

# pFUSE-hIgG1e2-Fc2

Plasmid containing a human engineered IgG1 Fc region

Catalog # pfc2-hg1e2

For research use only

Version 20K05-MM

## PRODUCT INFORMATION

### Content:

- 20 µg of pFUSE-hIgG1e2-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. Human IgG1 displays high ADCC and CDC, and is the most suitable for therapeutic use against pathogens and cancer cells.

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 activity<sup>1</sup>. 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

- **hIgG1e2-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.

The Fc region binds to neonatal FcR (FcRn), a receptor expressed on the surface of endothelial cells. This interaction, which is pH-dependent, protects the IgG from lysosomal degradation thus mediating the serum persistence of IgG antibodies. The human IgG1 Fc domain was engineered by introducing mutations in the FcRn binding sites leading to higher FcRn binding affinity and reduced pH dependence<sup>2</sup>. The engineered hIgG1e2 Fc contains the following mutations: M252Y/S254T/T256E and H433K/N434F.

- **hEF1-HTLV prom** is a composite promoter comprising the Elongation Factor-1α (EF-1α) core promoter<sup>3</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>4</sup>. 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 mRNA<sup>5</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*.

- **βGlo pAn:** The human beta-globin 3'UTR and polyadenylation sequence allows efficient arrest of the transgene transcription<sup>6</sup>.

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

2. Vaccaro C. *et al.* 2005. Engineering the Fc region of immunoglobulin G to modulate *in vivo* antibody levels. Nat Biotechnol. 23(10):1283-8.

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](mailto: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 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.

## RELATED PRODUCTS

Product	Catalog Code
Zeocin™	ant-zn-1

---

### [TECHNICAL SUPPORT](#)

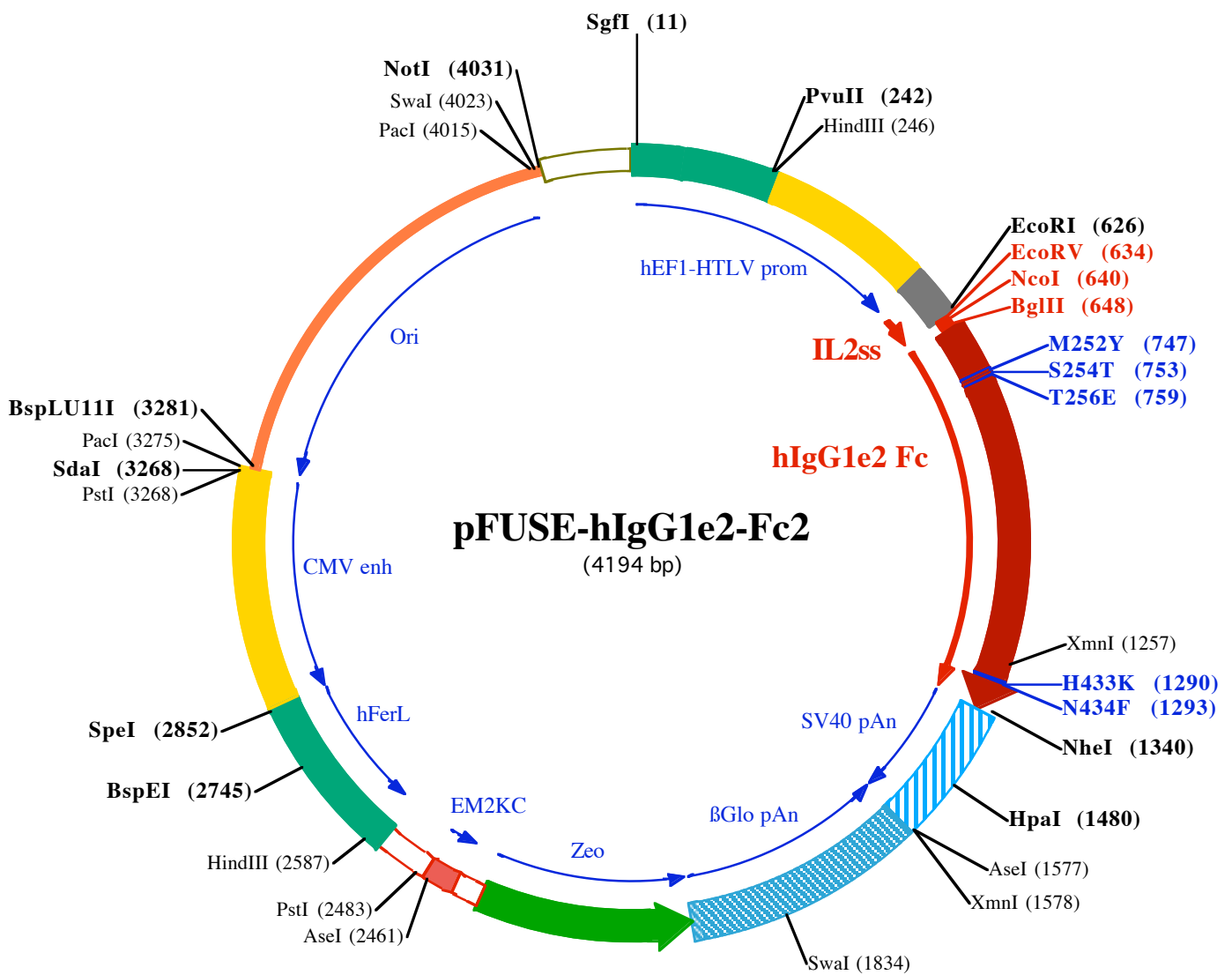
InvivoGen USA (Toll-Free): 888-457-5873

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](mailto:info@invivogen.com)



**SgfI (11)**  
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGGTAACCTGGGAAAGTGATGTCGTGTACTGGCTCCGCCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (246)**  
**PvuII (242)**  
201 GTGAACGTTCTTTTTGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGCTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
401 GGGCCTTTGTCCGCGCTCCCTTGGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT  
501 TCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCTACTCTGAGATCAcggcGAAGGAGGCCACCATGTACAGGATGCAACTCCTGTCTTGCA  
1MetTyrArgMetGlnLeuLeuSer CysI

**EcoRV (634) BglIII (648)**  
**EcoRI (626) NcoI (640)**  
601 TTGCACTAAGTCTTGCCTTGTCAAGATTCGATATCGCCATGGTTAGACTGTGACAAAACCTCACACATGCCACCGTCCAGCAGCTGAAGCTCTGGG  
10P IeAlaLeuSerLeuAlaLeuValThrAsnSer 1AspLysThrHisThrCysProProCysProAlaProGluLeuLeuGln  
S254T (753)  
701 GGGACGTCAGTCTTCTCTTCCCAAAACCAAGGACACCTCTACATCAACCGGAACTGAGGTACATGCGTGGTGGTGGAGCTGAGCCAGAA  
16yGlyProSerValPheLeuPheProProLysProLysAspThrLeuTyrIleThrArgGluProGluValThrCysValValValAspValSerHisGlu  
801 GACCTGAGGTCAAGTTCACCTGGTACGTGGACGGCGTGGAGTGCATAATGCCAAGCAAAGCCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGG  
50P AspProGluValLysPheAsnTrpTyrValIleAspGluValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValV  
901 TCAGCGTCTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCAT  
83a I SerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIle  
1001 CTCCAAGCAAAGGGCAGCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGAGGAGATGACCAAGAACCAGGTGAGCTGACCTGCTGGTCT  
116e SerLysAlaLysGlyGlnProArgGluProGluValTyrThrLeuProProSerArgGluGluMetThrLysAsnGluValSerLeuThrCysLeuVal  
1101 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGCGAGCCGAGAACTACAAGACCAAGCCCTCCGCTGGACTCCGACGGCT  
150P LysGlyPheTyrProSerAspIleAlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlyS  
N434F (1293)  
1201 CCTTCTCTCTACAGCAAGCTCACCGTGACAGAGCAGGTGGCGCAGGGGAACTCTTCTCATGCTCCGTGATGCATGAGGCTCTGAAGTCCACTA  
183r PhePheLeuTyrSerLysLeuThrValAspLysSerArgTyrGlnGlnGlyAsnValPheSerCysSerValIleHisGluAlaLeuLysPheHisTy  
H433K (1290)  
1301 CACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGAGTGTGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGC  
216r ThrGlnLysSerLeuSerLeuSerProGlyLys•••

**NheI (1340)**  
1401 AGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTATAAGCTGCAATAACAAGTTAACAACAATTGCATTCA

**HpaI (1480)**  
1501 TTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGGTATGGAATTAATTTAAAAATACAGCATAGCA  
AseI (1577)  
XmnI (1578)  
1601 AAACCTTAACCTCAAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCAATGTGCATTAGCTGTTTG  
1701 CAGCCTCACCTTCTTCATGAGTAAAGATATAGTATTTTTCCCAAGGTTTGAAGTACGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCAC

**Swal (1834)**  
1801 ATTCCCTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTC  
1901 ATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTAAATAGAAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTATCTCAGTCTCTG  
1254•••AspGln  
2001 CTCTCTGCCACAAAGTGCACGAGTTGCCGCGGGTGCAGCGGCGAACTCCCGCCCCAGGCTGCTCGCGATCTCGGTATCGCCGGCCGGAG  
1224GluGluAlaValPheHisValCysAsnGlyAlaProArgAspLeuAlaPheGluArgGlyTrpProGlnGluGlyIleGluThrMetAlaProGlySerA  
2101 GCGTCCCGAAGTTCGTGGACACGACCTCCGACCTCGCGTACGCTCGTCCAGCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACCACT  
884IleAspArgPheAsnThrSerValValGluSerTrpGluAlaTyrLeuGluValArgValTrpValTrpAlaLeuThrAsnAspProValValGlu  
2201 GGTCTGGACCGCTGATGAACAGGGTACGTCGTCGACACCGGCAAGTCTCTCCAGAACTCCGGGAGAACCCGAGCCGGTCCGCTGCA  
554nAspGlnValAlaSerIlePheLeuThrValAspAspArgValValGlyAlaPheAspAspGluValPheAspArgSerPheGlyLeuArgAspThrTrp  
2301 GAACCTGACCGCTCGCGCAGCTCGCGCGGGTGGACACCGGAACCGCACTGGTCAACTGGCCATGATGGCTCCTCctgtcaggagaggaagagaaga  
224PheGluValAlaGlyAlaValAspArgAlaThrLeuValProValAlaSerThrLeuLysAlaMet  
AseI (2461) PstI (2483)  
2401 aggttagtacaattgCTATAGTGAAGTATTATACTATGCAGATATACTATGCCAATGATTAATTGCAAACTAGGGCTGCAGgggttcatagtgccact

**HindIII (2587)**  
2501 tttctgcactgccccatctcctgccccacctttccaggcatagacagtcagtgacttacCAAACCTCACAGGAGGAGAAGGCAGAAAGCTTGAGACAGA  
2601 CCCGCGGACCGCGAACTGCGAGGGGACGTGGCTAGGGCGGCTCTTTTATGGTGCAGCCGCCCTCGGAGGCAGGGGCTCGGGGAGGCTAGCGGCCA

**BspEI (2745)**  
2701 ATCTGCGGTGGCAGGAGGGGGCCGAAGGCCGTGCCTGACCAATCCGGAGCACATAGGAGTCTCAGCCCCCGCCCCAAAGCAAGGGGAAGTACAGCGC

**SpeI (2852)**  
2801 CTGTAGCCGACGCTGTTGTGAAATGGGGCTTGGGGGGTGGGGCCCTGACTAGTCAAAACAAACTCCCATTTGACGCTCAATGGGGTGGAGACTTGGAA  
2901 ATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATGTTAATAGCGATGACTAATACGTAGATGTACTGCCAAGT  
3001 AGGAAAGTCCCATAAAGTCTACTGGGCATAATGCCAGCGGGCCATTTACCGTCAATGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGA  
3101 TGTAAGTCCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACC

PacI (3275)  
PstI (3268) SdaI (3268) BspLU11I (3281)

3201 TCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAG  
3301 CAAAAGGCCAGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT  
3401 GCGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTC  
3501 CGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCAC  
3601 GAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG  
3701 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG  
3801 CGCTCTGTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGCAAGCAG  
3901 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGG  
4001 TCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACA  
PacI (4015) SmaI (4023) NotI (4031)  
4101 TACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA