

pFUSE-hIgG2e1-Fc2

Plasmid containing a human engineered IgG2 Fc region

Catalog # pfc2-hg2e1

For research use only

Version 20K05-MM

PRODUCT INFORMATION

Content:

- 20 µg of pFUSE-hIgG2e1-Fc2 (IL2ss) 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-Fc2 (IL2ss) plasmids allow the secretion of Fc-Fusion proteins. They contain the IL2 signal sequence (IL2ss) for the generation of Fc-Fusion proteins derived from proteins that are not naturally secreted. 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.

Under certain circumstances, for example when depletion of the target cell is undesirable, abrogating effector functions is required. On the contrary, in the case of antibodies intended for oncology use, increasing effector functions may improve their therapeutic activity¹. Modifying effector functions can be achieved by engineering the Fc regions to either improve or reduce their binding to FcγRs or the complement factors. Amino acids substitutions have been made in the human IgG1 Fc region in order to increase or reduce its ADCC and CDC.

PLASMID FEATURES

• **hIgG2e1-Fc (human IgG2 engineered Fc):** 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 human IgG2 Fc mediates low CDC and very low ADCC. To further reduce its cytotoxicity, the Fc region was engineered to reduce its binding affinity to the first component of the complement C1q by substituting the lysine residue at position 322 by an alanine².

• **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1α (EF-1α) core promoter³ and the R segment and part of the U5 sequence (R-U5') of the Human T-Cell Leukemia Virus (HTLV) Type 1 Long Terminal Repeat⁴. 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.

• **IL2 ss:** The IL2 signal sequence contains 20 amino acids and share common characteristics with signal peptides of other secretory proteins. The intracellular cleavage of the IL2 signal peptide occurs after Ser20 and leads to the secretion of the antigenic protein.

• **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 mRNA⁵.

• **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 transcription⁶.

1. Carter PJ., 2006. Potent antibody therapeutics by design. Nature Reviews Immunology. Advance online publication.

2. Idusogie EE. *et al.*, 2000. Mapping of the C1q binding site on rituxan, a chimeric antibody with a human IgG1 Fc. J Immunol. 164(8):4178-84. .

3. 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.

4. 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.

5. 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.

6. 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

InvivoGen USA (International): +1 (858) 457-5873

InvivoGen Europe: +33 (0) 5-62-71-69-39

InvivoGen Hong Kong: +852 3622-3480

E-mail: info@invivogen.com

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

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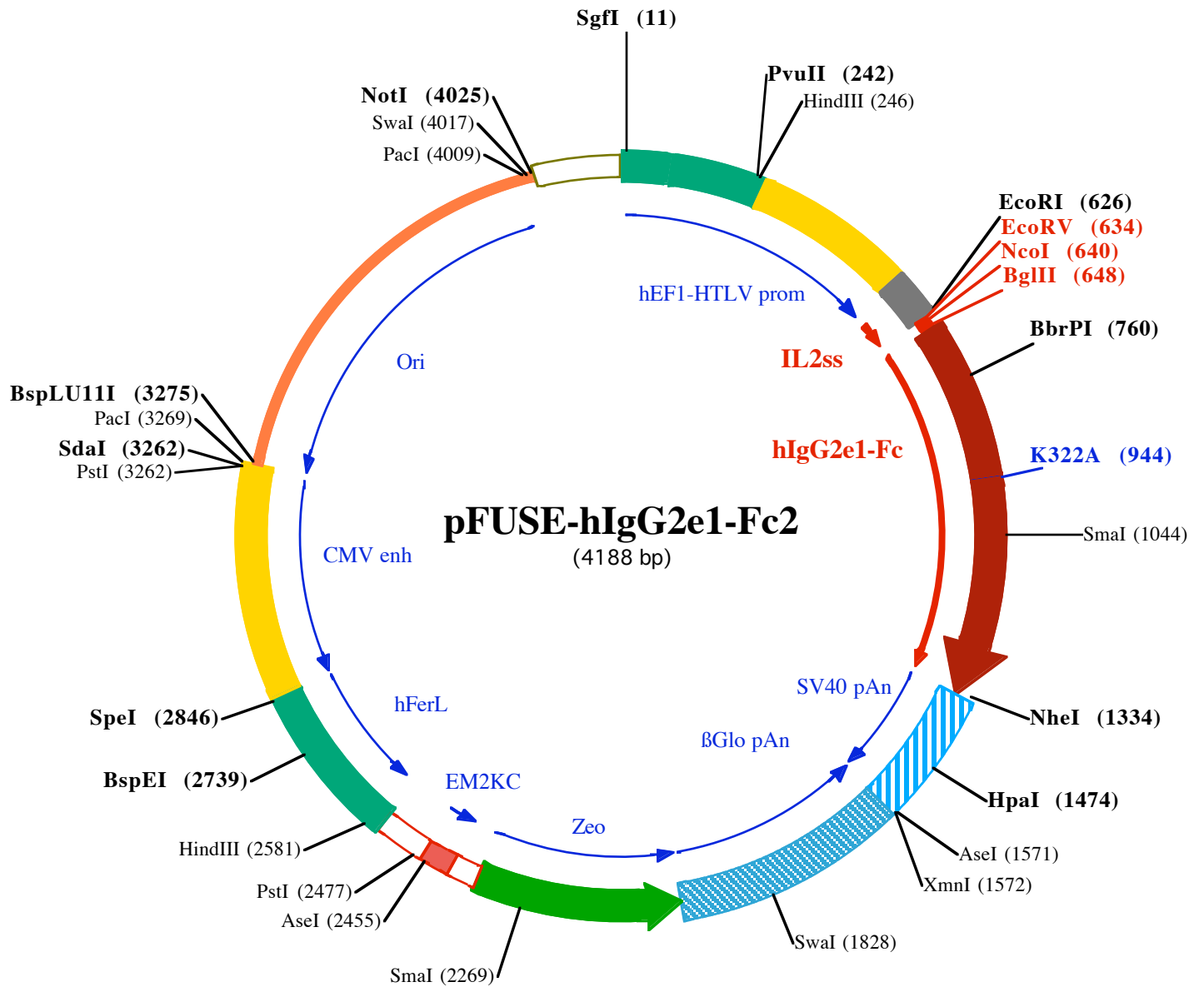
InvivoGen USA (Toll-Free): 888-457-5873

InvivoGen USA (International): +1 (858) 457-5873

InvivoGen Europe: +33 (0) 5-62-71-69-39

InvivoGen Hong Kong: +852 3622-3480

E-mail: info@invivogen.com



SgfI (11)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGTGCCTA

101 GAGAAGGTGGCGGGGTAACACTGGGAAAGTGATGTCGTGTAAGTGGTCCGCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (246)

PvuII (242)

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGACCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCAccggcGAAGGAGGGCCACCATGTACAGGATGCAACTCCTGTCTTGC A
1▶MetTyrArgMetGlnLeuLeuSerCysI

EcoRV (634) BglIII (648)

EcoRI (626) NcoI (640)

601 TTGCACTAAGTCTTGCCTTGTACGAAATTCGATATCGGCCATGGTTAGATCTGTGGAGTGGCCACCTTGCCAGCACCACCTGTGGCAGGACCTTCAGT
10▶leAlaLeuSerLeuAlaLeuVal 1▶ValGluCysProProCysProAlaProProValAlaGlyProSerVal

BbrPI (760)

701 CTTCTCTTCCCCAAAACCAAGGACACCCTGATGATCTCCAGAACCCTGAGGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTC
16▶I PheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAspProGluVal

801 CAGTTCAACTGGTACGTGGACGGCATGGAGGTGCATAATGCCAAGACAAAGCCAGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCTCA
50▶GlnPheAsnTrpTyrValAspGlyMetGluValHisAsnAlaLysThrLysProArgGluGluGluPheAsnSerThrPheArgValValSerValLeuT

K322A (944)

901 CCGTCGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCCTGGTCTCCAACAAAGGCTCCAGCCCCATCGAGAAAACCATCTCCAAAACCA
83▶hrValValHisGluAspTrpLeuAsnGlyLysGluTyrLysCysAlaValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSerLysThrLys

SmaI (1044)

1001 AGGCGAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTAC
116▶sGlyGluProArgGluProGluValTyrThrLeuProProSerArgGluGluMetThrLysAsnGluValSerLeuThrCysLeuValLysGlyPheTyr

1101 CCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGACGGGAGAACAACATAAGACCACCTCCCATGCTGGACTCCGACGGCTCTTCTTCTCT
150▶ProSerAspIleAlaValGluTrpGluSerAsnGlyGluProGluAsnAsnTyrLysThrThrProProMetLeuAspSerAspGlySerPhePheLeuT

1201 ACAGCAAGCTCACCGTGGACAAGAGCAGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAG
183▶yrSerLysLeuThrValAspLysSerArgTrpGluGluGluValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGluLysSer

NheI (1334)

1301 CCTCTCCTGTCTCCGGTAAATGAgTgccacgGCTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAA
216▶rLeuSerLeuSerProGlyLys...

HpaI (1474)

1401 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAACCAATTGCATTCATTTAT

AseI (1571)
XmnI (1572)

1501 GTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTCAAATGTGGTATGGAATTAATTCTAAATAACAGCATAGCAAACTT
125▶...AspGluGluGlu

1601 TAACCTCAAATCAAGCCTCTACTTGAATCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCT

1701 CACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAAGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTTCC

SwaI (1828)

1801 TTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATA

1901 TCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTC
125▶...AspGluGluGlu

2001 TGCCACAAAGTGCACGAGTTGCCGGCCGGTGCAGGCGGAACTCCCGCCCCACGGTCTGCTCGCCGATCTCGGTATGGCCGGCCGGAGGCGTCC
120▶AlaValPheHisValCysAsnGlyAlaProAspArgLeuAlaPheGluGlyTrpProGluGluGlyIleGluThrMetAlaProGlySerAlaAspA

2101 CGGAAGTTCGTGGACACGACTCCGACCCTCGGCTCAGCTGTCAGGCGCGCACCCACCCAGCCAGGCGGTGTTGTCGGCACCCCTGGTCTCCT
86▶rGlyPheAsnThrSerValValGluSerTrpGluAlaTyrLeuGluAspLeuGlyArgValTrpValTrpAlaLeuThrAsnAspProValValGluAspGlu

SmaI (2269)

2201 GGACCGCGCTGATGAACAGGGTACGTCGTCGCCGACCACCCGGCGAAGTCTGCTCCACGAAGTCCCGGGAGAACCCGAGCCGTCGGTCCAGAATC
53▶nValAlaSerIlePheLeuThrValAspAspArgValValGlyAlaPheAspAspGluValPheAspArgSerPheGlyLeuArgAspThrTrpPheGlu

2301 GACCGTCCGGCGACGTCGCGCGGTTGAGCACCAGGACCGACTGGTCAACTTGGCCATGATGGCTCCTCctgtcaggagaggaagagaagaagtta
20▶ValAlaGlyAlaValAspArgAlaThrLeuValProValAlaSerThrLeuLysAlaMet

AseI (2455) PstI (2477)

2401 gtacaattgCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAAACCTAGGGCTGCAgggttcatagtgcacttttctt
1▶ 1▶

HindIII (2581)

2501 gactgccccatctcctgcccaccctttccaggcatagacagtcaagtactacCAAACCTACAGGAGGGAGAAGGCAGAAGCTTGAGACAGACCCCGG
1▶

2601 GGACCGCCGAACCTGCGAGGGGACGTGGCTAGGGCGGCTCTTTTATGGTGCGCCGGCCCTCGGAGGCAGGGCGCTCGGGGAGGCTAGCGCCAATCTGC

BspEI (2739)

2701 GGTGGCAGGAGGGGGCCGAAGGCCGTGCCTGACCAATCCGGAGCAGATAGGAGTCTCAGCCCCCGCCCCAAAGCAAGGGGAAGTCACGCGCTGTAG

SpeI (2846)

2801 CGCCAGCGTGTGTGAAATGGGGCTTGGGGGGTGGGGCCCTGACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCC

2901 GTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAA
3001 GTCCCATAAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACT
3101 GCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATAACGTCATTATTGACGTCAATG

PacI (3269)
PstI (3262)
SdaI (3262) **BspLU11I (3275)**

3201 GCGGGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAG
3301 GCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA
3401 ACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGTCCCTCGTGCGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCCTT
3501 TCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCC
3601 CCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA
3701 GGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCT
3801 GCTGAAGCCAGTTACCTTCGGAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCAGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATT
3901 ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGG

PacI (4009) SwaI (4017) **NotI (4025)**
4001 CTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCT
4101 CTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA