

ID Construct **12ABHCNC** Map

Customer **UNIVERSITÄT REGENSBURG, Jennifer Flechsler**

Name of the gene **Igni_0341**

optimized for **Escherichia coli**

17.10.2012 08:34:36

BamHI NdeI

CACTATAGGGCGAATTGAAGGAAGGCCGTCAAGGCCGCATGGATCCCATATGGTGAAAGT
 1 -----+-----+-----+-----+-----+-----+
 GTGATATCCCGCTTAACTTCCTTCCGGCAGTTCCGGCGTACCTAGGGTATACCACTTTCA
 M_V_K_V_

TCCGAAACTGATGGCAACCCAGCATCCGGATAGCACCGTTGTTCTGATGCCGCAGGATGA
 61 -----+-----+-----+-----+-----+-----+
 AGGCTTTGACTACCGTTGGGTCGTAGGCCTATCGTGGCAACAAGACTACGGCGTCCTACT
 _P_K_L_M_A_T_Q_H_P_D_S_T_V_V_L_M_P_Q_D_E_

AGTTGAAGAGGCAATTCAGGATGTTCTGCCGCTGGATCAGGGTGGTCGTGGTTGTGATGA
 121 -----+-----+-----+-----+-----+-----+
 TCAACTTCTCCGTTAAGTCCTACAAGACGGCGACCTAGTCCCACCAGCACCAACACTACT
 _V_E_E_A_I_Q_D_V_L_P_L_D_Q_G_G_R_G_C_D_E_

AAAAATGGTTGATTATGAAGGTAAAGCCACCCCGTATAATCAGATGCGTGATATTATTGA
 181 -----+-----+-----+-----+-----+-----+
 TTTTACCAACTAATACTTCCATTTCCGGTGGGGCATATTAGTCTACGCACTATAATAACT
 _K_M_V_D_Y_E_G_K_A_T_P_Y_N_Q_M_R_D_I_I_E_

AGAGGTGCGCAAATATGATGTTGTTCCGGGTGAAGATTTTCTGATTACACCGCGTGTTC
 241 -----+-----+-----+-----+-----+-----+
 TCTCCACGCGTTTATACTACAACAAGGCCCACTTCTAAAAGACTAATGTGGCGCACAAGG
 _E_V_R_K_Y_D_V_V_P_G_E_D_F_L_I_T_P_R_V_P_

GAATCCGAAACTGGAAGATAAAGATCGTCATCTGCTGGCAATTACCGCAGCAGTTACCGC
 301 -----+-----+-----+-----+-----+-----+
 CTTAGGCTTTGACCTTCTATTTCTAGCAGTAGACGACCGTTAATGGCGTCGTCAATGGCG
N_P_K_L_E_D_K_D_R_H_L_L_A_I_T_A_A_V_T_A

AAATATGTATAGCCAGATGTATTTCAACACCGATGCCATCAAATATATCATTCTGCCGAT
 361 -----+-----+-----+-----+-----+-----+
 TTTATACATATCGGTCTACATAAAGTTGTGGCTACGGTAGTTTATATAGTAAGACGGCTA
N_M_Y_S_Q_M_Y_F_N_T_D_A_I_K_Y_I_I_L_P_M

GAGCACCAGCACCCCTGGAAGTGGCAGAAAGTTCAGCGTCGTATTCTGAAAGTTGAACGTCT
 421 -----+-----+-----+-----+-----+-----+
 CTCGTGGTTCGTGGGACCTTGACCGTCTTCAAGTCGCAGCATAAGACTTTCAACTTGCAGA
S_T_S_T_L_E_L_A_E_V_Q_R_R_I_L_K_V_E_R_L

BstBI

GGTTAGCGAAGAATTTAGCCTGCGTATTGAAGAATGGATTAACTGATTCCGCTGTTCTGA
 481 -----+-----+-----+-----+-----+-----+
 CCAATCGCTTCTTAAATCGGACGCATAAATTCTTACCTAATTTGACTAAGGCGACAAGCT
V_S_E_E_F_S_L_R_I_E_E_W_I_K_L_I_P_L_F_E

AACCGCAGAAAGCCACATGCATATTGATGAAATTGTTGAAGGTCTGCGCATTGCCTTCAT
 541 -----+-----+-----+-----+-----+-----+
 TTGGCGTCTTTTCGGTGTACGTATAACTACTTTAACAACCTCCAGACGCGTAACGGAAGTA
T_A_E_S_H_M_H_I_D_E_I_V_E_G_L_R_I_A_F_I

TAAAGAAATTGGCATGTTTGAGAACGAATTTTCGCATCTTTATGGGCAAAAGCGATAGCGG
 601 -----+-----+-----+-----+-----+-----+
 ATTTCTTTAACCGTACAAACTCTTGCTTAAAGCGTAGAAATACCCGTTTTTCGCTATCGCC
K_E_I_G_M_F_E_N_E_F_R_I_F_M_G_K_S_D_S_G

TATTCATAGCGGTCATATTGCAAGCAGCATTGGTGTTCGTATGGGTCTGCTGAAACTGTG
 661 -----+-----+-----+-----+-----+-----+
 ATAAGTATCGCCAGTATAACGTTTCGTGTAACCACAAGCATACCCAGACGACTTTGACAC
I_H_S_G_H_I_A_S_S_I_G_V_R_M_G_L_L_K_L_W

GAATTGGCAGAAAGATACCATGTTCAAAGTGTATCCGATTATCGGTATGGGTAAACCGCC
 721 -----+-----+-----+-----+-----+-----+
 CTTAACCGTCTTTCTATGGTACAAGTTTCACATAGGCTAATAGCCATACCCATTTGGCGG
N W Q K D T M F K V Y P I I G M G K P P

TCTGCGTGGTCACATGGCAGAATGGGTTATTGAAGATTGGGTTGAAGCATGGCGTGGTTA
 781 -----+-----+-----+-----+-----+-----+
 AGACGCACCAAGTGTACCGTCTTACCCAATAACTTCTAACCCAACCTTCGTACCGCACCAAT
L R G H M A E W V I E D W V E A W R G Y

PvuI

TTATACCGCAACCGTTCAGAGCGCACTGCGTTTTAATACCGATCGTAAAGATTATGTGCA
 841 -----+-----+-----+-----+-----+-----+
 AATATGGCGTTGGCAAGTCTCGCGTGACGCAAAATTATGGCTAGCATTTCTAATACACGT
Y T A T V Q S A L R F N T D R K D Y V H

BstEII

TACCATTACCGTGGTGACCAAAAAATAGCGGTAAACAGCCTCCGCTGGAACCTGCTGGGTTA
 901 -----+-----+-----+-----+-----+-----+
 ATGGTAATGGCACCACCTGGTTTTTATCGCCATTTGTCGGAGGCGACCTTGACGACCCAAT
T I T V V T K N S G K Q P P L E L L G Y

TGCAAAAGAAATGGTTAATGTTGCATGGCGTGCAAGCGAAGTTTATCTGAGCCGTCTGGA
 961 -----+-----+-----+-----+-----+-----+
 ACGTTTTCTTTACCAATTACAACGTACCGCACGTTTCGCTTCAAATAGACTCGGCAGACCT
A K E M V N V A W R A S E V Y L S R L E

ACGCTCTGGCAGATATGATTAGCTTTATGGCCAAATTTGTTACCCGTACCCGTGCACGTCT
 1021 -----+-----+-----+-----+-----+-----+
 TGCAGACCGTCTATACTAATCGAAATACCGGTTTAAACAATGGGCATGGGCACGTGCAGA
R L A D M I S F M A K F V T R T R A R L

AgeI

GGATAGCTATAAACGTCGTGCAAAAACCGGTAAAGAAATGCCTCGTGCAATTCGTTTTTG
 1081 -----+-----+-----+-----+-----+-----+
 CCTATCGATATTTGCAGCACGTTTTTGGCCATTTCTTTACGGAGCACGTTAAGCAAAAAAC
D S Y K R R A K T G K E M P R A I R F C

1141 TGCAAGCCTGTATAGCATGGGTCTGGGTCCGACCCTGATTGGTGCCGGTGTTATTGAAGA
 -----+-----+-----+-----+-----+-----+
 ACGTTCGGACATATCGTACCCAGACCCAGGCTGGGACTAACCACGGCCACAATAACTTCT
 _A_S_L_Y_S_M_G_L_G_P_T_L_I_G_A_G_V_I_E_E_

1201 ACTGGCAAGCGGCACCGCAGAAAACTGGAACATCTGCTGAAATTTGTTCCGCTGCTGCC
 -----+-----+-----+-----+-----+-----+
 TGACCGTTTCGCCGTGGCGTCTTTTGGACCTTGTAGACGACTTTAAACAAGGCGACGACGG
 _L_A_S_G_T_A_E_K_L_E_H_L_L_K_F_V_P_L_L_P_

1261 GAAAGATTTTGCATTTGATTATGCATTCACCGATCTGGAAGTGTTCAAACGTTATGTGGA
 -----+-----+-----+-----+-----+-----+
 CTTTCTAAAACGTAAACTAATACGTAAGTGGCTAGACCTTCACAAGTTTGCAATACACCT
 _K_D_F_A_F_D_Y_A_F_T_D_L_E_V_F_K_R_Y_V_D_

1321 TGAAAAAACCTTTGAAATTATCAAAAAAGATGTGGATGTGGTGAAAGAATACTTCGCCAA
 -----+-----+-----+-----+-----+-----+
 ACTTTTTTTGGAAACTTTAATAGTTTTTCTACACCTACACCACTTTCTTATGAAGCGGTT
 _E_K_T_F_E_I_I_K_K_D_V_D_V_V_K_E_Y_F_A_N_

1381 TGTTGAACCGCCTAAAAGCCCTCCGGAAGGTTATTTTGAAAACTGCGCGAACTGCGTGG
 -----+-----+-----+-----+-----+-----+
 ACAACTTGGCGGATTTTCGGGAGGCCTTCCAATAAACTTTTTGACGCGCTTGACGCACC
 _V_E_P_P_K_S_P_P_E_G_Y_F_E_K_L_R_E_L_R_G_

1441 TGCACTGGATGAAGCCGAAGTTAGCCGTGCAAAAGCAATTGTTATGGAAGTGGCCGAAAT
 -----+-----+-----+-----+-----+-----+
 ACGTGACCTACTTCGGCTTCAATCGGCACGTTTTCGTTAACAATACCTTGACCGGCTTTA
 _A_L_D_E_A_E_V_S_R_A_K_A_I_V_M_E_L_A_E_M_

NcoI

HincII

1501 GCGTGGTTTTCTGGGTAAACCATGGCTGGGCCTCATGGGCCTTCCTTTCACTGCCCGCTT
 -----+-----+-----+-----+-----+-----+
 CGCACCAAAAGACCCAATTGGTACCGACCCGGAGTACCCGGAAGGAAAGTGACGGGCGAA
 _R_G_F_L_G_*_

TCCAG
1561 -----
AGGTC