

ID Construct **13ABGMYC** Map

Customer **UNIVERSITÄT REGENSBURG, Jennifer Flechsler**

Name of the gene **Igni_0132**

optimized for **Escherichia coli**

06.07.2013 09:08:31

SphI

NheI

CACTATAGGGCGAATTGAAGGAAGGCCGTCAAGGCCGCATGCTAGCGTGTATAATCCGTT

1 -----+-----+-----+-----+-----+-----+

GTGATATCCCGCTTAACCTTCCTTCCGGCAGTTCGGCGTACGATCGCACATATTAGGCAA

V_Y_N_P_F

TGGTGATTATGTTTGGGAATTTTCGTAGTCCGCGTAGCAAATTTGGTCCGGGTGCACTGAA

61 -----+-----+-----+-----+-----+-----+

ACCACTAATAACAAACCTTAAAGCATCAGGCGCATCGTTTAAACCAGGCCACGTGACTT

G_D_Y_V_W_E_F_R_S_P_R_S_K_F_G_P_G_A_L_N

Pf1MI

TGAACTGAAAGTTGATCTGGAACGTCTGCGTGTTGAAAAACCGTTTCTGATTACCACCAA

121 -----+-----+-----+-----+-----+-----+

ACTTGACTTTCAACTAGACCTTGCAGACGCACAACCTTTTGGCAAAGACTAATGGTGGTT

E_L_K_V_D_L_E_R_L_R_V_E_K_P_F_L_I_T_T_K

AGGTTGGGTAAACGTGGTATTGTTGATCGTCTGCGTGAAATTCTGGGTAAAGATGTTCC

181 -----+-----+-----+-----+-----+-----+

TCCAACCCAATTTGCACCATAACAACCTAGCAGACGCACTTTAAGACCCATTTCTACAAGG

G_W_V_K_R_G_I_V_D_R_L_R_E_I_L_G_K_D_V_P

GTATTGGGATGGTGTGAACCGGAACCGAGCGCAGAAAGCGTTGAAGAAGCAGCAAAAGC

241 -----+-----+-----+-----+-----+-----+

CATAACCTACCACTTGGCCTTGGCTCGCGTCTTTCGCAACTTCTTCGTCGTTTTCG

Y_W_D_G_V_E_P_E_P_S_A_E_S_V_E_E_A_A_K_A

ACTGGCAGAAAGCGGTGCAGATAGCGTTATTGCAATTGGTGGTGGTAGCGCACTGGATAC
 301 -----+-----+-----+-----+-----+-----+-----+
 TGACCGTCTTTTCGCCACGTCTATCGCAATAACGTTAACCACCACCATCGCGTGACCTATG
L A E S G A D S V I A I G G G S A L D T

CGCAAAAATTGCAAACTCTGCTGGCAACCTATGGTGGTCGTGTTTCGTGATTATGTTGCACC
 361 -----+-----+-----+-----+-----+-----+-----+
 GCGTTTTTAACGTTTAGACGACCGTTGGATACCACCAGCACAAAGCACTAATACAACGTGG
A K I A N L L A T Y G G R V R D Y V A P

AgeI

GCCTTATGGTGAAGGTAAACCGGTTCCGGGTCCGGTTAAACCGATGGTTGCAGTTCCGAC
 421 -----+-----+-----+-----+-----+-----+-----+
 CGGAATACCACTTCCATTTGGCCAAGGCCAGGCCAATTTGGCTACCAACGTCAAGGCTG
P Y G E G K P V P G P V K P M V A V P T

AgeI

CACCGCAGGCACCGGTAGCGAAGTTACCAGCGTTGCAGTTGTTACCCTGAAAGATGTTGG
 481 -----+-----+-----+-----+-----+-----+-----+
 GTGGCGTCCGTGGCCATCGCTTCAATGGTCGCAACGTCAACAATGGGACTTTCTACAACC
T A G T G S E V T S V A V V T L K D V G

TGTTAAAGTTGGTATCAGCAGCGATTTTCTGCGTCCGAGCCTGGCACTGCTGGACCCGGA
 541 -----+-----+-----+-----+-----+-----+-----+
 ACAATTTCAACCATAGTCGTCGCTAAAAGACGCAGGCTCGGACCGTGACGACCTGGGCCT
V K V G I S S D F L R P S L A L L D P E

AgeI

ACTGACCATGACCGTTCCGCCTAAAGTTACCGCAGATACCGGTATGGATGCACTGACCCA
 601 -----+-----+-----+-----+-----+-----+-----+
 TGACTGGTACTGGCAAGGCGGATTTCAATGGCGTCTATGGCCATACCTACGTGACTGGGT
L T M T V P P K V T A D T G M D A L T H

TGCAGTTGAAAGCTATATCGCAAAACCGTATTGGGCACGTGAACGTCCGGAAGATCCGGC
 661 -----+-----+-----+-----+-----+-----+-----+
 ACGTCAACTTTTCGATATAGCGTTTTGGCATAACCCGTGCACTTGCAAGCCTTCTAGGCCG
A V E S Y I A K P Y W A R E R P E D P A

AAAACGTCCGGTTTATGTTGGTAGCTTTACCGTTACCGATGCACTGGCCGAACGTGCAAT
 721 -----+-----+-----+-----+-----+-----+
 TTTTGCAGGCCAAATACAACCATCGAAATGGCAATGGCTACGTGACCGGCTTGACACGTTA
K_R_P_V_Y_V_G_S_F_T_V_T_D_A_L_A_E_R_A_I

TGAACTGATTGGTAAATATCTGCGTCGTGCAGTTTATCAGGGTCGTACCGATCTGGAAGC
 781 -----+-----+-----+-----+-----+-----+
 ACTTGACTAACCATTATAGACGCAGCACGTCAAATAGTCCCAGCATGGCTAGACCTTCG
E_L_I_G_K_Y_L_R_R_A_V_Y_Q_G_R_T_D_L_E_A

BspMI

ACGTAGCGGTATGCTGATTGCAAGCTATCTGGCAGGTCTGGCATTGTTGTAATGCCGGTGT
 841 -----+-----+-----+-----+-----+-----+
 TGCATCGCCATACGACTAACGTTTCGATAGACCGTCCAGACCGTAAACCATTACGGCCACA
R_S_G_M_L_I_A_S_Y_L_A_G_L_A_F_G_N_A_G_V

TGGTCTGGCACATGCAGCAAGCTATCCGCTGGGTGGTCGTTATAAAGTTACACATGGTGA
 901 -----+-----+-----+-----+-----+-----+
 ACCAGACCGTGTACGTCGTTTCGATAGGCGACCCACCAGCAATATTTCAATGTGTACCACT
G_L_A_H_A_A_S_Y_P_L_G_G_R_Y_K_V_T_H_G_E

PstI

AGCAGTTGGTATTCTGCTGCCTGCAGTTCTGGAATTTAATGCACCGGCAAATTATGAAAA
 961 -----+-----+-----+-----+-----+-----+
 TCGTCAACCATAAGACGACGGACGTCAAGACCTTAAATTACGTGGCCGTTTAATACTTTT
A_V_G_I_L_L_P_A_V_L_E_F_N_A_P_A_N_Y_E_K

AgeI

AGCCAAACGTGTTGGCGAACTGCTGACCGGTGAAAAATGTCCGGAACGTGATCCTGCAAA
 1021 -----+-----+-----+-----+-----+-----+
 TCGGTTTGCACAACCGCTTGACGACTGGCCACTTTTTACAGGCCTTGCACTAGGACGTTT
A_K_R_V_G_E_L_L_T_G_E_K_C_P_E_R_D_P_A_K

PstI *EcoRV*

1081 ATGTGCAGAATGGGCAGCAAATGCAATTCGTGAACTGCAGCGTGATATCAAATTTACACC
-----+-----+-----+-----+-----+-----+
TACACGTCTTACCCGTCGTTTACGTTAAGCACTTGACGTCGCACTATAGTTTAAATGTGG
C A E W A A N A I R E L Q R D I K F T P

1141 GGGTCTGGAAGCAGTGGGTGTTAAAGAAGAGGATCTGATGGAAATGGCAAAGAAACCCT
-----+-----+-----+-----+-----+-----+
CCCAGACCTTCGTCACCCACAATTTCTTCTCCTAGACTACCTTTACCGTTTTCTTTGGGA
G L E A V G V K E E D L M E M A K E T L

BstEII

1201 GAATCAGAAACGTCTGCTGGCCACCAATCCGCGTCCGGTTACCGAAGAAGATGTTTATTG
-----+-----+-----+-----+-----+-----+
CTTAGTCTTTGCAGACGACCGGTGGTTAGGCGCAGGCCAATGGCTTCTTCTACAAATAAC
N Q K R L L A T N P R P V T E E D V Y W

SphI

NcoI

1261 GGTTTATAAACGTAGCATGCGCAACTATTAACCATGGCTGGGCCTCATGGGCCTTCCTTT
-----+-----+-----+-----+-----+-----+
CCAAATATTTGCATCGTACGCGTTGATAATTGGTACCGACCCGGAGTACCCGGAAGGAAA
V Y K R S M R N Y * _

1321 CACTGCCCCGCTTTCCAG
-----+-----
GTGACGGGCGAAAGGTC