–615; stop codon: 1564–1566
- $I\kappa B\alpha M$  only: Start codon (ATG): 584–586; stop codon: 1535–1537
- AG $\rightarrow$ GC (Ser $\rightarrow$ Ala) mutation: 677 & 678;T $\rightarrow$ G (Ser $\rightarrow$ Ala) mutation: 689
- SV40 early mRNA polyadenylation signal
  - Polyadenylation signals: 1727–1731 & 1756–1760; mRNA 3' ends: 1765 & 1777
- f1 single-strand DNA origin: 1824–2279 (Packages the noncoding strand of  $I\kappa B\alpha$  or  $I\kappa B\alpha M$ .)
- Bacterial promoter for expression of Kan<sup>r</sup> gene: -35 region: 2341–2346; -10 region: 2364–2369
  - Transcription start point: 2376
- SV40 origin of replication: 2620–2697
- SV40 early promoter
  - Enhancer (72-bp tandem repeats): 2453–2524 & 2525–2598 21-bp repeats: 2600–2620, 2621–2641 & 2643–2663 Early promoter element: 2676–2682 Major transcription start points: 2672, 2710, 2716 & 2721
- Kanamycin/neomycin resistance gene
  - Neomycin phosphotransferase coding sequences: start codon (ATG): 2804–2806; stop codon: 3596–3598
    - $G \rightarrow A$  mutation to remove *Pst* I site: 2986
  - $C \rightarrow A$  (Arg to Ser) mutation to remove *Bss*H II site: 3332
- Herpes simplex virus (HSV) thymidine kinase (TK) polyadenylation signal
- Polyadenylation signals: 3834–3839 & 3847–3852
- pUC plasmid replication origin: 4188–4826

\*All numbers are correct for pCMV-I $\kappa$ B $\alpha$ . For pCMV-I $\kappa$ B $\alpha$ M, add 1 bp for all sequence numbers after nucleotide number 593.

Propagation in E. coli

- Suitable host strains: DH5α, HB101 and other general purpose strains. Single-stranded DNA production requires a host containing an F plasmid such as JM101 or XL1-Blue.
- Selectable marker: plasmid confers resistance to kanamycin (50 µg/ml) to *E. coli* hosts.
- E. coli replication origin: pUC
- Copy number: ~500
- Plasmid incompatibility group: pMB1/CoIE1

References

- 1. Feig, B., et al. (1999) Surgery 126:399–405.
- 2. Brown, K., et al. (1995) Science 267:1485–1491.
- 3. Chen, Z. J., et al. (1995) Genes Devel. 9:1586–1597.
- 4. Mercury IκBα Dominant-Negative Vector Set (January 2000) *Clontechniques* XV(1):18–19.
- 5. Gorman, C. (1985) In DNA cloning: A practical approach, Vol. II. Ed. D.M. Glover. (IRL Press, Oxford, UK) pp. 143–190.

Note: The attached sequence file has been compiled from information in the sequence databases, published literature, and other sources, together with partial sequences obtained by Clontech. This vector has not been completely sequenced.

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