

# pDRIVE-rEF1 $\alpha$ /RU5'

A plasmid with a composite promoter consisting of the rat Elongation Factor-1 alpha and HTLV 5' UTR

Catalog # pdrive-ref1ru5

## For research use only

Version # 05B15-SV

## PRODUCT INFORMATION

### Content:

- 1 disk of lyophilized GT100 *E. coli* bacteria transformed by pDRIVE-rEF1 $\alpha$ /RU5'.
- GT100 genotype is: *F-*, *mcrA*,  $\Delta(mrr-hsdRMS-mcrBC)$ ,  $\emptyset 80lacZ\Delta M15$ ,  $\Delta lacX74$ , *recA1*, *endA1*.
- 4 pouches of *E. coli* Fast-Media® Zeo

### Shipping and storage:

- Products are shipped at room temperature.
- Transformed bacteria should be stored at -20°C. Bacteria are stable up to one year when properly stored.
- Store *E. coli* Fast-Media® Zeo at room temperature. Fast-Media® pouches are stable 18 months when stored properly.

### Quality control:

- Plasmid construct has been confirmed by restriction analysis and sequencing.
- Bacteria have been lyophilized, and their viability upon resuspension has been verified.
- Promoter activity has been confirmed by transient transfection of 293 cells as well as other selected cell lines.

## GENERAL PRODUCT USE

pDRIVE is an expression plasmid containing a native or composite promoter of interest. pDRIVE may be used to:

**Subclone a promoter of interest into another vector:** Unique restriction sites are present at each end of the promoter allowing convenient excision. The 5' sites include *Sda* I, *Pst* I, and *Spe* I. *Sda* I is compatible with *Nsi* I and *Pst* I. *Spe* I is compatible with *Avr* II, *Nhe* I and *Xba* I. The 3' restriction site is *Nco* I which includes the ATG start codon, and is compatible with *BspH* I, *Afl* III, *Pci* I and *Sty* I.

**Compare the activity of different promoters** in transient transfection experiments. Each pDRIVE promoter drives the expression of the *LacZ* reporter gene which allows for testing of the promoter's activity in transient transfection experiments. Furthermore, the *LacZ* gene is flanked by unique restriction sites (*Nco* I and *EcoR* I) for easy replacement with a different gene of interest.

## PROMOTER CHARACTERISTICS

Element	Name	Origin	Size bp
Promoter	EF-1 $\alpha$	Rat	349
5'UTR	HTLV	Viral	267
Enhancer	-	-	-

### **EF-1 $\alpha$ promoter**

The EF-1 alpha gene encodes for elongation factor-1 alpha which is one of the most abundant proteins in eukaryotic cells and is expressed in almost all kinds of mammalian cells. The promoter of this "housekeeping" gene exhibits a strong activity, higher than viral promoters such as SV40 and RSV promoters<sup>1</sup>, and on the contrary to the CMV promoter, yields persistent expression of the transgene *in vivo*<sup>2</sup>. The rat EF-1 $\alpha$  promoter shares a 45.05% homology to the human EF-1 $\alpha$  promoter.

### **HTLV R-U5' UTR**

The R segment and part of the U5 sequence (R-U5') of the HTLV Type 1 Long Terminal Repeat<sup>3</sup> has been coupled to the EF-1 $\alpha$  promoter to enhance stability of DNA and RNA. This modification not only increases steady state transcription, but also significantly increases translation efficiency possibly through mRNA stabilization.

## PLASMID FEATURES

- **LacZ gene** encodes  $\beta$ -galactosidase an enzyme that catalyzes the hydrolysis of X-Gal, producing a blue precipitate that can be easily visualized under a microscope.
- **SV40 pAn:** The Simian Virus 40 late polyadenylation signal enables efficient cleavage and polyadenylation reactions resulting in high levels of steady-state mRNA.
- **pMB1 Ori** is a minimal *E. coli* origin of replication with the same activity as the longer Ori.
- **EM7** is a bacterial promoter that enables the constitutive expression of the antibiotic resistance gene in *E. coli*.
- **Sh ble** gene confers zeocin resistance therefore allowing the selection of transformed *E. coli* carrying a pDRIVE plasmid.

**Note:** Stable transfection of clones cannot be performed due to the absence of an eukaryotic promoter upstream of the *Sh ble* gene.

## METHODS

### Growth of pDRIVE-transformed bacteria:

Use sterile conditions to do the following:

- 1- Resuspend the lyophilized *E. coli* by adding 1 ml of LB medium in the tube containing the disk. Let sit for 5 minutes. Mix gently by inverting the tube several times.
- 2- Streak bacteria taken from this suspension on a zeocin LB agar plate prepared with the *E. coli* Fast-Media® Zeo agar provided (see below).
- 3- Place the plate in an incubator at 37°C overnight.
- 4- Isolate a single colony and grow the bacteria in TB supplemented with zeocin using the Fast-Media® Zeo liquid provided (see below).
- 5- Extract the pDRIVE plasmid DNA using the method of your choice.

**Note:** For long-term storage of the pDRIVE-transformed bacteria, prepare a 20% glycerol stock of the bacteria grown in the overnight liquid culture and freeze at -80°C.

### Selection of bacteria with *E. coli* Fast-Media Zeo:

*E. coli* Fast-Media® Zeo is a new, fast and convenient way to prepare liquid and solid media for bacterial culture by using only a microwave. *E. coli* Fast-Media® Zeo is a TB (liquid) or LB (solid) based medium with zeocin, and contains stabilizers.

*E. coli* Fast-Media® Zeo can be ordered separately (catalog code # fas-zn-l, fas-zn-s).

### Method:

- 1- Pour the contents of a pouch into a clean borosilicate glass bottle or flask.
- 2- Add 200 ml of distilled water to the flask
- 3- Heat in a microwave on MEDIUM power setting (about 400Watts), until bubbles start appearing (approximately 3 minutes). **Do not heat a closed container. Do not autoclave Fast-Media®.**
- 4- Swirl gently to mix the preparation. **Be careful, the bottle and media are hot, use heatproof pads or gloves and care when handling.**
- 5- Reheat the media for 30 seconds and gently swirl again. Repeat as necessary to completely dissolve the powder into solution. But be careful to avoid overboiling and volume loss.
- 6- Let agar medium cool to 45°C before pouring plates. Let liquid media cool to 37°C before seeding bacteria.

**Note:** Do not reheat solidified Fast-Media® as the antibiotic will be permanently destroyed by the procedure.

### References:

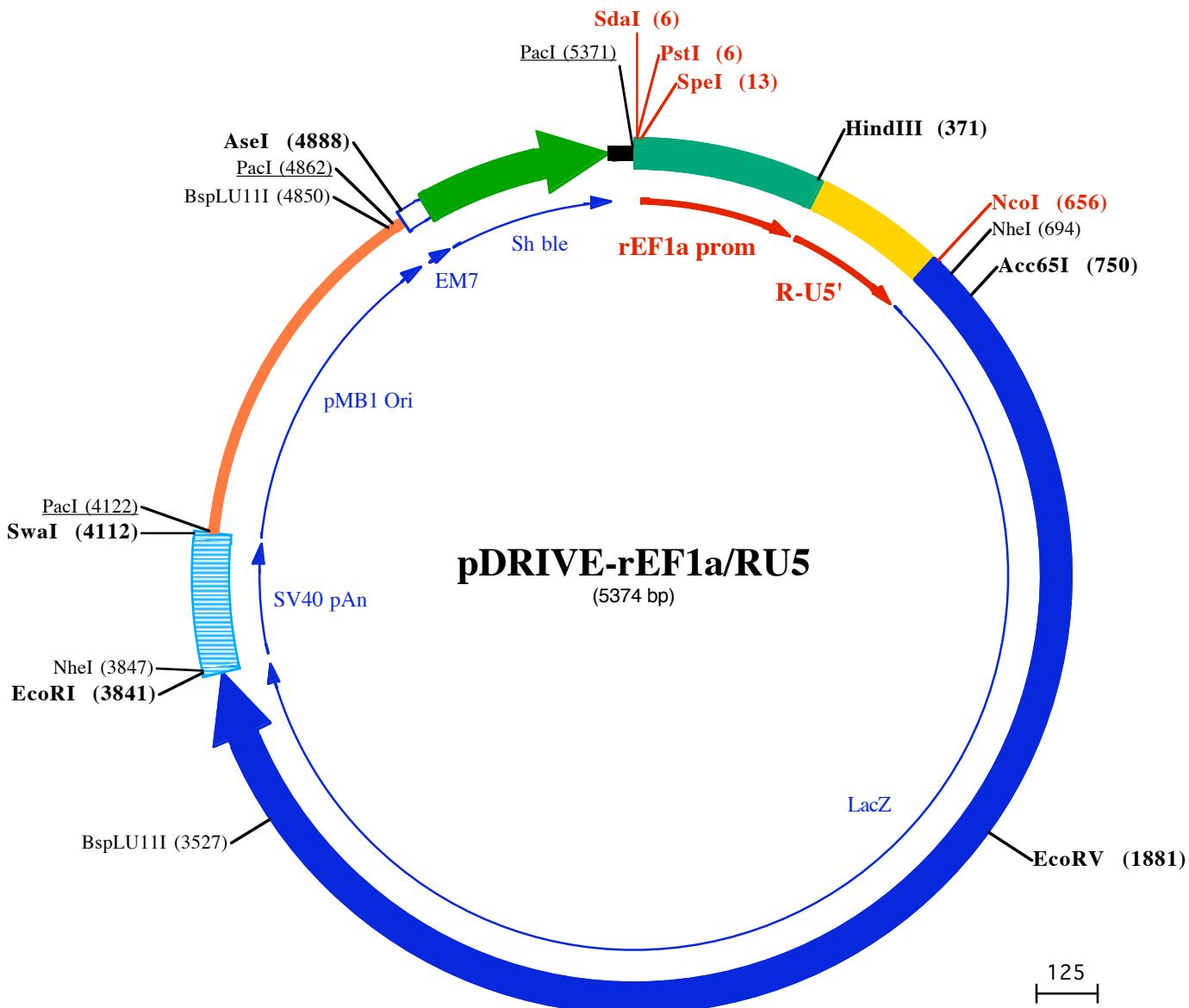
- 1- Kim DW *et al.* (1990). Gene. 91(2): 217-23.
- 2- Guo ZS *et al.* (1996). Gene Ther. 3(9):802-10
- 3- Takebe *et al* (1988). Mol. Cell Biol. 1: 466-472

## TECHNICAL SUPPORT

Toll free (US): 888-457-5873  
Outside US: (+1) 858-457-5873  
E-mail: info@invivogen.com  
Website: www.invivogen.com

**InvivoGen™**

3950 Sorrento Valley Blvd. Suite A  
San Diego, CA 92121 - USA



**PstI (6)**  
**SdaI (6)**      **SpeI (13)**

1 CCTGCAGGGCCCACTAGTGGAGCCGAGAGTAATTACACAAAGGAGGGATGCCCTCGCAAGGGGAGAGCCCAGGGACCCTCAAATTCTCACAGAC

101 CCAAATCCCTGTAGCCGCCAACGACAGCGCGAGGAGCATGCGCCAGGGCTGAGCGCGGGTAGATCAGAGCACACAAGCTCACAGTCCCCGGCGTGGG

201 GGGAGGGGCCGCTGAGCGGGGCCAGGGAGCTGGCGGGCAAACCTGGAAAGTGGTGTGCTGGCTCCGCCCTTCCCAGGGTGGGGAGA

**HindIII (371)**

301 ACGGTATAAGTCGGTAGTCCTGGACGTTCTTCGAACGGTTGCCAGAACGCCAGCTGAAGCTCGAGGGGCTCGATCTCTCTTC

401 CGCGCCCGCCCTACCTGAGGCCATCCACGCCGGTAGTCGCGTTCTGCCGCCCTCCGCCCTGTTGCTGAACCTGCGTCCGCCGCTAGG

501 TAAGTTAAAGCTCAGTCAGGCGAGACCGGGCTTGTCGGCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCCACGCTTGCCTGACCCCTGCTGC

**NcoI (656)**  
**Acc65I (750)**  
**NeI (694)**

601 TCAACTCTACGTCTTGTTCGTTCTGTCGCCGTTACAGATCAAGGCCCATGGGGGTTCTCATCATCATCATCATGGTATGGCTAGCA  
 1► Met Gl y Gl y Ser Hi s Hi s Hi s Hi s Hi s Hi s Gl y Me t Al a Ser M

701 TGACTGGTGACAGCAAATGGTCGGGATCTGTACGACGATGACGATAAGGATACCTAAGGATCAGCTGGAGTTGATCCCCTGCTTTAACACGTCGTA  
 15► et Thr Gl y Gl y Gl n Met Gl y Arg Asp Leu Tyr Asp Asp Asp Lys Val Pro Lys Asp Gl n Leu Gl y Val Pro Val Val Leu Gl n Arg Arg As  
 801 CTGGGAAACCCCTGGCTTACCCA ACTTAATGCCCTGACGACATCCCCCTTCCGAGCTGGCTAATAGCGAAGAGGCCGACCGATGCCCTTC  
 48► p Trp Gl u Asn Pro Gl y Val Thr Gl n Leu Asn Arg Leu Al a Al a Hi s Pro Pro Phe Al a Ser Trp Arg Asn Ser Gl u Gl u Al a Arg Thr Asp Arg Pro Ser  
 901 CAACAGTTGCGCAGCCTGAATGGCAATGGCCTTGCCTGGTCCGGACCAGAAGCGGTGCGGAAAGCTGGCTGGAGTGGCGATCTCCTGAGGCCG  
 82► Gl n Gl n Leu Arg Ser Leu Asn Gl y Gl u Trp Arg Phe Al a Trp Phe Pro Al a Pro Gl u Al a Val Pro Gl u Ser Trp Leu Gl u Cys Asp Leu Pro Gl u Al a a  
 1001 ATACTGTCGTCGCCCCCTCAAACCTGGCAGATCACGGTTACAGATGCCCATCTACACCAACGTAACCTATCCATTACGGTCAATGCCGTTGTTCC  
 115► sp Th Val Val Val Pro Ser Asn Trp Gl n Met Hi s Gl y Tyr Asp Al a Prol i e Tyr Th Val Asn Pro Pro Phe Val Pr  
 1101 CACGGAGAATCCGACGGGTTACTCGCTCACATTAAATGTTGATGAAAGCTGGTACAGGAAGGCCGACGCCAATTATTTGATGGCTTAACTCG  
 148► o Thr Gl u Asn Pro Thr Gl y Cys Tyr Ser Leu Thr Phe Asn Val Asp Gl u Ser Trp Leu Gl n Gl u Gl y Gl n Thr Arg I l e l e Phe Asp Gl y Val Asn Ser  
 1201 GCGTTTCATCTGTTGTCACGGGCGCTGGGTCGGTACGCCAGGGCAGCTGGCTGCTGAATTGACCTGAGCGCATTTCACGCCGAGGAAA  
 182► Al a Phe Hi s Leu Trp Cys Asn Gl y Arg Trp Val Gl y Tyr Gl y Gl n Asp Ser Arg Leu Pro Ser Gl u Phe Asp Leu Ser Al a Phe Leu Arg Al a Gl y Gl u a  
 1301 ACCGCCTCGCGGTATGGTGTGCTGGAGTACGGCAGTTCTGGAAAGATCAGGATATGTGGCGGTAGGGCCATTTCGTCAGTCTCGTGT  
 215► sn Arg Leu Al a Val Met Val Leu Arg Trp Ser Asp Gl y Ser Tyr Leu Gl u Asp Gl u Asp Met Trp Arg Met Ser Gl y l e Phe Arg Asp Val Ser Leu Le  
 1401 GCATAAACCGACTACACAAATCAGCGATTCCATGTTGCACTCGCTTAATGATGATTTCAGCCGGCTGTACTGGAGGCTGAAGTTCAGATGTGCGGC  
 248► u Hi s Lys Pro Trh Gl n l e Ser Asp Phe Hi s Val Al a Thr Arg Phe Asn Asp Phe Ser Arg Al a Val Leu Gl u Al a Gl u Val Gl n Met Cys Gl y  
 1501 GAGTTGGTGTACTACCTACGGTACAGGTTCTTATGGCAGGGTAAACCGCAGGGCAGCGCAGCGCCTTCGGCGTGAAATTATCGATGAGC  
 282► Gl u Leu Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gl n Gl y Gl u Thri Gl n Val Al a Ser Gl y Thri Al a Pro Phe Gl y Gl u l e l e Asp Gl u A  
 1601 GTGGTGGTTATGCCGATCGCTCACACTACGTCTGAACGTCGAAAACCGAAACTGTGGAGGCCGAATCCGAATCTATCGTGGTGTGA  
 315► r Gl y Gl y Tyr Al a Asp Arg Val Thr Leu Arg Leu Asn Val Gl u Asn Pro Lys Leu Trp Ser Al a Gl u l e Pro Asn Leu Tyr Arg Al a Val Val Gl u Le  
 1701 GCACACCCCGACGGCACGCTGATTGAAGCAGAACGCTCGGATGTCGGTTCCGAGGTGGATTGAAATTGGTCTGCTGCTGAACGCCAAGCCG  
 348► u Hi s Thr Al a Asp Gl y Thr Leu l e Gl u Al a Gl u Al a Cys Asp Val Gl y Phe Arg Gl u Val Arg l e Gl u Asn Gl y Leu Leu Asn Gl y Lys Pro

**EcoRV (1881)**

1801 TTGCTATTCGAGGCCAACCGTCACGAGCATCCTCTGCATGGTCAGGTATGGATGAGCAGACGATGGTCAGGATATCTGCTGATGAAGCAGA  
 382► Leu Leu l e Arg Gl y Val l Asn Arg Hi s Gl u Hi s Hi s Pro Leu Hi s Gl y Gl n Val Met Asp Gl u Gl n Thr Met Val Gl n Asp l e Leu Leu Met Lys Gl n A  
 1901 ACAACTTAAACCGCTGCCTGTCATTATCCGACCATCGCTGTGGTACACGCTGTGCGACCGCTACGCCCTGATGTTGGTGTGAAGCCAATAT  
 415► sn Asn Phe Asn Al a Val Arg Cys Ser Hi s Tyr Pro Asn Hi s Pro Leu Trp Tyr Thri Leu Cys Asp Arg Tyr Gl y Leu Tyr Val Val Asp Gl u Al a Asn l l  
 2001 TGAAACCCACGGCATGGCCAATGTCGCTGACCGATGATCCCGCTGGTACCGCGATGAGCGAACCGCTAACCGCAATGGTGCAGCGATCGT  
 448► e Gl u Thri Hi s Gl y Met Val Pro Met Asn Arg Leu Thri Asp Pro Arg Trp Leu Pro Al a Met Ser Gl u Arg Met Val Gl n Arg Asp Arg  
 2101 AATACCCGGAGTGTGATCATCTGGTCGCTGGGAATGACCGCCTGCTAACGACGCGCTGTATCGCTGGATCAAATCTGTCGATCCTTCCC  
 482► Asn Hi s Pro Ser Val l l e l e Trp Ser Leu Gl y Asn Gl u Ser Gl y Al a Asn Hi s Asp Al a Leu Tyr Arg Trp l e Lys Ser Val Asp Pro Ser A  
 2201 GCCCGGTGCACTATGAAGGGCGCGAGGCCAACCGCCACCGATATTATTCGGCGATGTCAGCGCGCTGGATGAAGACGCCCTCCCGCTGT  
 515► rg Pro Val Gl n Tyr Gl u Gl y Gl y Al a Asp Thr Thr Al a Thr Asp l e l e Cys Pro Met Tyr Al a Arg Val Asp Gl u Asp Gl n Pro Phe Pro Al a Va  
 2301 GCGAAATGGTCATCAAAATGGCTTCGCTACCTGGAGAGACCGGCCGCTGATCCTTGCATAACGCCAACCGCAGGGTAACAGTCTGGCGT  
 548► p Pro Lys Trp Ser l l e Lys Trp Leu Ser Leu Pro Gl y Gl u Thri Arg Pro Leu l e Lys Pro Leu Gl y Tyr Al a Hi s Al a Met Gl y Asn Ser Leu Gl y Gl y  
 2401 TTCGCTAAATACTGGCAGGCCCTTCGCTAGTATCCCCTGAGGGCTTCGCTGGGACTGGTGTGATCAGTCGCTGATTAATATGATGAAACAG  
 582► Phe Al a Lys Tyr Trp Gl n Al a Phe Arg Gl n Tyr Pro Arg Leu Gl n Gl y Gl y Phe Val Trp Asp Trp Val Asp Gl u Ser Leu l l e Lys Tyr Asp Gl u Asn G  
 2501 GCAACCCGGTGGCTGGCTACGGCGGTGATTTGGCGATACGCCAACGATCGCCAGTTCTGATGAAGGGCTGGCTTCCGACCGCACCGCATCC  
 615► l y Asn Pro Trp Ser Al a Tyr Gl y Gl y Asp Phe Gl y Asp Thr Pro Asn Asp Arg Gl n Phe Cys Met Asn Gl y Leu Val Phe Al a Asp Arg Thr Pro Hi s Pr  
 2601 AGCGCTGACGGAAAGCAAAACACCAGCAGCAGTTTCCAGTCCGTTATCCGGAAACCATCGAAGTGGCAGCACGCAATCTGTCGATAGCGAT  
 648► o Al a Leu Thr Gl u Al a Lys Hi s Gl n Gl n Gl y Gl y Phe Arg Leu Ser Gl y Gl n Thr l l e Gl u Val Thri Ser Gl u Tyr Leu Phe Arg Hi s Ser Asp  
 2701 AACGAGCTCTGCACTGGATGGTGGCGCTGGATGGTAAGCGCTGGCAAGCGGTGAAGTGGCTCCACAAGGTAACAGTGGTATTGAAAC  
 682► Asn Gl u Leu Leu Hi s Trp Met Val Al a Leu Asp Gl y Lys Pro Leu Al a Ser Gl y Gl u Val Pro Leu Asp Val Al a Pro Gl n Gl y Lys Gl n Leu l l e Gl U  
 2801 TGCCTGAACCTACCGCAGGGAGAGCGCCGGAACTCTGGCTCACAGTACGGTAGTGCACCGAACGCCGACGGCATGGTCAAGGCCAAGCGGGCATCAG  
 715► eu Pro Gl u Leu Pro Gl n Pro Gl u Ser Al a Gl y Gl n Leu Trp Leu Thri Val Arg Val Val Gl n Pro Asn Al a Thri Al a Trp Ser Gl u Al a Gl y Hi s l l e Se  
 2901 CGCCTGGCAGCAGTGGCGCTGGCGAAAACCTCAGTGTGACGCTCCCGCCGCGTCCACGCCATCCGCATCTGACCAACAGCGAAATGGATTTGC  
 748► r Al a Trp Gl n Gl n Trp Arg Leu Al a Gl u Asn Leu Ser Val Thri Leu Pro Al a Al a Ser Hi s Al a l e Pro Hi s Leu Thri Thri Ser Gl u Met t Asp Phe Cys  
 3001 ATCGAGCTGGTAATAAGCGTTGGCAATTAAACGCCAGTCAGGCTTCTTCACAGATGTTGGATTGGCATAAAAACAACGCTGACGCCGCTGCGC  
 782► l l e Gl u Leu Gl y Asn Lys Arg Trp Gl n Phe Asn Arg Gl n Ser Gl y Phe Leu Ser Gl n Met Trp l l e Gl y Asp Lys Gl n Leu Leu Thri Pro Leu Arg A  
 3101 ATCAGTTACCCCGCTGCCGATAACGACATTGGCTAAGTGAAGCGACCCGATTGACCTTAACGCCCTGGCTGAACGCCCTGGAAAGGCCGGG  
 815► sp Gl n Phe Thr Ar Gl a Pro Leu Asp Asn Asp l e Gl y Val Ser Gl u Al a Thri Arg l e Asp Pro Asn Al a Trp Val Gl u Arg Trp Lys Al a Al a Gl y Hi  
 3201 TTACCAAGGCCAGCAGCGTTGCTAGTGCACGGCAGATACACTTGTGATGCGGTGCTGATTACGACCGCTCACGCCAGCATCAGGGAAAACC  
 848► s Tyr Gl n Al a Gl u Al a Al a Leu Leu Gl n Cys Thr Al a Asp Thr Leu Al a Asp Al a Val Leu l l e Thri Thri Al a hi s Al a Trp Gl n Hi s Gl y Lys Thri  
 3301 TTATTTATCAGCCGAAACCTACCGGATTGATGGTAGTGGCAAATGGCATTACCGTTGATGTTGAAGTGGCAGCGATACCCGATCCGGCGG  
 882► Leu Phel l e Ser Arg Lys Thri Tyr Arg l l e Asp Gl y Ser Gl y Gl n Met Al a l l e Thri Val Asp Val Gl u Val Al a Ser Asp Thr Pro Hi s Pro Al a Arg l  
 3401 TTGGCCTGAACCTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAAACTGGCTCGGATTAGGGCCGCAAGAAAATATCCGACGCCCTACTGCGCCTGTT  
 915► l e Gl y Leu Asn Cys Gl n Leu Al a Gl n Val Al a Gl u Arg Val Asn Trp Leu Gl y Leu Gl y Pro Gl n Gl u Asn Tyri Pro Asp Arg Leu Thri Al a Al a Cys Ph

BspLU1II (3527)

3501 TGACCGCTGGATCTGCCATTGTCAGACATGTATAACCCGTACGTCTTCCGAGCGAAAACGGTCTGCCTGCGCTGGGACGCCGAATTGAATTATGGCCA  
948▶ eAspArgTrpAspLeuProLeuSerAspMetTyrThrProTyrValPheProSerGl uAsnGl yLeuArgCysGl yThrArgGl uLeuAsnTyrGl yPro  
3601 CACCACTGGCGCGCGACTTCAACATCAGCGCTACAGTAACAGCAACTGATGAAACCAGCCATCCCCTGCTGCACGCCAGAGAAGGCA  
982▶ HisGl nTrpArgGl yAspPheGl nPheAsnI IeSerArgTyrSerGl nGl nLeuMetGl uThrSerHisArgHi sLeuLeuHisAl aGl uGl yT  
3701 CATGGCTGAATATCGACGGTTCCATATGGGGATTGGTGGCGACGACTCTGGAGCCCGTAGTATCGCGGAATTACAGCTGAGCGCCGGTCGCTACCA  
1015▶ hr TrpLeuAsnI IeAspGl yPheHi sMetGl yIleGl yGl yAspAspSerTrpSerProSerValSerAl aGl uLeuGl nLeuSerAl aGl yArgTyrHi

NheI (3847)

EcoRI (3841)

3801 TTACCAAGTTGGTCTGGTGTCAAAAATAATAATCTAGTCGAGAATTGCTAGCTGACATGATAAGATAACATTGATGAGTTGGACAACCACAAGTAGAA  
1048▶ sTyrGl nLeuVal TrpCysGl nLys \*\*\*

3901 TGCAGTAAAAAAATGCTTATTGTGAAATTGTGATGCTATTGTTATTGTGAAATTGTGATGCTATTGCTTATTGTGTAACCATTATAAGCTGC

4001 AATAAACAGTTAACACAATTGCATTCTATTGTTAGGTTAGGGGAGGTGTGGAGGTTTTAAAGCAAGTAAACCTCTACAAATGTG

PacI (4122)

SwaI (4112)

4101 GTAGATCCATTAAATGTTAAATTAACTAGCCATGACCAAAATCCCTAACGTGAGTTTCTGTTCACTGAGCTCAGACCCCCTAGAAAAGATCAAAGGA  
4201 TCTTCTGAGATCCTTTTTCTGCGCGTAATCTGCTGCTGCAAACAAAAAACCCGCTACAGCGTGGTTGTTGCCGATCAAGAGCTACCAA  
4301 CTCTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATAACCAAAACTGTTCTCTAGTGTAGCCGTAGTAGGCCACACTCAAGAACTCTGAGC  
4401 ACCGCCTACATACCTCGCTCTGCTAACCTGTTACCAAGTGGCTGCTGCCAGTGGCATAAGTCGTCTTACCGGTTGACTCAAGACGATAGTTACCG  
4501 GATAAGGCGCAGCGTCGGCTAACGGGGGTTCTGCACACAGCCAGCTGGAGCGAACGACCTACACCGAACACTGAGATAACCTACAGCGTAGCT  
4601 GAGAAAGGCCACGCCCTCCGAAGGGAAAGGCGACAGGTATCCGTAAGCGGAGGGTCGAAACAGGAGAGCGCACGAGGAGCTCCAGGGGAA  
4701 CGCCTGGTATCTTATAGCTCTGCGGTTGCCACCTGACTTGAGCGTCATTGTGATGCTCGTAGGGGGCGGAGCCTATGGAAAAACGCC

PacI (4862)

BspLU1II (4850)

AseI (4888)

4801 AGCAACCGGCCCTTTACGGTTCTGGCTTTGCTGGCTTTGCTCACATGTTCTAACATTAAATTTCAAAAGTAGTTGACAATTATCATCGGCA  
4901 TAGTATATCGGCATAGTATAATCGACTCACTATAAGAGGGCCATCATGGCCAAGTTGACCGAGTGCTGTCCCAGTGCTCACAGCCAGGGATGTGGCTGGA  
5001 GCTGTTGAGTTCTGACTGACAGGTTGGGTTCTCAGAGATTGAGGGATGACTTGAGGTGAGAGATGATGTCACCCGTTCATCTCAG  
5101 CAGTCAGGACCAAGGTGGCTGACAACACCCCTGGCTGGGTGGTGAGAGGACTGGATGAGCTGTATGCTGAGTGGAGTGAGGTGGTCTCCACCAA  
5201 CTTCAGGGATGCCAGTGGCCCTGCCATGACAGAGATTGGAGAGCAGCCCTGGGGAGAGAGTTGCCCTGAGAGACCCAGCAGGCAACTGTGTGCACTT

PacI (5371)

5301 GTGGCAGAGGAGCAGGACTGAGGATAAGAATTGTAACAAAAACCCGCCGGGGTTTTGTTAATTAA