

pFUSE-mIgG1-Fc1

Plasmid containing a mouse IgG1 Fc region

Catalog code: pfuse-mg1fc1

<https://www.invivogen.com/pfuse-migg1-fc>

For research use only

Version 20K04-MM

PRODUCT INFORMATION

Contents:

- 20 µg of pFUSE-mIgG1-Fc1 plasmid provided as lyophilized DNA
- 1 ml of Zeocin™ (100 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 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 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. Three murine isotypes are available: IgG1, IgG2a and IgG3. The Fc region mediates effector functions, such as antibody-dependent cellular cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC). In ADCC, the Fc region of an antibody binds to Fc receptors (FcγRs) on the surface of immune effector cells such as natural killers and macrophages, leading to the phagocytosis or lysis of the targeted cells. In CDC, the antibodies kill the targeted cells by triggering the complement cascade at the cell surface. IgG isoforms exert different levels of effector functions increasing in the order of mIgG1 < mIgG3 < mIgG2a.

WARNING: mIgG1-Fc has a very low affinity to Protein A and Protein G making it difficult to purify.

PLASMID FEATURES

• **mIgG1 Fc (mouse):** 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.

The Fc region of mouse IgG1 mediates low CDC and no ADCC¹.

• **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1α (EF-1α) core promoter² and the R segment and part of the U5 sequence (R-U5') of the Human T-Cell Leukemia Virus (HTLV) Type 1 Long Terminal Repeat³. 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 mRNA⁴.

• **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*.

• **βGlo pAn:** The human beta-globin 3'UTR and polyadenylation sequence allows efficient arrest of the transgene transcription⁵.

1. Kipps TJ. *et al.*, 1985. Importance of immunoglobulin isotype in human antibody-dependent, cell-mediated cytotoxicity directed by murine monoclonal antibodies. *J Exp Med.* 161(1):1-17.

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.

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

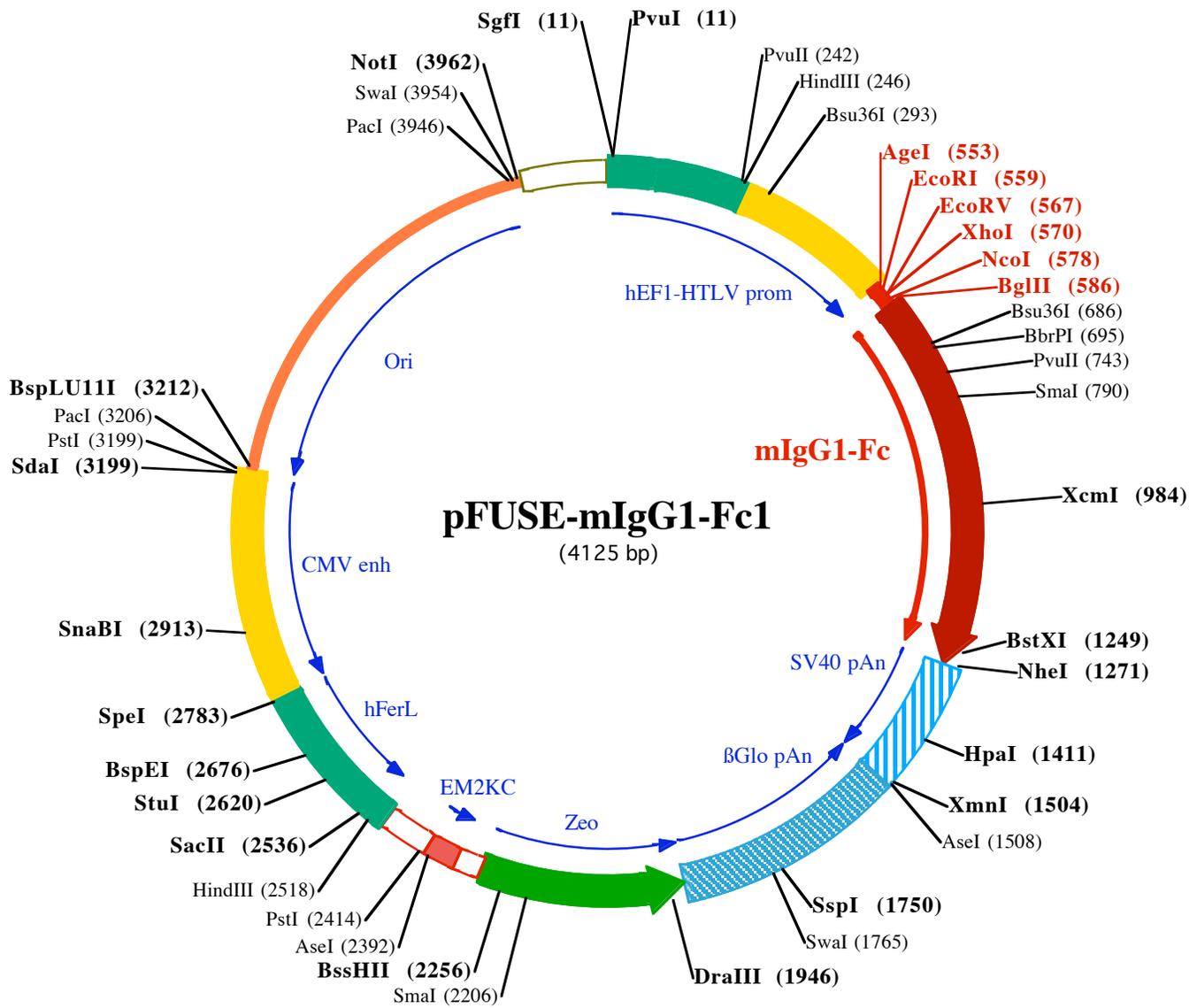
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PvuI (11)
SgfI (11)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGTTCGCAATTGAACGGGTGCCTA
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (246)
201 GTGAACGTTCTTTTTCGCAACGGGTTGCGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCGCCCTACCTGAGGGC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGTTAAGTTTAAAGCTCAGTTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

EcoRI (559) **XhoI (570)** **BglII (586)**
AgeI (553) **EcoRV (567)** **NcoI (578)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGTGAATTCGATATCTCGAGCACCATGGTTAGATCTGGTTGTAAG
1► Gl yCysLys
BbrPI (695)
601 CCTTCATATGTACAGTCCAGAAAGTATCATCTGTCTTACTTCCCCCAAAGCCAAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTACAGTGTG
4► ProCysI l eCysThr Val P roGl uVal l Ser Ser Val Phe l l ePheP roP roLysP roLysAspVal l euThr l l eThr LeuThr P roLysVal l Thr CysV

PvuII (743) **SmaI (790)**
701 TTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCAGTTCAGCTGGTTGTAGATGATGTGGAGTGCACACAGCTCAGACGCAACCCCGGAGGAGCA
37► a l Val Val Asp l l eSer LysAspAspP roGl uVal l Gl nPheSer T rpPheVal l AspAspVal l Gl uVal l Hi sThr Al aGl nThr Gl nP roArgGl uGl uGl
801 GTTCAACAGCACTTCCGCTCAGTCAGTGAACCTCCATCATGCCACAGACTGGCTCAATGGCAAGGAGTTCAAATGCAAGGTCAACAGTGCAGCTTTC
70► nPheAsnSer Thr PheArgSer Val l Ser Gl uLeuP ro l l eMetHi sGl nAspT rpLeuAsnGl yLysGl uPheLysCysArgVal l AsnSer Al aAl aPhe

XcmI (984)
901 CCTGCCCCATCGAAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCAAGGATA
104► P roAl aP ro l l eGl uLysThr l l eSer LysThr LysGl yArgP roLysAl aP roGl nVal l TyrThr l l eP roP roP roLysGl uGl nMe tAl aLysAspL
1001 AAGTCAGTCTGACCTGCATGATAACAGACTTCTCCCTGAAGACATTACTGTGGAGTGGCAGTGAATGGCAGCCAGCGGAGAAGTCAAGAACTCA
137► ysVal l Ser LeuThr CysMe t l l eThr AspPhePheP roGl uAsp l l eThr Val l Gl uT rpGl nT rpAsnGl yGl nP roAl aGl uAsnTyrLysAsnThr Gl
1101 GCCATCATGGACACAGATGGCTTACTTCTGCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGAGGAAATCTTACCTGCTGTGTATA
170► nP ro l l eMetAspThr AspGl ySer TyrPheVal l TyrSer LysLeuAsnVal l Gl nLysSerAsnT rpGl uAl aGl yAsnThr PheThr CysSer Val l eU

BstXI (1249) **NheI (1271)**
1201 CATGAGGCGTGCACAACCACCTACTGAGAAGAGCCTCCCACTCTCCTGGTAAATGATCCAGTGTGCTAGCTAGCTGGCCAGACATGATAAGATACATT
204► Hi sGl uGl yLeuHi sAsnHi sHi sThr Gl uLysSer LeuSer Hi sSer P roGl yLys •••
1301 GATGAGTTGGACAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCA

HpaI (1411)
1401 ATAAACAAGTTAAACAACAACAAATGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGG

AseI (1508) **XmnI (1504)**
1501 TATGGAATTAATCTAAAATACAGCATAGCAAAAATTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCA
1601 GGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCAAGGTTTGAACCTAGCTCTTCATT

SspI (1750) **SwaI (1765)**
1701 TCTTTATGTTTTAAATGCAGTGCACCTCCACATTCCTCTTTTAGTAAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTA
1801 TTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAG

DraIII (1946)
1901 AAAGCGAGTCTTCTAGCTTATCTCAGTCTGCTCTGCTGCCACAAGTGCACGAGTTCGCGCGGGTTCGCGAGGGCAACTCCCGCCCCACGGCTG
125► •••AspGl nGl uGl uAl aVal l PheHi sVal l CysAsnGl yAl aP roAspArgLeuAl aPheGl uArgGl yT rpP roGl n
2001 CTGCGCATCTCGGTATGGCCGGCCGGAGGCGTCCCGAAGTTCGTGGACACGACTCCGACCCTCGGCGTACAGCTCGTCCAGCGCCGCCACCCAC
99► Gl uGl y l l eGl uThr Me tAl aP roGl ySer Al aAspArgPheAsnThr Ser Val l Val l Gl uSer T rpGl uAl aT yrLeuGl uAspLeuGl yA rgVal l T rpV
2101 ACCAGGCCAGGGTGTGTCCGGCACCTGGCTGACCGCGCTGATGAACAGGGTCACTGCTCCCGACCACCGCGAAGTCTCTCCACGCA
65► Al l T rpAl aLeuThrAsnAspP roVal l Val l Gl nAspGl nVal l Al aSer l l ePheLeuThr Val l AspAspArgVal l Val l Gl yAl aPheAspAspGl uVal l Ph
2201 AGTCCCGGAGAACCCGAGCCGGTTCGAGTCCAGAACTCGACCGCTCCGGCGAGTTCGCGCGGTCGAGCACCAGGACGGCAGTGGTCAACTGGCCATGAT
32► eAspArgSer PheGl yLeuArgAspThr T rpPheGl uVal l Al aGl yAl aVal l AspArgAl aThr LeuVal l P roVal l Al aSer Thr LeuLysAl aMe t
2301 GGCTCCTCgtgcaggagagaagaagaaggttagtacaattgCTATAGTAGTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTC
AseI (2392)

PstI (2414)
2401 AAAGTAGGCTGCAGgttcatagtccacttttctgactgccccatctcctgccaccctttccaggcatagacagtcagtgacttacCAAACCTCA

HindIII (2518) **SacII (2536)**
2501 CAGGAGGAGAAGGCAGAAGCTTGAGACAGACCCCGGACCGCCGAAGTGCAGGGGACGTGGCTAGGGCGCTCTTTTATGTTGCGCCGCCCTCGG

StuI (2620) **BspEI (2676)**
2601 AGGACGGGCGCTCGGGAGGCTAGCGGCCAATCTGCGGTGGCAGGAGCGGGCCGAAGGCGTGCCTGACCAATCCGGAGCACATAGGAGTCTCAGCC

SpeI (2783)
2701 CCCC GCCCAAAGCAAGGGGAAGTCACCGCCTGTAGCGCCAGCGTGTGTGAAATGGGGCTTGGGGGTTGGGGCCCTGACTAGTCAAACCAAACCTC
2801 CCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCGGTAATAG

SnaBI (2913)
2901 CGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCACTGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCACTGACGTCAAT

3001 AGGGGGCGTACTTGCCATATGATACACTTGATGTAAGTGGCAAGTGGGCGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGC

PstI (3199)

SdaI (3199)

3101 GTTACTATGGGAACATACGTATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAG

PacI (3206) **BspLU11I (3212)**

3201 GTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAG

3301 CATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTG

3401 TTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTA

3501 GGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA

3601 CACGACTTATGCCACTGGCAGCAGCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTGAAGTGGTGGCCTAACTACG

3701 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGC

3801 TGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAG

PacI (3946) SmaI (3954) **NotI (3962)**

3901 TGGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTG

4001 TGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTCAAGTGCA

4101 GGTGCCAGAACATTTCTATCGAA