

STOP

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pCpGfree-vitroBLacZ

A LacZ expression plasmid completely devoid of CpG dinucleotides, selectable with Blasticidin

Catalog code: pcpgvtb-lz

<https://www.invivogen.com/pcpgfree-vitro-blasticidin>

For research use only

Version 20F08-MM

PRODUCT INFORMATION

Contents:

- 20 µg of pCpGfree-vitroBLacZ plasmid provided as lyophilized DNA
- *E. coli* GT115 strain provided lyophilized on a paper disk
- 2 x 1 ml blasticidin at 10 mg/ml

Storage and stability:

- Product is shipped at room temperature.
- Upon receipt, store lyophilized DNA at -20°C.
- Resuspended DNA should be stored at -20°C.
- Store blasticidin at 4°C or -20°C. *

*The expiry date is specified on the product label.

Quality control:

- Plasmid construct has been confirmed by restriction analysis and sequencing.
- Plasmid DNA was purified by ion exchange chromatography and lyophilized.

GENERAL PRODUCT USE

pCpGfree-vitro plasmids represent innovative tools to study the effects of CpG dinucleotides in numerous applications. DNA vaccination exploits the immunostimulatory character of certain CpG motifs to prime and boost the immune response. However, these immunostimulatory CpG motifs are antagonized by CpG dinucleotides in certain distinct base contexts, termed neutralizing CpG motifs. Both types of CpG motifs are usually present in plasmidic DNAs, and therefore may lead to an unfavorable immune response. pCpGfree-vitro is the ideal tool to overcome this problem, and may be used to study the effects of these two types of CpG motifs by adding them in different configurations to the pCpGvitro backbone.

CpG dinucleotides are key elements in a number of cellular functions associated with chromatin. Several large multisubunit complexes, consisting of methyl-CpG binding (MBD) proteins and histone deacetylases, have been implicated in the regulation of chromatin dynamics. These complexes are recruited to methylated CpG dinucleotides by DNA methyltransferases (DNMTs) and induce chromatin remodelling. However the specific roles of these complexes are still to be explored. Due to the absence of CpG dinucleotides within its backbone, pCpGfree-vitro is not the target of DNMTs and thus MBD proteins. Therefore, it provides a useful model to study the other proteins involved in these complexes, in particular the histone deacetylases. It can also be used to analyze the effects of CpG methylation on the regulation and duration of gene expression.

PLASMID FEATURES

pCpGfree-vitro is a family of expression vectors devoid of CpG dinucleotides that are selectable in mammalian cells. All the elements required for replication and selection of the plasmids in bacteria, and gene expression in mammalian cells have been modified to remove all CpG dinucleotides.

- **Composite CpG-free promoter** combining the mouse CMV enhancer, the human elongation factor 1 α core promoter and 5'UTR containing a synthetic intron (I 126). This composite promoter yields high and ubiquitous expression of the LacZ gene.

• **LacZ** encodes β -galactosidase an enzyme that catalyzes the hydrolysis of X-Gal, producing a blue precipitate that can be easily visualized under a microscope. This CpG-free allele of the lacZ reporter gene can be easily subcloned and replaced by a gene of interest.

• **CpG-free polyadenylation signals (pAn)**: The polyadenylation signals utilized are CpG-free versions of the SV40 late and human β -globin polyadenylation signals. These polyA enable efficient cleavage and polyadenylation reactions resulting in high levels of steady-state mRNA.

• **CpG-free matrix attached regions (MARs)** are AT-rich sequences that are able to form barriers between independent expression cassettes.

• **CpG-free Blasticidin resistance gene (bsr- Δ CpG)**: The CpG-free blasticidin resistance gene is active both in *E. coli* and mammalian cells.

• **CpG-free SV40 promoter** works in tandem with a bacterial promoter located within a synthetic intron (I-EC2K). This composite promoter drives the expression of the resistance gene in both mammalian cells and *E. coli*.

• **CpG-free *E. coli* R6K gamma origin of replication**: This origin is activated by the R6K specific initiator protein π , encoded by the *pir* gene. Expression of the *pir* gene is necessary for the replication and amplification of pCpGvitro plasmids. *E. coli* GT115 strain expresses a *pir* mutant gene that allows higher plasmid copy number.

1. Wu F. et al. 1995. A DNA segment conferring stable maintenance on R6K gamma-origin core replicons. J Bacteriol. 177(22):6338-45. 2. Bode J. et al., 1996. Scaffold/matrix-attached regions: topological switches with multiple regulatory functions. Crit Rev Eukaryot Gene Expr. 6(2-3):115-38.

METHODS

Plasmid resuspension

Quickly spin the tube containing the lyophilized plasmid to pellet the DNA. To obtain a plasmid solution at 1 µg/ μ l, resuspend the DNA in 20 μ l of sterile H₂O. Store resuspended plasmid at -20°C.

Reconstitution of *E. coli* GT115 strain under sterile conditions

1. Reconstitute *E. coli* GT115 by adding 1 ml of LB medium in the tube containing the paper disk. Let sit for 15 minutes. Mix gently by inverting the tube several times. Let sit 5 more minutes.
2. Streak bacteria taken from this suspension on a LB agar plate.
3. Place the plate in an incubator at 37°C overnight.
4. Isolate a single colony and grow the bacteria in *E. coli* growth medium.
5. Prepare competent cells utilizing your preferred protocol.

Plasmid amplification and cloning:

Plasmid amplification and cloning can be performed in competent *E. coli* GT115.

Blasticidin usage

Blasticidin should be used at 25-100 µg/ml in bacteria and 1-30 µg/ml in mammalian cells. Blasticidin is supplied at 10 mg/ml in HEPES buffer.

RELATED PRODUCTS

Product	Description	Cat. Code
ChemiComp GT115 cells	Competent <i>E. coli</i> cells	gt115-11
Blasticidin	Selection antibiotic	ant-bl-05

TECHNICAL SUPPORT

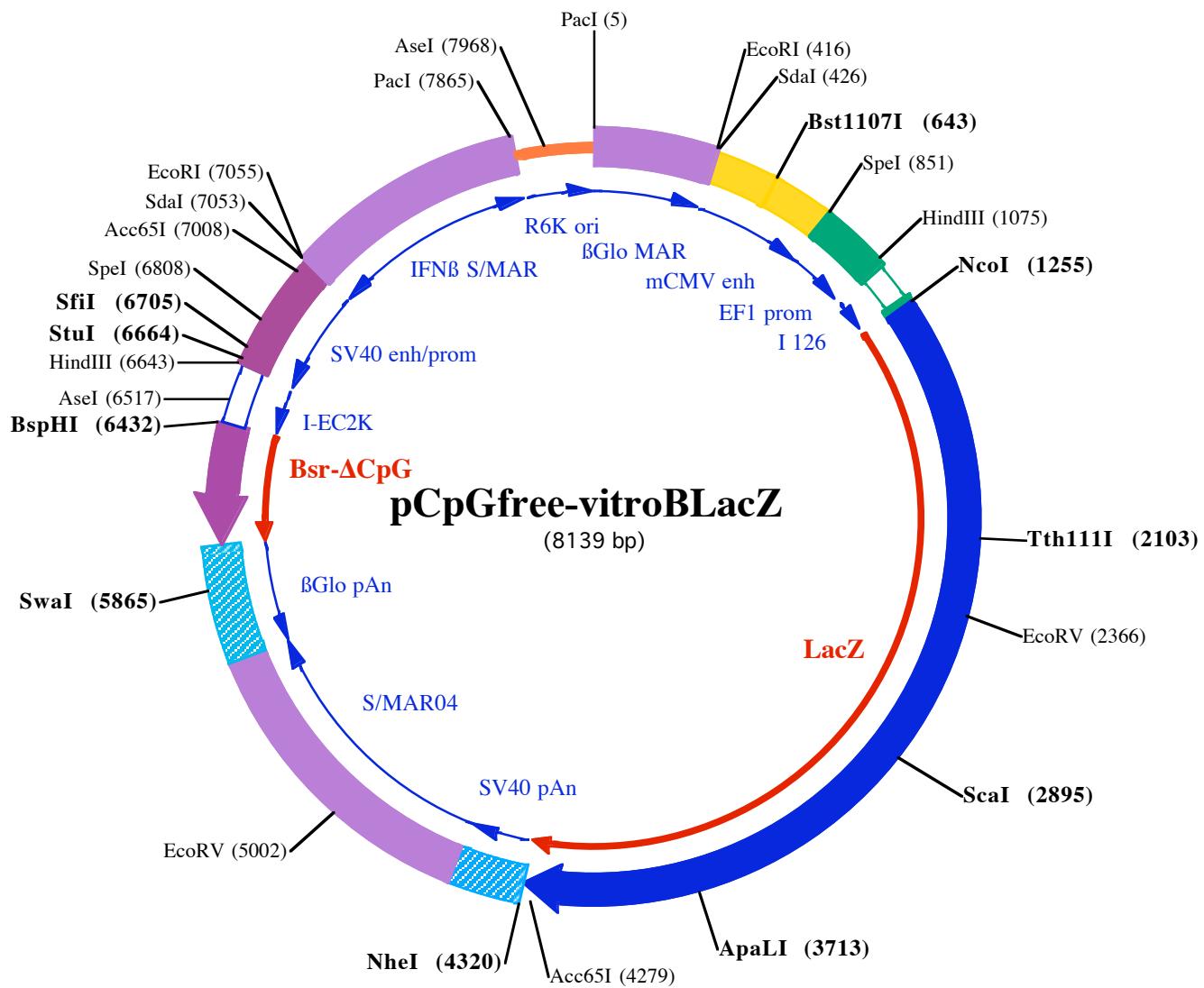
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PacI (5)
1 TTAATTAAAATTATCTCAAGGCATGTGAACGGCTGTCTGGTTTATCTGACTTCATCTGACCTCTGTGACCTGAAACATATTATAATTCCAT

101 TAAGCTGTGATGATAGATTATCATATGTATTTCTAAAGGATTTGTAAGAACTAATTGAACTTGTAAAGTCTTACACTACCC

201 AATAAAATAAAATCTTGTTCAGCTCTGTCTTCTATAAATATGACAAGTTTGTGAGTGTGTTTATCTCTTCTATATAT

301 ACACACATGTGTCATTCTATAAATATACAATTGAAATAAAAATTATTAGCAATATTGAAAACCACTGATTTGTTATGTGAGCAA

SdaI (426)
EcoRI (416)
401 ACAGCAGATTAAAGGAATTCCCTGCAGGAGTCATGGAAAAACCCATTGGAGCCAAGTACACTGACTCAATAGGACTTCCATTGGTTTGCCCAGT
501 ACATAAGGTCAATAGGGGGTGAGTCACAGGAAAGTCCATTGGAGCCAAGTACATTGAGTCATAGGACTTCCATTGGTTTGCCCAGTACATAAG

Bst1107I (643)
601 GTCAATGGGAGGTAAGCCAATGGGTTTCCATTACTGACATGTATACTGAGTCATTAGGACTTCCATTGGTTTGCCCAGTACATAAGGTCAATA

701 GGGGTGAATCAACAGGAAAGTCCATTGGAGCCAAGTACACTGAGTCATAGGACTTCCATTGGTTTGCCCAGTACAAAAGGTCAATAGGGGTGA

SpeI (851)
801 GTCAATGGGTTTCCATTATTGGCACATACATAAGGTCAATAGGGTGACTAGTGGAGAAGAGCATGCTTGAGGCTGAGTGCCCTCAGTGGCAGA
901 GAGCACATGCCACAGTCCCTGAGAAGTGGGGGGGGGGCAATTGAACTGGTGCCTAGAGAAGGTGGGCTGGTAAACTGGAAAGTGTG

HindIII (1075)
1001 GGTGACTGGCTCCACCTTTCCCCAGGGTGGGGAGAACCATATAAGTCAGTAGTCAGCTGTGAACATTCAAGCTCTGCCTCCCTCGTGA
1101 GTTGGtaagtcaactgactgtctatgcctggaaagggtggcaggagatggggcagtcaggaaaagtggcactatgaaccTGAGCCCTAGAcaatt

NcoI (1255)
1201 gtactaacccctttcttcccttcgtacagGTTGGTGTACAGTAGCTTCCACCATGGACCTGTTGCTGCAAAAGGAGAGACTGGAGAACCTGG
1301 AGTACCCAGCTAACAGACTGGCTGCCACCCCTCCCTTGCTGAGGAACCTGAGGAAGCAGACAGGCCAGCCAGCTCAGGTCT
15► yVal Thr Gl nLeuAsnArgLeuAl aAl aHi sProProPheAl aSer TrpArgAsnSer Gl uGl uAl aArgThrAspProSer Gl nGl nLeuArgSer
1401 CTCATGGAGAGTGGAGGTTGCTGGTCCCTGCCCTGAAGCTGCTGAGCTTGGCTGGAGTGTGACCTCCAGAGGCTGACACTGTTGTTG
49► LeuAsnGl yGl uTrpArgPheAl aTrpPheProAl aProGl uAl aVal iProGl uSer TrpLeuGl uCysAspLeuProGl uAl aAspThr Val Val Val P
1501 CCAGCACTGGCAGATCATGGCTATGCCCCATCACCATGCTCACCTTCACTGTAACCCCCCATCACTGTAACCCCCCTTGTGCCACTGAGAACCCAC
82► rroSerAsnTrpGl nMetHi sGl yTyrAspAl aProI eTyrThrAsnVal Thr TyrProI eTyr Val AsnProPheProVal ProThr Gl uAsnProTh
1601 TGGCTGCTCACAGCTGACCTTCAATGTTGATGAGACTGGCTGAAGAAGCCAGAGCAGATCTGGCATCTTGTGAGGACTCACTGCCCTCACCTGG
115► rGl yCysTyrSerLeuThrPheAsnValAspGl uSer TrpLeuGl nGl uGl yGl nThr ArgI l eI ePheAspGl yVal AsnSer Al aPheHisLeuTrp
1701 TGCATGGCAGGTGGCTGGCTATGGCCAAGACAGCAGGCTGCCCTCTGAGTTGACCTCTGCTCCCTCAGAGCTGGAGAACACAGCTGGCTGCA
149► CysAsnGl yArgTrpVal Gl yTyrGl yGl nAspSer ArgLeuProSer Al aPheAspLeuArgAl aGl yGl uAsnArgLeuAl aVal M
1801 TGGTGCCTAGGTGGCTGATGGCAGCTACCTGGAAAGCAACATGTTGAGGATGTGGCATCTGGCATCTGGCTGCAAGGCCAAC
182► etVal LeuArgTrpSerAspGl ySer TyrLeuGl uAspGl nAspMetTrpArgMetSer Gl l eI ePheArgAspVal Ser LeuLeuHi sLysProThr Th
1901 CCAGATTCTGACTCCATGTTGCCACAGGTTCAATGATGACTTCAGCAGAGCTGCTGGAGGCTGAGATGTGTTGAGAACCTCAGAGACTAC
215► rGl nI eSerAspPheHisValAl aThrArgPheAsnAspPheSer ArgAl aVal LeuGl uAl aGl uVal Gl nMetCysGl yGl uLeuArgAspTyr

Tth111I (2103)
2001 CTGAGAGTCACAGTGGCCTCTGGCAAGGTGAGACCCAGGTGGCCCTCTGGCACAGCCCCCTTGGAGGAGAGATCATTGATGAGAGAGGAGCTATGCT
249► LeuArgVal Thr Val Ser LeuTrpGl nGl yGl uThr Gl nVal Al aSer Gl yThr Al aProPheGl yGl yGl uI l eI eAspGl uArgGl yGl yTyrAl aA
2101 ACAGTCACCCCTGAGGCTCAATGTGGAGAACCCCAAGCTGTGCTGAGATCCCCACCTCTACAGGCTGTGGAGCTGACACTGCTGATGG
282► spArgVal Thr LeuAsnLeuAsnVal Gl uAsnProLyLeuTrpProLeuTrpProLeuTrpProLeuTrpProLeuTrpProLeuTrpProLeuTrpProLeuTrp
2201 CACCCCTGATGAACTGGCTGATGTTGATGAGGATTGAGAATGGCTGCTGCTGAATGGCAAGGCCCTGTCATCAGGCTGAGATGGAGCAT
315► yThr LeuI l eGl uAl aGl uAl aCysAspVal Gl yPheArgGl uVal ArgI l eI uAsnGl yLeuLeuLeuAsnGl yLysProLeuLeuI l eArgGl y

EcoRV (2366)
2301 GTCAACAGGCATGAGCACCCCTCTGCATGGACAAGTGTGGATGAACAGACAATGGCAAGATCTCTGCTAATGAAGCAGAACACTTCAATGCT
349► ValAsnArgHi sGl uHi sHi sProLeuHi sGl yGl nValMetAspGl uGl nThr MetVal Gl nAspI l eLeuLeuMetLysGl nAsnAsnPheAsnAl aV
2401 TCAGGTGCTCTCACTACCCCAACACCCTCTGGTACACCCCTGTGACAGGTATGGCTGTATGTTGATGAAGCCAACATTGAGACACATGGCAT
382► aI ArgCysSer Hi sTyrProAsnHi sProLeuTrpTyrThrLeuCysAspArgTyrGl yLeuTyrVal Val AspGl uAl aAsnI l eGl uThr Hi sGl yMe
2501 GGTGCCCATGAACAGGCTCACAGTACCCAGGCTGCTGAGAGTGGCTGCTGAGATGGCTGAGAGATGGCTGAGAGAACAGGAAACCCCTGTG
415► tVal ProMetAsnArgLeuThrAspProArgTrpLeuProAl aMetSer Gl uArgVal Thr ArgMetVal Gl nArgAspArgAsnHi sProSer Val
2601 ATCATCTGGCTCTGGCAATGAGCTGGACATGGAGCCAACCATGATGCTCTACAGGTTGATGAAGCTGGAGGCCAGCAGACTGTCAGTATG
449► l eI l eTrpSer LeuGl yAsnGl uSer Gl yHi sGl yAl aAsnHi sAspAl aLeuTyrArgTrpI l eLysSer Val AspProSer ArgProVal Gl nTyrG
2701 AAGGAGGTGAGGAGCACACCCACAGCACATCTGGCTGAGGATGTGGCTGAGGACCCCTCCCTGCTGAGGAGCAT
482► l uGl yGl yAl aAspThr Thr Al aThrAspI l eI eCysProMetTyrAl aArgVal AspGl uAspGl nProPheProAl aVal ProLysTrpSer I I

ScaI (2895)
2801 CAAGAAGTGGCTCTCTGCTGGAGAGACCCAGACCTCTGATCTGTGAATATGCACTGGCAACTCTGGAGGCTTGCCAAGTACTGG
515► eLysLysTrpLeuProGl yGl uThr ArgProLeuI l eLeuCysGl uTyrAl ahI sAl aMetGl yAsnSer LeuGl yGl yPheAl aLysTyrTrp
2901 CAAGCCTCAGACAGTACCCAGGCTGCAAGGAGATTGGTGGACTGGTGGACCAACTCTCATCAAGTATGATGAGAATGGCAACCCCTGGCTG
549► Gl nAl aPheArgGl nTyrProArgLeuGl nGl yGl yPheVal TrpProTrpVal AspGl nSer LeuI l eLysTyrAspGl uAsnGl yAsnProTrpSer A
3001 CCTATGGAGGAGACTTGGTGCACCCCAATGACAGGCGATTCTGCTGAATGGCTGGCTTGCAGACAGGCCACCTGCCCTCACAGAGGC
582► l aTyrGl yGl yAspPheGl yAspThr ProAsnAspArgGl nPheCysMetAsnGl yLeuVal PheAl aAspArgThr ProHi sProAl aLeuThr Gl uAl
3101 CAAGCACCGCAACAGTCTCCAGGCTGCTGGAGCACCATCTGAGGAGCATCTGACACTCTGGAGGCTTCTGACATGAGCTCTGCAC
615► aLysHi sGl nGl nPhePheGl nPheArgLeuSer Gl yGl nThr I l eI uVal I l eI ProLeuAspVal Al aProGl nGl yLysGl nLeuI l eGl uLeuProGl uLeuProG
3201 TGGATGGTGGCCCTGGATGGCAACGGCTCTGGCTTCTGGTGGAGGCTGCTGGCTGAGGCTGCTGAGCTGCTGAGCTGCCCT
649► TrpMetVal Al aLeuAspGl yLysProLeuAl aSer Gl yGl uVal I l eI ProLeuAspVal Al aProGl nGl yLysGl nLeuI l eGl uLeuProGl uLeuProG
3301 AGCCAGAGTCTGGACAACCTGGCTAACAGTGAGGGTGGTCAAGGCCAACAGCTGGAGGCTGAGGCCACATCTGCTGAGCAGCAG
682► l nProGl uSer Al aGl yGl nLeuTrpLeuThr Val ArgVal Val Gl nProAsnAl aThr Al aTrpSer Gl uAl aGl yHi sI l eSer Al aTrpGl nGl nTr
3401 GAGGCTGGCTGAGAACCTCTCTGCTGGACCCCTGCTGCTCATGCATCCTCACCTGACAACTCTGAATGGACTCTGCATTGAGCTGGCAAC
715► pArgLeuAl aGl uAsnLeuSer Val Thr LeuProAl aAl aSer Hi sAl aI l eProHi sLeuThr Thr Ser Gl uMetAspPheCysI l eGl uLeuGl yAsn
3501 AAGAGATGGCAGTCAACAGGAGCTGGCTCTGTCTCAGATGGAGAGAACAGCAGCTCTACCCCTCAGGGACCAATTACCAAGGG
749► LysArgTrpGl nPheAsnArgGl nSer Gl yPheLeuSer Gl nMetTrpI l eGl yAspLysLysLys nLeuLeuThr ProLeuArgAspGl nPheThr ArgA
3601 CTCTCTGGACAATGATTGGAGTCTGGAGGCCACAGGATTGACCCAAATGCTGGTGGAGGTTGAGGCTGCTGGACACTACAGGCTGAGGC
782► l aProLeuAspAsnI l eGl yVal Ser Gl uAl aThr ArgI l eAspProAsnAl aTrpVal Gl uArgTrpLysAl aAl aGl yHi sTyrGl nAl aGl uAl
ApalI (3713)
3701 TGCCCTGCTCCAGTCACAGCACCCCTGGCTGATGCTTGTGATCACCAAGCCATGCTGGCAGCACCAAGGCAAGACCCCTGTTCATCAGCAGA
815► aAl aLeuLeuGl nCysThr Al aAspThr LeuAl aAspAl aVal LeuI l eThr Thr Al aHi sAl aTrpGl nHi sGl nGl yLysThr LeuPhel l eSer Arg

3801 AAGACCTACAGGATTGATGGCTCTGGACAGATGCCAATCACAGTGGATGGAGGGTGCCTTGACACACCTCACCTGAAGGATTGGCTGAACGT
 849▶ LysThr TyrArgI IeAsnGlySer Gl nMeIaAl aIeIeThr ValAspVal Gl uValAl aSerAspThr ProHi sProAl aArgI IeGl yLeuAsnCysG
 3901 AACTGGCACAGGTGCTGAGAGGGTGAACCTGGCTGGGCTTAGGCCCTCAGGAGAACCTACCCCTGACAGGCTGACAGCTGCTGCTGGGACT
 882▶ I nLeuAl aGl nVaIaI aGl uArgValAsnTrpLeuGl yLeuGl yProGl nGl uAsnTyrProAspArgLeuThr Al aAl aCysPheAspArgTrpAspLe
 4001 GCCTCTGTGACATGTACACCCCTATGTGTTCCCTCTGAGAATGGCCTGAGGTGTCACAGGGAGCTGAACATGGCTCACAGTGGAGGGAA
 915▶ uProLeuSerAspMetTyrThr ProTyrVal PheProSer Gl uAsnGl yLeuArgCysGl yThr ArgGl uLeuAsnTyrGl yProHi sGl nTrpArgGl y
 4101 GACTTCCAGTTAACATCTCCAGGACTCTCAGAACAGCTCATGGAAACCTCTCACAGGCACCTGCTCCATGCAGAGGGGAACCTGGCTGAACATTG
 949▶ AspPheGl nPheAsnI IeSerArgTyrSer Gl nGl nLeuMetGl uThr Ser HisArgHi sLeuLeuHi sAl aGl uGl IyThr TrpLeuAsnI IeA
 Acc65I (4279)

4201 ATGGCTTCCACATGGCATTGGAGAGATGACTCTGGTCTCCTCTGCTGCTGAGTTCCAGTTCTGCTGGCAGGTACCACTACAGCTGGTGTG
 982▶ pGl yPheHi sMetGl I IeGl yGl yAspAspSer TrpSer ProSer Val Ser Al aGl uPheGl nLeuSer Al aGl yArgTyrHi sTyrGl nLeuVal Tr

NheI (4320)

4301 GTGCCAGAAGTAAACCTGAGCTAGCTGGCCAGACATGATAAGATAACATTGATGAGTTGGACAAACCAACTAGAATGCAGTAAAAAAATGTTATT
 1015▶ pCysGl nLys●●

4401 TGTGAAATTGTGATGCTATTGTTTGTAAACCATTATAAGCTGCAATAAACAGTTAACACAATTGATTCTATTTATGTTCAGGTTCAAG
 4501 GGGAGGTGAGGTTAAAGCAAGTAAACCTCTACAAATGGTATGGATTGAGCCCCACTGTGTTCATCTTACAGATGAAACTGACAT
 4601 TCAGAGGAGTTAGTTAACCTGCTAGGTGATTCTAGCTAAATAAGTCAAGAGAAGATTCAATCCAAGGTGATTCTGAAGCTGTGCTAACATT
 4701 ACACCAAGCTACAACCTATTATAAAATAAAAGTCAGCTTCAAGGGCTTCAGGTGTCCTGACTTACAAGCTGTGCCATTAGTAAC
 4801 TGAGCCTTGATGAAGTAGTCTTCATTAGTAACTAAATTCTAGCTGCCAGCTGATTGAAGGCTGGGACAAATTCAAACATG
 EcoRV (5002)

4901 CATCTACAACAAATATATCTCAATGTTAGTCTCAAATTCTATTGACTTCAACTCAAGAGAATATAAGAGCTAGTCTTATACACTTTAAAGGTATG
 5001 ATATCATCTGAAAGTAACAAATTGATGCAATTGAACTTATCATGGTGTATTACACAATGTGTTCTCCCTGCAATGTATTCTTCT
 5101 CTAATTCTCCATTGATCTTCATACACAATCTGTTGATGTATGTTGGATGCACTTCAACTCCAAAAGACAGAGCTAGTTACTTCTC
 5201 CTGGTGCTCAAGCACTGATTGATCTGATTCAAGGCCCTTGAATTGACTGGATCATTTCACCTCTAGGATGGCTCCAGGCAACTG
 5301 TGTTCACCCAGAGACTACATTGATCTTGAACCTTCAAGGCCCTTGAACCTTCAAGGCCCTTGAACAGTGTCTAAAATAATGTGAA
 5401 ATTAAACAATATAAAAGGAGAAGCAAGGAGAGAACACAGGTGTTGCTAAAGGAGATTTGCTGAGCTAAACATCTATATTCA
 5501 ATAGTGAGGAGACAAAGTTATACCTTTATCTGGCTTTAAGGAGATTTGCTGAGCTAAACATCTATATTCA
 5601 CAATACCTCAATTCAAACAGCATAGCAAACCTTAACTCCAACAGCTACTGAACTCTTCTGAGGGATGAAGGCATAGGCATAG
 5701 GGGCTGTTGCCAATGTGATTAGCTGTTGCAGCCTCACCTCTCATGGAGTTAACAGATAGTGTATTCCAGGTTGAACAGCTTCATT

SwaI (5865)

5801 TCTTTATGTTAAATGCACTGACCTCCCACATCCCTTTAGTAAAATATTCAAGAAATAATTAAATACTATTGCAATGAAATAATGTTTTA
 5901 TTAGGCAGAATCCAGATGCTCAAGGCCCTCATATAATCCCCAGTTAGTGTAGTGGACTTAGGAACAAAGAACCTTAATAGAAATTGGACAGCAAG
 6001 AAAGCTCTAGCTTAGTTCTGGTATTCAGTGGATCAGCTCTCAATGGTTGCTTGACAGCTGCTTACATCTCAATCAGAACAAAGCAATC
 141▶ AsnArgThr TyrLysLeuProI IeLeuGl IGl IleIeThr LysVal LeuLysGl yAsnMetGl IuIeLeuVal PheCysAspP
 6101 GGGGCATAGTCTGAGTGGCTCCCTGCACATGCCACAGGGGGACACCACTCTGATGGACCTGTCACCTCATCAGGGGTGCTCACGCCACAA
 111▶ RoAlaI TyrAspSer I IeLeuGl IuArgCysMetGl yCysProSer Val ValArgI IeSerArgAspVal Gl uAspSer TyrProHi sArgValAl aValII
 6201 TGGTGTCAAAGCTCTGCCCATTGGAGACTCGACACCAATGGCAATGCCCTGACACACAGTGACCCCTGCCATGTAGGCTTCAATGTGGACAGC
 784▶ ThrAspPheAspLysGl nGl yAsnSer Val Al aSer Gl I IeAl aIeAl aIeAl aIeAl aIeAl aIeAl aIeAl aIeAl aIeAl a
 6301 AGAGATGATTCTCTGCTCTGGCTCTGATGGCAGCACCAACATGGCTCTGTGCTCATAGACCATGGTGTATTCTCAGTGGCAACTTCCAC
 454▶ Ser I IeIeGl uGl yThr LysThr ArgI IeAl aAl aIyValHi sHi sLysAsnAspGl uTyrLeuMetThr I IeLysGl uThrAl aVal Gl uVal LeuG
 BspHI (6432)

6401 TCAAGGCTGCTGAGAGATGTTGAAGGTCTCATGATGGCTCCTCctgtcaggagaggaaagagaaggtagtacaattgCTATAGTGAGTTGAT
 111▶ IuLeuAspGl nGl nSer I IeAsnPheThr LysMet

AspI (6517)

6501 TATACTATGCTTATGATTAATTGTCAAACTAGGGCTGCAgggttcatagtgccactttccctgcactgccccatctcccccacccctccaggcata

HindIII (6643) **StuI (6664)**

6601 gacagtcatgtacttacAAACTCACAGGAGGGAGAAGGCAGAGCTTTGCAAAAGCCTAGGCTCCAAAAAGCTCCTCACTACTCTGGAATAGC
 6701 TCAGAGGCCAGGGCCCTgGGCCTCTGCATAAATAAAAAAATTAGTCAGCCTGGGctgggtggggcaggggtggggccactggCAGGGTG

SpeI (6808)

6801 GGGGGCACTAGTGGGACTATGGTGACTAATTGAGATGCTGATGCTTGCACTTCTGCCTGCTGGGAGCCTGGGACTTCCACACCTGGTGTG
 6901 GACTAATTGAGATGCATGCTTGCAACTTCTGCCTGCTGGGAGCCTGGGACTTCCACACCTAACGTACACACATTCCACAGCTGGTCTTCAGC

EcoRI (7005)

7001 CTCAGAAGGTACCTAACCAAGTCTCTTTAGAGGTTATTCAGGCCCTGCAAGGAACTTCAGTCAATATGTCACCCAAAAAGCTTTGTTAAC
 7101 TCAACCTCATCTAAAATGATATAGAACGCCAAAGACAATAACAAAATATTCTGTAGAACAAAATGGGAAAGAATGTCACAAATCAAGATT
 7201 TAGAGCAAAGCATGAGATGTTGGGATAGACAGTGAGGCTGATAAAATAGAGTAGAGCTCAGAACAGACCCATTGATATATGTAAGTGACCTATGAA
 7301 AAAATGGCATTAAATGGAAAATGATGATTTCTTTAGAAAAACAGGAAATATTTATATGAAAAAATAAAAGGAAACCCATATG

7401 CATAACCACACACACAAAAATTCCAGTGAATTATAAGTCTAAATGGAGAAGGCAAACCTTAAATCTTTAGAAAATAATAGAACATGCCATCAAG
7501 ACTTCAGTGTAGAGAAAAATTCTTATGACTCAAAGTCTAACCAAGAAAAGATTGTTAATTAGATTGCATGAATATTAAGACTTATTTAAATT
7601 AAAAACCATTAAGAAAAGTCAGGCCATAGAATGACAGAAAATTTGCAACACCCCAGTAAAGAGAATTGTAATATGCAGATTATAAAAGAAGTCTA
7701 CAAATCAGTAAAAATAAAACTAGACAAAATTGAAACAGATGAAAGAGAAACTCTAATAATCATTACACATGAGAAACTCAATCTCAGAAATCAGAGA
7801 ACTATCATTGCATATACACTAAATTAGAGAAATTAAAGGCTAACATCTGGCTTAATTAAAGTTACCTAGGAAACCTTAAACCTTAAAG
7901 CCTTATATATTCTTTTTCTTATAAAACTTAAACCTTAGAGGCTATTAAAGTTGCTGATTATATTAAATTATTGTTCAAACATGAGAGCTTAGTA
8001 CATGAAACATGAGAGCTTAGTACATTAGCCATGAGAGCTTAGTACATTAGCCATGAGGTTAGTTCAAAACATGAGAGCTTAGTACATTAAACATGA
8101 GAGCTTAGTACATACACAGGTTGAACGTGCTGATT

PacI (7865) →
AseI (7968)