

pMOD2-Hygro

A plasmid containing a synthetic hygromycin resistance gene

Catalog code: pmod2-hygro

<https://www.invivogen.com/pmod2-hygro>

For research use only

Version 22C07-MM

PRODUCT INFORMATION

Contents

- 20 µg of lyophilized plasmid DNA

Storage and Stability

- Product is shipped at room temperature.
- Lyophilized DNA should be stored at -20°C.
- Resuspended DNA should be stored at -20°C and is stable at least for 1 year.

Quality control

- Plasmid construct has been confirmed by restriction analysis and full-length open reading frame (ORF) sequencing.
- Plasmid DNA was purified by ion exchange chromatography.

GENERAL PRODUCT USE

pMOD2 plasmids contain genes that have been chemically synthesized. The DNA sequences of these genes were modified by optimizing the codon usage, reducing or eliminating the CpG motifs and avoiding secondary DNA structures without changing the amino acid sequence of the wild type proteins.

pMOD2 may be used to subclone the synthetic gene into another vector. Each synthetic gene is flanked by unique restriction sites allowing convenient excision. Furthermore, two multiple cloning sites (MCS) have been added on both ends of the synthetic gene. They contain several restriction sites that are compatible with many other enzymes, thus facilitating cloning.

METHODS

Plasmid resuspension

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

Plasmid amplification and cloning

Plasmid amplification and cloning can be performed in *E. coli* GT116 or other commonly used laboratory *E. coli* strains, such as DH5α.

Ampicillin usage

Ampicillin (not provided) can be used for *E. coli* at 50-100 µg/ml in liquid or solid media.

PLASMID FEATURES

• Multiple cloning sites

MCS1 located upstream of the synthetic gene, contains the following restriction sites:

NdeI, BstEII, AvrII, MfeI, BglIII, AflIII, HindIII, PmeI, BspHI

MCS2 located downstream of the synthetic gene, contains the following restriction sites:

NheI, BamHI, Ec1136II, SacI, EcoRV, PaeI

Each restriction site is compatible with many other enzymes, increasing the cloning options.

• **Synthetic hygromycin resistance gene (CpG-free hph):** The *E. coli* *hph* gene codes for a phosphotransferase that confers resistance to Hygromycin B. The native *hph* gene is a 1023 bp gene rich in CpG dinucleotides (103 CpGs). In the synthetic *hph* gene, all the CpG motifs have been removed and codon usage optimized.

• **pMB1 ori** is a minimal *E. coli* origin of replication to limit vector size, but with the same activity as the longer Ori.

• **Amp:** The ampicillin resistance gene allows the selection of transformed *E. coli* carrying a pMOD2 plasmid.

RELATED PRODUCTS

| Product | Description | Cat. Code |
|-----------------|--------------------------|-----------|
| ChemiComp GT116 | Competent <i>E. coli</i> | gt116-11 |

TECHNICAL SUPPORT

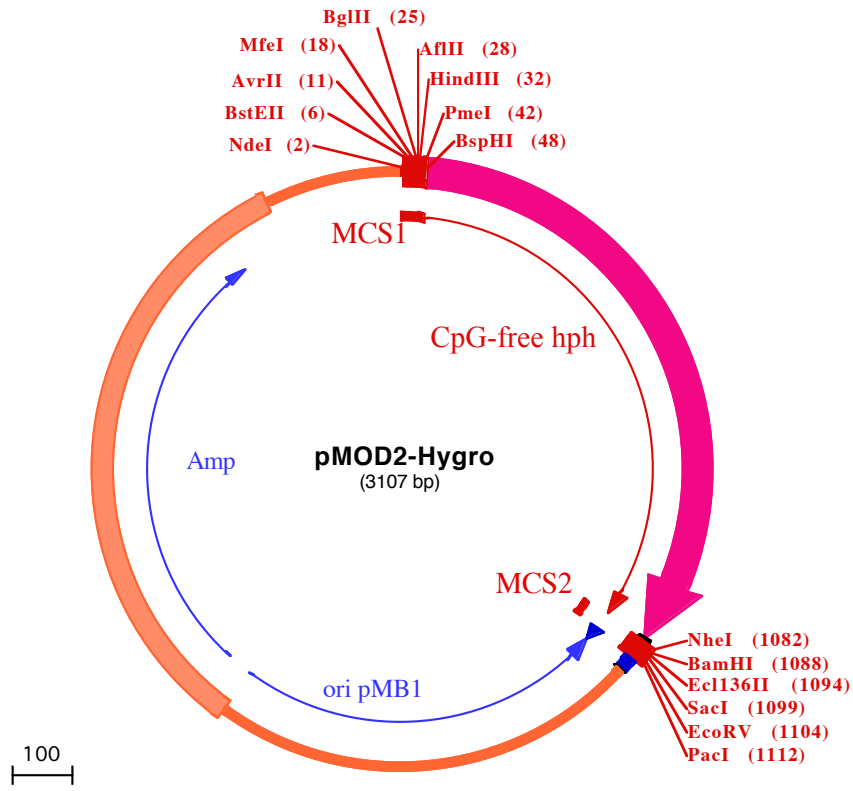
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InvivoGen Asia: +852 3622-3480

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HindIII (32)

BstEII (6) **MfeI (18)** **AflIII (28)**
NdeI (2) **AvrII (11)** **BglII (25)** **PmeI (42)** **BspHI (48)**

1 CATATGGTGACCTAGGACAATTGTAGATCTTAAGCTTAGTTAAACATCATGAAGAAACCTGAAGCTGACAGCAACTTCTGTTGAGAAGTTTCTCATTGAA
101 AAATTTGATTCTGTTTCTGATCTCATGCAGCTGTCTGAAGGTGAAGAAAGCAGAGCCTTTTCTTTTGTGTTGGAGGAAGAGTTATGTTCTGAGGGTCA
180 K F D S V S D L M Q L S E G E E S R A F S F D V G G R G Y V L R V
201 ATCTTGTGCTGATGGTTTTACAAAGACAGATATGTTACAGACACTTGGCTGTGCTGCTGCAATTCCAGAAGTTCTGGACATGGAGGATTTTC
51 N S C A D G F Y K D R Y V Y R H F A S A A L P I P E V L D I G E F S
301 TGAATCTCTCACTACTGCATCAGCAGAAGAGCACAAGGAGTCACTCTCCAGGATCTCCCTGAAACTGAGCTGCCAGCTGTTCTGCAACTGTTGCTGAA
84 E S L T Y C I S R R A Q G V T L Q D L P E T E L P A V L Q P V A E
401 GCAATGGATGCCATTGAGGATTCTGAGCAGCTGATCTGAGCAGCTGATTTGGTCTTTTGGTCCCAAGGCATTGGTCAGTACACCCTGGAGGGATTTCA
118 A M D A I A A A D L S Q T S G F G P F G P Q G I G Q Y T T W R D F
501 TTTGTGCCATTGCTGATCTCATGTCTACTGGCAGACTGTGATGGATGACACAGTTTCTGCTTCTGTTGCTCAGGCACTGGATGAACCTCATGCTGTG
151 I C A I A D P H V Y H W Q T V M D D T V S A S V A Q A L D E L M L W
601 GGCAGAAGATTGCTTGAAGTCAGACACCTGGTCCATGCTGATTTTGAAGCAACAATGTTCTGACAGACAATGCCAGAACTCACTGCAGTCACTGACTGG
184 A E D C P E V R H L V H A D F G S N N V L T D N G R I T A V I D W
701 TCTGAAGCCATGTTTGGAGATTCTCAATATGAGGTTGCCAACATTTTTTTGGAGACCTGGCTGGCTTGCATGGAACAACAAGATATTTTGAA
218 S E A M F G D S Q Y E V A N I F F W R P W L A C M E Q Q T R Y F E
801 GAAGACACCCAGAAGCTGGTGGTCCCGCAGACTGAGAGCCTACATGCTCAGAATTGGCCTGGACCAACTGTATCAATCTCTGGTTGATGGAACTTTGA
251 R R H P E L A G S P R L R A Y M L R I G L D Q L Y Q S L V D G N F D
901 TGATGCTGCTTGGGCACAAGAGATGTGATGCCATTGTAGGCTGGTGTCTGGAAGCTGTTGGAAGAATCAAATGCAAGAAAGGCTGCTGCTGTTGG
284 D A A W A Q G R C D A I V R S G A G T V G R T Q I A R R S A A V W

SacI (1099)

1001 ACTGATGGATGTTGTAAGTTCTGGCTGACTCTGGAACAGGAGACCCTCCACAAGACCCAGAGCCAAGGAATGAatattaGCTAGCGGATCTGAGCTC
318 T D G C V E V L A D S G N R R P S T R P R A K E •

BamHI (1088)
NheI (1082) **Ecl136II (1094)**

PaeI (1112)
EcoRV (1104)

1101 TGATATCTTAATAAAAACCCGCTTCGGCGGGTTTTTTATGCATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTCTGGCG
1201 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGGTTTT
1301 CCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACCAGGATACCTGTCCGCTTTCTCCCTTCCGGGAAGCGTGGCGCTTCTCAT AG
1401 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCAGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGT
1501 AACATCGCTTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA
1601 CAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG
1701 TAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT
1801 TTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGGTCATGCATGAGACAATAACCTGATAAATGCTTCAATAA
1901 TATTGAAAAAGGAAGTATGAGTATCAACATTTCCGTGTCGCCCTTATTCCTTTTTTGGCGGCATTTTGCCTTCTGTTTTGCTCACCCAGA AACGC
2001 TGGTGAAGTAAAAGATGCTGAAGATCAGTTGGGTGACGAGTGGGTTACATCGAAGTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGA
280 L V K V K D A E D Q L G A R V G Y I E L D L N S G K I L E S F R P E
2101 AGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTCCGCCGATACAC
61 E R F P M M S T F K V L L C G A V L S R I D A G Q E Q L G R R I H
2201 TATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGTGCATAACCATGA
95 Y S Q N D L V E Y S P V T E K H L T D G M T V R E L C S A A I T M
2301 GTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGAGGCTAAGCGCTTTTTTGACAACATGGGGGATCATGTAACCTCGCCTTGA
128 S D N T A A N L L L T T I G G P K E L T A F L H N M G D H V T R L D
2401 TCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACCTGGC
161 R W E P E L N E A I P N D E R D T T M P V A M A T T L R K L L T G
2501 GAACTACTTACTCTAGCTTCCCGGCAACAATTAAGACTGGATGGAGCGGGATAAAGTTGCAAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGT
195 E L L T L A S R Q Q L I D W M E A D K V A G P L L R S A L P A G W
2601 TTATTGCTGATAAATCTGGAGCCGTTGAGCGTGGGTCTCGCGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAC
228 F I A D K S G A G E R G S R G I A A L G P D G K P S R I V V I Y T
2701 GACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAAGTGTGAGCAAGTTTACTCA
261 T G S Q A T M D E R N R Q I A E I G A S L I K H W •
2801 TATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACATTAACCTATAAAAAAT
2901 AGGCGTATCACGAGGCCCTTCTGCTCGCGCTTTCGGTGATGACGGTGAACACTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTGTCTGTAAG
3001 CGGATCCCGGGAGCAGACAAGCCCGTCAAGGCGCGTCAAGCGGTTGGCGGGTGTGCGGGCTGGCTTAACATGCGGCATCAGAGCAGATTGTACTGAG
3101 AGTGCAC