

pFUSE-mIgG2B-Fc1

Plasmid containing a mouse IgG2B Fc region

Catalog # pfuse-mg2bfc1

For research use only

Version 20K04-MM

PRODUCT INFORMATION

Content:

- 20 µg of pFUSE-mIgG2B-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 (when Fc portion is fused to a naturally secreted protein). 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.

In vivoGen provides pFUSE-Fc vectors featuring Fc regions from different species and isotypes. Several murine isotypes are available: IgG1, IgG2a & b, 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.

PLASMID FEATURES

- **mIgG2B 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 IgG2B mediates high ADCC and CDC.
- **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 *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 transcription⁴.

References:

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

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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

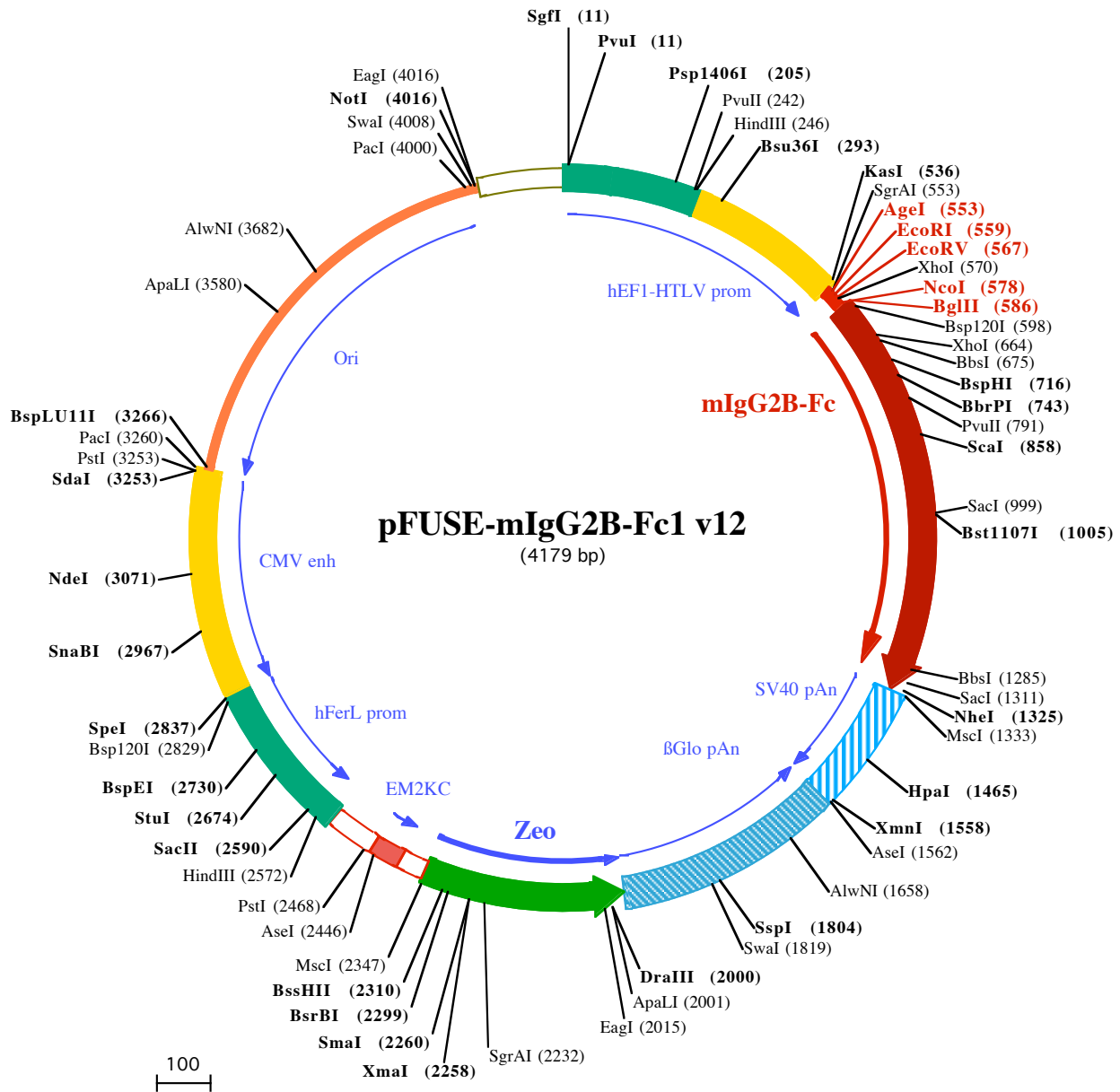
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PvuI (11)
SgfI (11)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (205) **HindIII (246)** **PvuII (242)** **Bsu36I (293)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGCGTTGAGTGCAGTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

EcoRI (559) **KasI (536)** **AgeI (553)** **XhoI (570)** **BglII (586)** **Bsp120I (598)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTGAATTCGATATCTCGAGCACCATGGTTAGATCTCCAGCGGG
1 P S G
601 CCCATTTCAACAATCAACCCTGTCTCCATGCAAGGAGTGTACAAATGCCAGCTCCTAACCTCGAGGGTGGACCATCCGTTCTTCCCTCCAA
4 P I S T I N P C P P C K E C H K C P A P N L E G G P S V F I F P P
BspHI (716) **BbrPI (743)** **PvuII (791)**
701 ATATCAAGGATGACTCATGATCTCCCTGACACCAAGGTCACGTGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTGT
37 N I K D V L M I S L T P K V T C V V V D V S E D D P D V Q I S W F V
ScaI (858)
801 GAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAACCCCTCCCATCCAGCACCAGGAC
70 N N V E V H T A Q T Q T H R E D Y N S T I R V V S T L P I Q H Q D
SacI (999)
901 TGGATGAGTGGCAAGGATTCAATGCAAGGTCAACAACAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGCTC
104 W M S G K E F K C K V N N K D L P S P I E R T I S K I K G L V R A
Bst1107I (1005)
1001 CACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCTGGGCTTCAACCTGGAGACATCAGTGT
137 P Q V Y I L P P P A E Q L S R K D V S L T C L V V G F N P G D I S V
1101 GGAGTGGACCAGCAATGGCATAACAGGAGAACTACAAGGACCCGACCCAGTCTGGACTCTGACGGTCTTACTTATATACAGCAAGCTCGATATA
170 E W T S N G H T E E N Y K D T A P V L D S D G S Y F I Y S K L D I
BbsI (1285)
1201 AAAACAAGCAAGTGGGAGAAAACAGATTCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGTCTCCGG
204 K T S K W E K T D S F S C N V R H E G L K N Y Y L K K T I S R S P
MscI (1333)
SacI (1311) **NheI (1325)**
1301 GTAATGAGCTCAGCACCCACAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAAGTGAATGCAGTGAATAAATGCT
237 G K •

HpaI (1465)
1401 TTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTATTTATGTTTCAGGT

AseI (1562) **XmnI (1558)**
1501 TCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTTAAAATACAGCATAGCAAACTTTAACCTCCA
AlwNI (1658)
1601 AATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTT
1701 TCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTA

SspI (1804) **SwaI (1819)**
1801 AAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGT

DraIII (2000)
1901 TTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCCTGCTCCTGCCACAAA
125 D Q E E A V F
ApaLI (2001) **EagI (2015)**
2001 GTGCACGAGTTGCCGGCGGGTGCAGGCGGAACTCCCGCCCCACGGTCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGTCCCGGAAGTTC
117 H V C N G A P D R L A F E R G W P Q E G I E T M A P G S A D R F N
2101 GTGACACGACCTCCGACACTCGGCGTACAGCTCGTCCAGGCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACACCTGGTCTGGACCGCGC
83 T S V V E S W E A Y L E D L G R V W V W A L T N D P V V Q D Q V A S
XmaI (2258) **SmaI (2260)** **BsrBI (2299)**
2201 TGATGAACAGGGTACGTCGTCGCCGACACACCGCGAAGTGTCTCCACGAAGTCCCGGGAAGCCGAGCCGGTCCGTCGAGAACTCGACCGCTCC
50 I F L T V D D R V V G A F D D E V F D R S F G L R D T W F E V A G
BssHII (2310) **MscI (2347)**
2301 GGCACGTCGCGCGGTGAGCACCGGAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCctgtcaggagaggaaagagaagaaggttagtacaattg
17 A V D R A T L V P V A S T L K A M

2401 CTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAAC TAGGGCTGCAGggttcatagtgccacttttctgcactgccc
← AseI (2446) PstI (2468)

2501 catctcctgccaccctttccaggcatagacagtcagtgacttacCAAAC TACAGGAGGAGAAGGCAGAAGCTTGAGACAGACCCGCGGACCGCG
HindIII (2572) SacII (2590)
←

2601 AACTGCGAGGGGACGTGGCTAGGGCGGCTTCTTTTATGGTGC CGCCCTCGGAGGCAGGGCGCTCGGGGAGCCTAGCGGCAATCTGCGGTGGCAGG
StuI (2674)

2701 AGGCGGGGCCGAAGGCCGTGCTGACCAATCCGGAGCACATAGGAGTCTCAGCCCCCGCCCAAGCAAGGGGAAGTACGCGCCTGTAGCGCCAGCGT
BspEI (2730)

2801 GTTGTGAAATGGGGCTTGGGGGGTTGGGGCCCTGACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAA
Bsp120I (2829) SpeI (2837)
←

2901 ACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAA
SnaBI (2967)

3001 GGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGG
NdeI (3071)

3101 GCAGTTTACCGTAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGT
PacI (3260)

3201 CGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC
PstI (3253) SdaI (3253) BspLU11I (3266)
←

3301 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG
3401 GACTATAAAGATACCAGGCGTTTCCCCCTGGAAGTCCCTCGTGCCTCTCTGTTCCGACCCCTGCCGTTACCGGATACCTGTCGCGCTTTCTCCCTTC

3501 GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAG
ApaLI (3580)

3601 CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA
AlwNI (3682)

3701 GAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCC
3801 AGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGA

3901 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCAATGGCTAGTTAAT
PacI (4000)

4001 TAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAA
EagI (4016) NotI (4016)
SwaI (4008)

4101 AACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA