

ID Construct **12ABJHBC** Map

Customer **UNIVERSITÄT REGENSBURG, Jennifer Flechsler**

Name of the gene **Igni_1058**

optimized for **Escherichia coli**

23.10.2012 09:00:27

BamHI

CACTATAGGGCGAATTGAAGGAAGGCCGTCAAGGCCGCATGGATCCATGCTGGGTGGTGC
 1 -----+-----+-----+-----+-----+-----+
 GTGATATCCCGCTTAACCTCCTTCCGGCAGTTCCGGCGTACCTAGGTACGACCCACCACG
 M L G G A

ACTGGCACTGTATAGCCTGCTGCGTCTGTGGACCGCAGATCAGGCACTGCAAGAAGTTCG
 61 -----+-----+-----+-----+-----+-----+
 TGACCGTGACATATCGGACGACGCAGACACCTGGCGTCTAGTCCGTGACGTTCTTCAAGC
 L A L Y S L L R L W T A D Q A L Q E V R

TAAAGTTCTGGTTGTTGGTGCCGGTGTATGGGTCATGGTATTGCACAGGTTGCAGCAAT
 121 -----+-----+-----+-----+-----+-----+
 ATTTCAAGACCAACAACCACGGCCACAATACCCAGTACCATAACGTGTCCAACGTCGTTA
 K V L V V G A G V M G H G I A Q V A A M

GAGCGGTCTGAATGTTCGTATGATTGATATTAAACAAGAATTTCTGGATCGCGCAATGGA
 181 -----+-----+-----+-----+-----+-----+
 CTCGCCAGACTTACAAGCATACTAACTATAATTTGTTCTTAAAGACCTAGCGCGTTACCT
 S G L N V R M I D I K Q E F L D R A M E

ACGCATTAAAGAAAGCCTGGAAAACTGTATGCCAAAGGCAAACCTGAAAGAACCGCCTGA
 241 -----+-----+-----+-----+-----+-----+
 TGCCTAATTTCTTTTCGGACCTTTTTGACATACGGTTTCCGTTTGACTTTCTTGGCGGACT
 R I K E S L E K L Y A K G K L K E P P E

AGAAGTTCTGAAACGTATTGAAACAATGGTTGCCAATCCGGATGATGAAAGCAGCTATGC
 301 -----+-----+-----+-----+-----+-----+
 TCTTCAAGACTTTGCATAACTTTGTTACCAACGGTTAGGCCTACTACTTTTCGTCGATACG
E_V_L_K_R_I_E_T_M_V_A_N_P_D_D_E_S_S_Y_A

CGAAGCAGCAAAAAGATGTTGATTTTGTATTGAAGCCGTGCCGGAAGAACTGGAAGTGA
 361 -----+-----+-----+-----+-----+-----+
 GCTTCGTCGTTTTCTACAATAAAACAATACTTCGGCACGGCCTTTTTGACCTTGACTT
E_A_A_K_D_V_D_F_V_I_E_A_V_P_E_K_L_E_L_K

ACGTGCAGTTTTTAGCGTGCTGGATAAATATGCACCGCCTCATGCAATTCTGGCAAGCAA
 421 -----+-----+-----+-----+-----+-----+
 TGCACGTCAAAAATCGCACGACCTATTTATACGTGGCGGAGTACGTTAAGACCGTTCGTT
R_A_V_F_S_V_L_D_K_Y_A_P_P_H_A_I_L_A_S_N

TACCAGCAGCATTCCGATTACCGAAATTGCAAAAGCAACCAAACGTCCGGATAAAGTTGT
 481 -----+-----+-----+-----+-----+-----+
 ATGGTCGTCGTAAGGCTAATGGCTTTAACGTTTTCGTTGGTTTGCAGGCCTATTTCAACA
T_S_S_I_P_I_T_E_I_A_K_A_T_K_R_P_D_K_V_V

SphI

TGGCATGCATTTTTTCAATCCGCCTGTTATTCTGAAACTGGTTGAAGTTGTTTCGTGGCAA
 541 -----+-----+-----+-----+-----+-----+
 ACCGTACGTAAAAAAGTTAGGCGGACAATAAGACTTTGACCAACTTCAACAAGCACCGTT
G_M_H_F_F_N_P_P_V_I_L_K_L_V_E_V_V_R_G_K

AGAAACCAGTGATGAAACCGTGAAAATTACCGTTGAACTGGCCAAAAAATGGGCAAAGT
 601 -----+-----+-----+-----+-----+-----+
 TCTTTGGTCACTACTTTGGCACTTTTAATGGCAACTTGACCGTTTTTTTACCGTTTTCA
E_T_S_D_E_T_V_K_I_T_V_E_L_A_K_K_M_G_K_V

TCCGATTGTGGTGAACAAAGATGTTCCGGGTTTTATTGTGAATCGTATCATGGCACGTTT
 661 -----+-----+-----+-----+-----+-----+
 AGGCTAACACCACTTGTTTCTACAAGGCCCAAAATAACACTTAGCATAGTACCGTGCAAA
P_I_V_V_N_K_D_V_P_G_F_I_V_N_R_I_M_A_R_F

TCTGAATGAAGGTTGTTGGCTGGTTGAACGTGGTGGTTTATACCAAAGAACAGGTTGATGC
 721 -----+-----+-----+-----+-----+-----+-----+
 AGACTTACTTCCAACAACCGACCAACTTGCACCACAAATATGGTTTCTTGTCCAACCTACG
L N E G C W L V E R G V Y T K E Q V D A

AGCACTGCGCTATAAACTGAATTTTCCGATGGGTGCATTTGAGCTGGCAGATTATGTTGG
 781 -----+-----+-----+-----+-----+-----+-----+
 TCGTGACGCGATATTTGACTTAAAAGGCTACCCACGTAACTCGACCGTCTAATACAACC
A L R Y K L N F P M G A F E L A D Y V G

TCTGGATGTTCTGGTTCATCTGATGGAAGCAATGAAAGAACGTGGTATGAATCTGACCAT
 841 -----+-----+-----+-----+-----+-----+-----+
 AGACCTACAAGACCAAGTAGACTACCTTCGTTACTTTCTTGCACCATACTTAGACTGGTA
L D V L V H L M E A M K E R G M N L T I

TTGTCCGCTGTTCAAAAACTGCTGGAAGAAGGTAACTGGGCGTTAAAAGCGGTGAAGG
 901 -----+-----+-----+-----+-----+-----+-----+
 AACAGGCGACAAGTTTTTTGACGACCTTCTTCCATTTGACCCGCAATTTTCGCCACTTCC
C P L F K K L L E E G K L G V K S G E G

AgeI

CTTTTACAAATATCCGGCACCGGGCAAGTTCAAAAAACCGTTGTTAAAGCAAGCGCAGC
 961 -----+-----+-----+-----+-----+-----+-----+
 GAAAATGTTTATAGGCCGTGGCCCGTTCAAGTTTTTTGGCCAACAATTTTCGTTTCGCGTCG
F Y K Y P A P G K F K K P V V K A S A A

AGAAGGTGTTGATTACATTAGCATTGTTGATACCGCAGTTAATGAAGGTGCATGGCTGGT
 1021 -----+-----+-----+-----+-----+-----+-----+
 TCTTCCACAACCTAATGTAATCGTAACAACCTATGGCGTCAATTACTTCCACGTACCGACCA
E G V D Y I S I V D T A V N E G A W L V

BspMI

AGAAAATGGTGTTGCAGGTCCGGAAGAAGTTGATACCGCCACCGTTCTGGGTCTGAATCT
 1081 -----+-----+-----+-----+-----+-----+-----+
 TCTTTTACCACAACGTCCAGGCCTTCTTCAACTATGGCGGTGGCAAGACCCAGACTTAGA
E N G V A G P E E V D T A T V L G L N L

1141 GCGGATGGGTATCCTGAAACTGGGTGATAGCCTGGGTCTGGATAATGTTCTGGATAGCAT
 -----+-----+-----+-----+-----+-----+
 CGGCTACCCATAGGACTTTGACCCACTATCGGACCCAGACCTATTACAAGACCTATCGTA
P M G I L K L G D S L G L D N V L D S I

PvuII

1201 CAACGAAAAAAAAAGAAAAATATGGCCTGGAAGATTATCGTCCGGTTCAGCTGCTGGAAAA
 -----+-----+-----+-----+-----+-----+
 GTTGCTTTTTTTTCTTTTTATACCGGACCTTCTAATAGCAGGCCAAGTCGACGACCTTTT
N E K K E K Y G L E D Y R P V Q L L E N

1261 TATGGTTAAGGAAGGTAAATGCGGAGTAAAATGCGGCAAAGGTTTTTATGAATATGAAGT
 -----+-----+-----+-----+-----+-----+
 ATACCAATTCTTCCATTTACGCCTCATTTTACGCCGTTTCCAAAAATACTTATACTTCA
M V K E G K C G V K C G K G F Y E Y E V

BglIII

1321 GAGCGAAGAAGATCTGGGCGAAATCAAAGTTCGTCTGGAAGGTGAAGCACTGTGGATTAT
 -----+-----+-----+-----+-----+-----+
 CTCGCTTCTTCTAGACCCGCTTTAGTTTCAAGCAGCACTTCCACTTCGTGACACCTAATA
S E E D L G E I K V R R E G E A L W I I

1381 TCTGAATCGTCCGAAACAGCGTAATGCACTGACACCGGAAATGCTGCTGAAAATGGCCGA
 -----+-----+-----+-----+-----+-----+
 AGACTTAGCAGGCTTTGTGCGATTACGTGACTGTGGCCTTTACGACGACTTTTACCGGCT
L N R P K Q R N A L T P E M L L K M A E

1441 AGTTGCACAGAAAGCATGTGAAGATGAAGGTGTTTCGTGCAATTGTTCTGTATGGTGGTGA
 -----+-----+-----+-----+-----+-----+
 TCAACGTGTCTTTTCGTACACTTCTACTTCCACAAGCACGTTAACAAGACATACCACCACT
V A Q K A C E D E G V R A I V L Y G G D

BspMI

1501 TGTTTTTAGCGCAGGTTTTGATCTGACCGTGATGAAAGATGTAGATCCGACCAAAGCACC
 -----+-----+-----+-----+-----+-----+
 ACAAAAATCGCGTCCAAAACCTAGACTGGCACTACTTTCTACATCTAGGCTGGTTTCGTGG
V F S A G F D L T V M K D V D P T K A P

AgeI

1561 GGAAACCGTTGCACGTCCTTTCAAAAACTGGCACTGGCACTGGAAGGTTGTCCGAAACC
-----+-----+-----+-----+-----+-----+
CCTTTGGCAACGTGCAGGAAAGTTTTTTGACCGTGACCGTGACCTTCCAACAGGCTTTGG
E T V A R P F K K L A L A L E G C P K P

AgeI

1621 GGTTATTGCATATATTACCGTTATGCACTGGGTGGTGGTCTGGAAGTTGCAATGATGGC
-----+-----+-----+-----+-----+-----+
CCAATAACGTATATAATGGCCAATACGTGACCCACCACCAGACCTTCAACGTTACTACCG
V I A Y I T G Y A L G G G L E V A M M A

BglIII

1681 AGATCTGCGTCTGGCAACCGAAGATAGCCTGCTGGGTGAGCCGAAATTAATGTTGGTAT
-----+-----+-----+-----+-----+-----+
TCTAGACGCAGACCGTTGGCTTCTATCGGACGACCCAGTCGGCCTTTAATTACAACCATA
D L R L A T E D S L L G Q P E I N V G I

1741 TATGCCTGGTGGTGGTGGCACCCAGCGTCTGCCTCGTCTGGTTGGTCTGGGTCGTGCAAT
-----+-----+-----+-----+-----+-----+
ATACGGACCACCACCACCGTGGGTGCGCAGACGGAGCAGACCAACCAGACCCAGCACGTTA
M P G G G G T Q R L P R L V G L G R A M

PvuII

1801 GCAGCTGGTTCTGCTGGGTGATCCGATTGATGCAGTTGAAGCAGAAAAATGGGGTCTGGT
-----+-----+-----+-----+-----+-----+
CGTCGACCAAGACGACCCACTAGGCTAACTACGTCAACTTCGTCTTTTTACCCCAGACCA
Q L V L L G D P I D A V E A E K W G L V

1861 TAATTGGGCAGTGCCGAAACGTATTGCAGATAGCGAAGTTCGTCTGCTGGTTAAAAAACT
-----+-----+-----+-----+-----+-----+
ATTAACCCGTCACGGCTTTGCATAACGTCTATCGCTTCAAGCAGACGACCAATTTTTTGA
N W A V P K R I A D S E V R L L V K K L

1921 GAGCAGCAAACCGAAAGAAGCACTGGCCCTGGCAAAAAAGCAGTTCGTGTTGCACAAGA
 -----+-----+-----+-----+-----+-----+
 CTCGTCGTTTGGCTTTCTTCGTGACCGGGACCGTTTTTTTCGTCAAGCACAAACGTGTTCT
S S K P K E A L A L A K K A V R V A Q E

1981 GGTTCCGCTGATTGATGGTCTGGAAATGGAAGCCGAAGCATTTGCACGTGCACTGGCCAC
 -----+-----+-----+-----+-----+-----+
 CCAAGGCGACTAACTACCAGACCTTTACCTTCGGCTTCGTAAACGTGCACGTGACCGGTG
V P L I D G L E M E A E A F A R A L A T

2041 CGAAAAATGCCAAAGAAGGTATTGCAGCATTTCTGGAAAAACGCAAACCGAATTTCAAATA
 -----+-----+-----+-----+-----+-----+
 GCTTTTACGGTTTCTTCCATAACGTCGTAAAGACCTTTTTGCGTTTGGCTTAAAGTTTAT
E N A K E G I A A F L E K R K P N F K *

EcoRI
 AGAATTCCTGGGCCTCATGGGCCTTCCTTTCACTGCCCCTTTCCAG
 2101 -----+-----+-----+-----+-----+
 TCTTAAGGACCCGGAGTACCCGGAAGGAAAGTGACGGGCGAAAGGTC

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