

pFUSE-hIgG1-Fc1

Plasmid designed for the construction of Fc-Fusion proteins

Catalog # pfuse-hg1fc1

For research use only

Version 20K04-MM

PRODUCT INFORMATION

Content:

- 20 µg of pFUSE-hIgG1-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

pFUSE-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).

pFUSE-Fc plasmids yield high levels of Fc-fusion proteins. The level of expression is usually in the µg/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.

pFUSE-Fc plasmids allow the secretion of Fc-Fusion proteins. As Fc-Fusion proteins are secreted, they can be easily detected in the supernatant of pFUSE-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 pFUSE-Fc vectors featuring Fc regions 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

- **hIgG1-Fc (human):** 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. Human IgG1 displays high ADCC and CDC, and is the most suitable for therapeutic use against pathogens and cancer cells.
- **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1α (EF-1α) core promoter¹ and the R segment and part of the U5 sequence (R-U5') of the Human T-Cell Leukemia Virus (HTLV) Type 1 Long Terminal Repeat². The EF-1α promoter exhibits a strong activity and yields long lasting expression of a transgene *in vivo*. The R-U5' has been coupled to the EF-1α 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 mRNA³.
- **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 *Streptallosteichus hindustanus*. The same resistance gene confers selection in both mammalian cells and *E. coli*.
- **BGlo pAn:** The human beta-globin 3'UTR and polyadenylation sequence allows efficient arrest of the transgene transcription⁴.

1. 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.

2. 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.

3. 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.

4. 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.

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 H₂O. 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.

RELATED PRODUCTS

Product	Catalog Code
Zeocin™	ant-zn-1

TECHNICAL SUPPORT

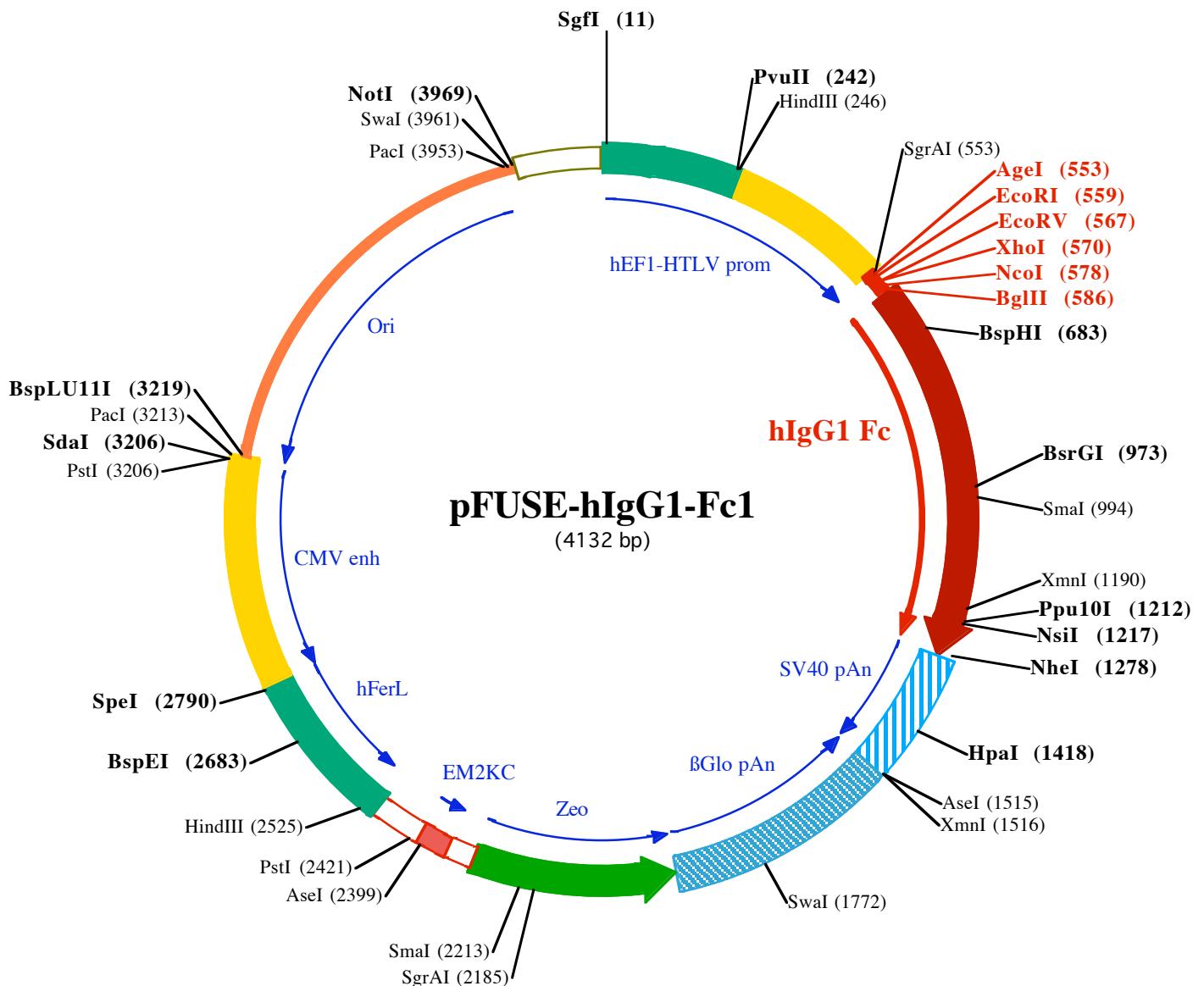
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SgII (11)

1 GGATCTCGATCGCTCCGGTCCCCGTCAGTGGCAGAGGCACATGCCAACAGTCCCAGAAGTTGGGGAGGGTCGCAATTGACGGTGCCTA

101 GAGAAGGTGGCGGGGAAACTGGAAAGTGTGCTGACTGGCTCGCTTTCCGAGGGGGAGAACCGTATAAGTCAGTAGTCGCC

HindIII (246)
PvuII (242)

201 GTGAACGTTTTTCGCAACGGTTGCCAGAACACAGCTGAAGCTTGAGGGCTCGCATCTCCCTCACCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCTCTGCCGCCCTGTTGCCCTGAAGTGCCTGAGCTAGTAAGTTAAAGCTCAGGTGAGACC

401 GGGCCTTGTCCGGCTCCCTGGAGCTACCTAGACTCAGCCGGCTCCACGCTTGCTGACCTGCTCAACTCTACGCTTTGTTGTT

EcoRI (559) XbaI (570) BglIII (586)

AgeI (553) EcoRV (567) NcoI (578)

501 TCTGTTGCGCCGTTACAGATCCAAGCTGTGACCCGGCCACCTGAGATCACCGGTAATTGATATCTCGAGCACCATGGTAGATCTGACAAA
ACT → AspLysThr

BspHI (683)

601 CACACATGCCACCGTGGCCAGCACCTGAACCTCTGGGGGACCGTCAGTCTCTCCCTTCCCCCAAACCAAGGACACCCATCGATCTCCGGACC
4► Hi s Thr CysProProCysProAl aProGl uLeuLeuGl yGl yProSer Val PheLeuPheProProLysProLysAspThr LeuMet I I eSer ArgThr P

701 CTGAGGTACATCGCTGGTGGACGTCAGGCCAGAACCCCTGAGGTCAAGTCAACTGGTAGTGGACGCCGTGGAGGTGATAATGCCAACAAA
37► r oGl uVal Thr CysVal Val Val AspVal Ser Hi s Gl uAspProGl uVal LysPheAsnTrpTyrVal AspGl yVal Gl uVal Hi s AsnAl alysThr Ly

801 GCCCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCCTCACCCTGACCAGGACTGGCTGAATGCCAGGAGTACAAGTGAAGGTC
70► s ProArgGl uGl uGl nTyrAsnSer Thr TyrArgVal Val Ser Val LeuThr Val LeuHi s Gl nAspTrpLeuAsnGl yLysGl uTyrLysCysLyVal

SmaI (994)

901 TCCAACAAAGCCCTCCAGCCCCATCGAGAAAACATCTCAAAGCCAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCATCCGGAGG
104► SerAsnLysAl aLeuP roAl aProI l eGl uLysThr I I eSer LysAl aLysGl yGl nProArgGl uProGl nVal I TyrThr LeuP roProSer ArgGl uG

1001 AGATGACCAAGAACAGGTGACGCTGCTGTCAAAGCTCTATCCAGCAGCATCGCTGGAGTGGAGAGACATGGCAGCGGAGAACAA
137► l uMetThr LysAsnGl nVal Ser LeuThr CysLeuVal LysGl yPheTyrProSerAspI l eAl aVal Gl uTrpGl uSerAsnGl yGl nProGl uAsnAs

XmnI (1195)

1101 CTACAAGACCACGCCCTCCGTGACTCCGACGGCTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTC
170► nTyrLysThr Thr ProProVal LeuAspSer AspGl ySer PhePheLeuTyrSer LysLeuThr Val AspLysSer ArgTrpGl nGl yAsnVal Phe

NheI (1278)

1201 TCATGCTCGTGTGACTCACGAGGCTCTGACAACACACTACACGCAGAGAGCCTCTCTCGCTCGGGTAAATGAGTGTAGCTGGCAGACATGATAAG
204► Ser CysSer ValMetHi s Gl uAl aLeuHi s AsnHi s TyrThr Gl nLysSer LeuSer LeuSer ProGl yLys***

1301 ATACATTGATGAGTTGGACAAACACAACTAGAATGCACTGAGTAAAAATGCTTTATGTGAAATTGTGATGCTATTGCTTATTGTAACCACTATA

HpaI (1418)

1401 AGCTCAATAAACAGTTAACACAACAAATTGCATTCTTTATGTTCAGGTTAGGGGGAGGTGAGGTTAAAGCAAGTAAACCTCTACA

AscI (1515)
XmnI (1516)

1501 AATGTTGATGAAATTCTAAACATACAGCATAGCAAAACTTAACTCTCAAATCAAGCTCTACTTGAATCCTTCTGAGGGATGAATAAGGCATA
→ ←

1601 GGATCAGGGCTTGTCCAATGTCATTAGCTGTTGAGCCTCACCTCTTATGGAGTTAAAGATATAGTGTATTTCCAAGGTTGAACTAGCT

SwaI (1772)

1701 CCTCATTCTTATTTAAATGCACTGACCTCCACATCCCTTTAGTAAATATTCAAATAATTAAATACATATTGCAATGAAATAAATAG

1801 TTTTTATTAGGCAGAACATCCAGATGCTCAAGGCCCTCATATAATCCCCAGTTAGTTAGTTGACTTAGGAACAAAGAACCTTAATAGAAATTGGA

1901 CAGCAAGAAAGCAGCTCTAGTTATCTCAGTCAGCTGCTCTGCCAACAGTGCACGCAGTGGCCGGGTCGCGAGGGCAACTCCGCC
125► *••AspGl nGl uGl uAl aVal PheHi s Val CysAsnGl yAl aProAspArgLeuAl aPheGl uArgGl yTr

2001 ACGGCTGCTCGCGATCGGTACGGTACGGCGGGGGGGAGGGCTCCCGAAGTCGACAGCACCTCGCCACTCGGCACAGCTCGCCAGGGCG
101► pProGl nGl uGl yI I eGl uThr MetAl aP roGl ySer Al aAspArgPheAsnThr Ser Val Val Gl uUser TrpGl uAl aTyrLeuGl uAspLeuGl yArg

2101 CACCCACACCCAGGGCAGGGTGTGGCGCACCCCTGGTCTGGACCCGCTGATGACAGGGTACGTCGCCCCGACACCGCGAAGTCG
68► Val TrpVal TrpAl aLeuThrAsnAspProVal Val Gl nAspGl nVal Al aSer I I ePheLeuThr Val AspAspArgVal Val Gl yAl aPheAspAspG

SmaI (2213)

2201 TCCACGAAGTCCGGAGAACCCGAGCCGTCGGTCCAGAACACTGACCGCTCCGGGACGTCGCGCGCGTGGAGCAGGGAAACGGCACTGGTCAACTGG
34► l uVal PheAspArgSer PheGl yLeuArgAspThr TrpPheGl uVal Al aGl yAl aVal AspArgAl aThr LeuVal P roVal Al aSer Thr LeuLysAl

2301 CCATGATGGCTCCTgtcaggagaggaaagagaaggtagataattgCTATAGTGAGTTGATTATACTATGCAGATATACTATGCCAATGATT
1► aMet ←

PstI (2421)

2401 ATTGTCAAACATAGGGCTGCAgggttcatagtgcacccatcttcgtactgccccatctctgcccaccccttccaggcatagacagtcaacttgacttC

HindIII (2525)

2501 AAACATCACAGGAGGGAGAACAGAGCTGAGACAGACCCGGGACCCGAACTGCGAGGGGAGTGGCTAGGGCGCTTTATGGTGCAGCG
→ ←

BspEI (2683)

2601 CCCTCGGAGGCAGGGCGCTGGGAGGCCATCGGCCAATCTCGGTGGCAGGAGGCCGGCAAGGCCGTGCCTGACCAATCCGGAGCACAGGT

SpeI (2790)

2701 CTCAGCCCCCGCCCAAAGCAAGGGAAAGTCACGCCCTGTAGGCCAGCGTGGTAAATGGGGCTTGGGGGGCTGACTAGTCAGTC
→ ←

2801 CAAACTCCCATTGACGTCATGGGTGGAGACTTGGAAATCCCGTGAATCCACGCCATTGATGACTGCAAAACCGCATCATCATG

2901 GTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTATGACTGGCATAATGCCAGGGGCCATTACCGTATTGA

3001 CGTCAATAGGGGGCTACTTGGCATATGATACTTGTGACTGCCAAGTGGCAGTTACCGTAATAACTCCACCCATTGACGTCAATGAAAGTCCC

3101 TATTGGCTTACTATGGAAACATACGTCATTGACGTCATGGCGGGGGTCGTTGGCGGTAGGCCAGGGGGCATTACCGTAAGTTATGTAACG

PacI (3213)
PstI (3206) SdaI (3206) BspLU11I (3219)

3201 CCTCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCTGGCGTTTCCATAGGCTCCGCCCCC
3301 TGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCCTTCCCCCTGGAAGCTCCCTCGTGC
3401 TCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCGCCCTTCTCCCTCGGAAGCGTGGCGCTTCTAGCTCACGCTGTAGGTATCTCAGT
3501 CGGTGTAGGTCGTCGCTCCAAGCTGGCTGTGACGAACCCCCGTTAGCCCACCGCTGCCCTATCCGTAACTATCGTCTGAGTCCAACCC
3601 GGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCCTGCTACAGAGTTGAAGTGGTGCCT
3701 AACTACGGCTACACTAGAAGAACAGTATTGGTATCTGCCTCTGTAAGCCAGTTACCTCGAAAAAGAGTTGGTAGCTCTTGATCCGGAAACAAA
3801 CCACCGCTGGTAGCGGTGGTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTAAGAAGATCCTTGATCTTCTACGGGTCTGA

PacI (3953) SwaI (3961) NotI (3969)

3901 CGCTCAGTGGAACGAAACTCACGTTAAGGGATTTGGTCATGGTAGTTAATTAACATTAAATCAGCGGCCGCAATAAAATATCTTATTTCTTAC
4001 ATCTGTGTTGGTTTTGTGAATCGTAACATACGCTCTCCATAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGCCCCAGTGC
4101 AAGTCAGGTGCCAGAACATTCTATCGAA