

# pINFUSE-hIgG4-Fc1

Plasmid designed for the construction of Fc-Fusion proteins

Catalog # pfc1-hgin40

For research use only

Version 20K06-MM

## PRODUCT INFORMATION

### Content:

- 20  $\mu$ g of pINFUSE-hIgG4-Fc1 plasmid provided as lyophilized DNA.
- 1 ml of Zeocin™ (100 mg/ml)

### Storage and Stability:

- Product is shipped at room temperature.
- Lyophilized DNA should be stored at -20°C and is stable 3 months.
- Resuspended DNA should be stored at -20°C and is stable up to 1 year.
- Store Zeocin™ at 4 °C or at -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

pINFUSE-Fc is a family of plasmid developed to facilitate the construction of Fc-fusion proteins by fusing the effector region of a protein to the Fc region of an immunoglobulin G (IgG).

pINFUSE-Fc plasmids yield high levels of Fc-fusion proteins. The level of expression is usually in the  $\mu$ g/mL range. They can be transfected in a variety of mammalian cells, including myeloma cell lines, CHO cells, monkey COS cells and human embryonic kidney (HEK)293 cells, cells that are commonly used in protein purification systems.

pINFUSE-Fc plasmids allow the secretion of Fc-Fusion proteins. As Fc-Fusion proteins are secreted, they can be easily detected in the supernatant of pINFUSE-Fc-transfected cells by SDS-PAGE. Furthermore, functional domains can be identified by immunoblotting and ligand blotting.

Fc-Fusion proteins can be easily purified by single-step protein A or protein G affinity chromatography.

InvivoGen provides pINFUSE-Fc vectors featuring Fc regions containing introns from different species and isotypes. In humans, there are four isotypes: IgG1, IgG2, IgG3 and IgG4. The Fc region mediates effector functions, such as antibody-dependent cellular cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC). IgG isoforms exert different levels of effector functions increasing in the order of IgG4<IgG2<IgG1≤IgG3.

## PLASMID FEATURES

- **human genomic IgG2-Fc (with introns):** The Fc region comprises the CH2 and CH3 domains of the IgG heavy chain and the hinge region. The hinge serves as a flexible spacer between the two parts of the Fc-fusion protein, allowing each part of the molecule to function independently. A short intron is present between each region (one intron between the hinge and CH2 and one intron between CH2 and CH3). The presence of introns is known to enhance the level of gene expression as splicing is known to promote rapid and efficient mRNA export<sup>1</sup>. Human IgG4 displays low ADCC and CDC.
- **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1 $\alpha$  (EF-1 $\alpha$ ) core promoter<sup>2</sup> and the R segment and part of the U5 sequence (R-U5') of the Human T-Cell Leukemia Virus (HTLV) Type 1 Long Terminal Repeat<sup>3</sup>. The EF-1 $\alpha$  promoter exhibits a strong activity and yields long lasting expression of a transgene *in vivo*. The R-U5' has been coupled to the EF-1 $\alpha$  core promoter to enhance stability of RNA.
- **MCS:** The multiple cloning site contains several restriction sites that are compatible with many other enzymes, thus facilitating cloning.
- **SV40 pAn:** the Simian Virus 40 late polyadenylation signal enables efficient cleavage and polyadenylation reactions resulting in high levels of steady-state mRNA<sup>4</sup>.
- **ori:** a minimal *E. coli* origin of replication to limit vector size, but with the same activity as the longer Ori.
- **CMV enh / hFerL prom:** This composite promoter combines the human cytomegalovirus immediate-early gene 1 enhancer and the core promoter of the human ferritin light chain gene. This ubiquitous promoter drives the expression of the Zeocin™-resistance gene in mammalian cells.
- **EM2KC** is a bacterial promoter that enables the constitutive expression of the antibiotic resistance gene in *E. coli*. EM2KC is located within an intron and is spliced out in mammalian cells.
- **Zeo:** Resistance to Zeocin™ is conferred by the *Sh ble* gene from *Streptoalloteichus hindustanus*. The same resistance gene confers selection in both mammalian cells and *E. coli*.
- **$\beta$ Glo pAn:** The human beta-globin 3'UTR and polyadenylation sequence allows efficient arrest of the transgene transcription<sup>5</sup>.

## TECHNICAL SUPPORT

InvivoGen USA (Toll-Free): 888-457-5873

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## 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 H<sub>2</sub>O. Store resuspended plasmid at -20 °C.

### Plasmid amplification and cloning

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

### Zeocin™ usage

This antibiotic can be used for *E. coli* at 25 µg/ml in liquid or solid media and at 50-200 µg/ml to select Zeocin™-resistant mammalian cells.

### References:

1. Nott A, et al. 2003. A quantitative analysis of intron effects on mammalian gene expression. *RNA*. 9(5):607-17.
2. Kim DW *et al.* 1990. Use of the human elongation factor 1 alpha promoter as a versatile and efficient expression system. *91(2):217-23*.
3. Takebe Y. *et al.* 1988. SR alpha promoter: an efficient and versatile mammalian cDNA expression system composed of the simian virus 40 early promoter and the R-U5 segment of human T-cell leukemia virus type 1 long terminal repeat. *Mol Cell Biol*. 8(1):466-72.
4. Carswell S. & Alwine JC. 1989. Efficiency of utilization of the simian virus 40 late polyadenylation site: effects of upstream sequences. *Mol Cell Biol*. 9(10):4248-58.
5. Yu J. & Russell JE. 2001. Structural and functional analysis of an mRNP complex that mediates the high stability of human beta-globin mRNA. *Mol Cell Biol*. 21(17):5879-88.

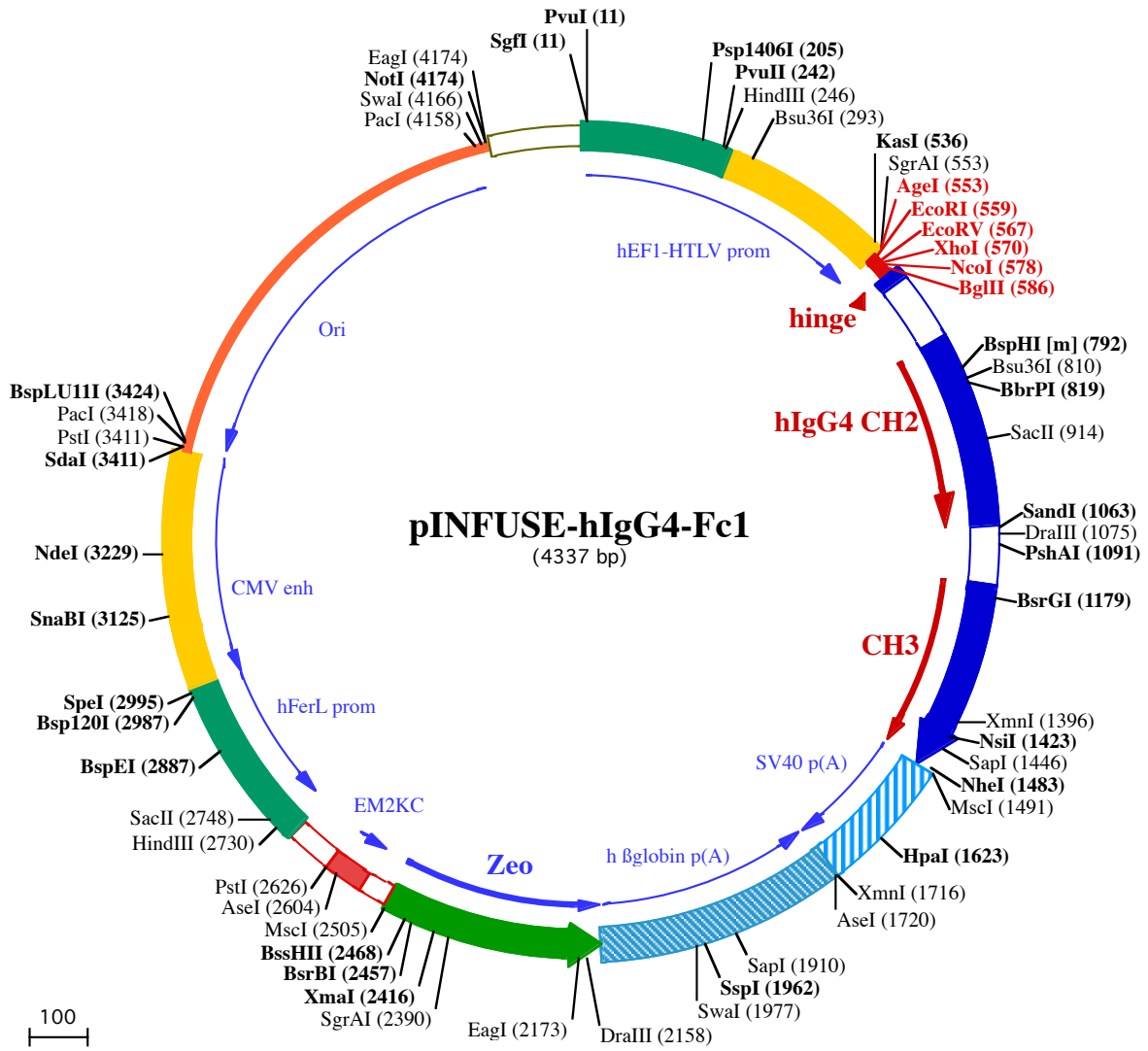
## RELATED PRODUCTS

Product	Catalog Code
Zeocin™	ant-zn-1

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**PvuI (11)**  
**SgfI (11)**  
 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (246)**  
**Psp1406I (205)** **PvuII (242)** **Bsu36I (293)**  
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**EcoRI (559)**  
**AgeI (553)** **XhoI (570)**  
**KasI (536)** **SgrAI (553)** **EcoRV (567)** **NcoI (578)** **BglII (586)**  
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTGAATTCGATATCTCGAGCACCATGGTTAGATCTCCCCATGC  
 601 CCATCATGCCAGGtaagccaaccaggcctcgccctcagctcaaggcgggacaggtgcctagagttagcctgcatcaggggacaggccccagccgggt  
 4▶ P S C P 1▶ P P C

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**BspHI [m] (792)**  
 701 gctgagcatccacctccatctcttctcagCACCTGAGTTCCTGGGGGACCATCAGTCTTCTGTTCCTGTTCCCCAAAACCAAGGACACTCTCATGATCT  
 1▶ P E F L G G P S V F L F P P K P K D T L M I

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**BbrPI (819)**  
**Bsu36I (810)**  
 801 CCCGGACCCTGAGGTCAGTGCCTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTCAACTGGTACGTGGATGGCGTGGAGTGCATAATGC  
 23▶ S R T P E V T C V V V D V S Q E D P E V Q F N W Y V D G V E V H N A  
**SacII (914)**  
 901 CAAGCAAAGCCGCGGAGGAGCAGTCAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAGGACTGGTGAACGGCAAGGAGTACAAG  
 56▶ K T K P R E E Q F N S T Y R V V S V L T V L H Q D W L N G K E Y K

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**DraIII (1075)** **SandI (1063)** **PshAI (1091)**  
 1001 TGCAAGTCTCCAACAAAGCCCTCCCGTCTCCATCGAGAAAACCATCTCCAAGCCAAAGTgggaccacaggggtgagggccacatggacagaggt  
 90▶ C K V S N K G L P S S I E K T I S K A K

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**BsrGI (1179)**  
 1101 cagctcggcccaccctctgccctgggagtgaccgctgtgccaacctctgtccctacagGGCAGCCCCGAGAGCCACAGGTGTACACCTGCCCCATCCC  
 1▶ Q P R E P Q V Y T L P P S  
 1201 AGGAGGAGATGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGA  
 14▶ Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E

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**XmnI (1396)**  
 1301 GAACAACATAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAAT  
 47▶ N N Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N

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**NsiI (1423)** **SapI (1446)** **NheI (1483)**  
 1401 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACAGAAAGCCCTCCTGTCTCTGGGTAATAAAGCTAGCTGGCCAGACATG  
 81▶ V F S C S V M H E A L H N H Y T Q K S L S L S L G K •  
 1501 ATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCA

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**HpaI (1623)**  
 1601 TTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTATTTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCT

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**AseI (1720)** **XmnI (1716)**  
 1701 CTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAG  
 1801 GCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAC

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**SapI (1910)** **SspI (1962)** **SwaI (1977)**  
 1901 TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAT  
 2001 AAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAA

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**DraIII (2158)** **EagI (2173)**  
 2101 TTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTCTGCCACAAAGTGCACGCAGTTGCCGGCCGGTTCGCGCAGGGCGAACTCCCG  
 125▶ • D Q E E A V F H V C N G A P D R L A F E R  
 2201 CCCCCAGGCTGCTCGCCGATCTCGGTGATGGCCGGCCGGAGGCGTCCCGGAAGTTCGTGGACACGACCTCCGACACTCGGCGTACAGCTCGTCCAGG  
 103▶ G W P Q E G I E T M A P G S A D R F N T S V V E S W E A Y L E D L

2301 CCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACCACTGGTCTGGACCGCGCTGATGAACAGGGTCACGTCGTCCCGGACCACCCGGCGAAGT  
69 G R V W V W A L T N D P V V Q D Q V A S I F L T V D D R V V G A F D  
XmaI (2416) BsrBI (2457) BssHII (2468)  
2401 CGTCCTCCACGAAGTCCCGGGAGAACCAGCCGGTCCGTCAGAACTCGACCGCTCCGGCGACGTCGCGCGCGGTGAGCACCGGAACGGCACTGGTCAA  
36 D E V F D R S F G L R D T W F E V A G A V D R A T L V P V A S T L  
MscI (2505)  
2501 CTTGGCCATGATGGCTCCTCctgtcaggagaggaaagagaagaaggttagtacaattgCTATAGTGAGTTGTATTATACTATGCGATATACTATGCCAA  
3 K A M  
AseI (2604) PstI (2626)  
2601 TGATTAATTGTCAAACACTAGGGCTGCAgggttcatagtgccacttttctgcactgccccatctcctgccacccttccaggcatagacagtcaagtac  
HindIII (2730) SacII (2748)  
2701 ttacCAAACCTCACAGGAGGGAGAAGGCAGAAGCTTGAGACAGACCCGCGGACCGCCGAACCTGCGAGGGGACGTGGCTAGGGCGGCTCTTTTATGGTGC  
BspEI (2887)  
2801 GCCGGCCCTCGGAGGCAGGGCGCTCGGGGAGGCTAGCGCCAATCTGCGGTGGCAGGAGCGGGGCCGAAGCCGTGCTGACCAATCCGGAGCACATA  
SpeI (2995)  
2901 GGAGTCTCAGCCCCCGCCCAAAGCAAGGGGAAGTCACGCGCTGTAGCGCCAGCGTGTGTGAAATGGGGGCTTGGGGGGTTGGGGCCCTGACTAGT  
Bsp120I (2987)  
3001 CAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCA  
SnaBI (3125)  
3101 TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTC  
NdeI (3229)  
3201 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAA  
3301 GTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTTGGCGGTGTCAGCCAGGCGGGCCATTTACCGTAAGTTATG  
PacI (3418)  
3401 TAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGC  
PstI (3411) SdaI (3411) BspLU11I (3424)  
3501 CCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCG  
3601 TGGCTCTCCTGTTCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCT  
3701 CAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC  
3801 AACCCGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGT  
3901 GGCCTAACTACGGCTACTAGAAAGCAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA  
4001 ACAAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG  
EagI (4174)  
4101 TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTC  
PacI (4158) SmaI (4166) NotI (4174)  
4201 ATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCC  
4301 AGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA