

ID Construct **14AGDG6C** Map

Customer **UNIVERSITÄT REGENSBURG, Jennifer Flechsler**

Name of the gene **Igni_0379**

optimized for **Escherichia coli**

15.09.2014 08:24:31

SphI

NheI

CACTATAGGGCGAATTGAAGGAAGGCCGTCAAGGCCGCATGCTAGCGTTTATCATGATCC
 1 -----+-----+-----+-----+-----+-----+
 GTGATATCCCGCTTAACCTCCTTCCGGCAGTTCGGCGTACGATCGAAATAGTACTAGG
 V_Y_H_D_P_

AgeI

GGGTAAACCGGTTTCATAAAATCATTGAAGAACGTGCACGTGAGAGTCCGGATAAAGTTGC
 61 -----+-----+-----+-----+-----+-----+
 CCCATTTGGCCAAGTATTTTAGTAACTTCTTGACGTGCACTCTCAGGCCTATTTCAACG
 _G_K_P_V_H_K_I_I_E_E_R_A_R_E_S_P_D_K_V_A_

BglII

ACTGGTTTATGAAGATGGCACCGAACTGACCTATAAAGATCTGATTAGCAAAGCAAAGC
 121 -----+-----+-----+-----+-----+-----+
 TGACCAAATACTTCTACCGTGGCTTGACTGGATATTTCTAGACTAATCGTTTCGTTTTCG
 _L_V_Y_E_D_G_T_E_L_T_Y_K_D_L_I_S_K_A_K_A_

CGTTGCCAATCTGCTGTATGAAAATAAAGTTCGCAAATGCGATACCGTGTTCTGATTAT
 181 -----+-----+-----+-----+-----+-----+
 GCAACGGTTAGACGACATACTTTTATTTCAAGCGTTTACGCTATGGCACAAGGACTAATA
 _V_A_N_L_L_Y_E_N_K_V_R_K_C_D_T_V_F_L_I_M_

GTTTAACCGTCCGGAATTTGTTACCAGCCTGCTGGGTGCACTGTATGCCGGTGACGTGT
 241 -----+-----+-----+-----+-----+-----+
 CAAATTGGCAGGCCTTAAACAATGGTCGGACGACCCACGTGACATACGGCCACGTGCACA
 _F_N_R_P_E_F_V_T_S_L_L_G_A_L_Y_A_G_A_R_V_

BglIII

PvuII

301 TGTATTGTTGATGCACTGACCCAGAAAGAAGATCTGGCATTTCAGCTGAATGATAGCGC
-----+-----+-----+-----+-----+-----+
ACAATAACAACACTACGTGACTGGGTCTTTCTTCTAGACCGTAAAGTCGACTTACTATCGCG
V I V D A L T Q K E D L A F Q L N D S A

PstI

361 ACCGAAAGTTGTTTCTGGCAGATGAAGAAGTTCTGCAGCGCGAAAGCGAAACCCTGAAAGG
-----+-----+-----+-----+-----+-----+
TGGCTTTCAACAAGACCGTCTACTTCTTCAAGACGTCGCGCTTTCGCTTTGGGACTTTCC
P K V V L A D E E V L Q R E S E T L K G

BglIII

421 TTATGCAGTTCTGACCGAAAAAGATCTGAGCAGCGCAAGCGGTGAACATGAAGTTGTTGT
-----+-----+-----+-----+-----+-----+
AATACGTCAAGACTGGCTTTTTCTAGACTCGTCGCGTTCGCCACTTGTACTTCAACAACA
Y A V L T E K D L S S A S G E H E V V V

BspMI

BspMI

BspMI

481 TGGTTATGAAGATGATGCCCCGTGTTTTCTATTATGCAGGTATTGCAGGTCGTACCATGCA
-----+-----+-----+-----+-----+-----+
ACCAATACTTCTACTACGGGCACAAAAGATAATACGTCCATAACGTCCAGCATGGTACGT
G Y E D D A R V F Y Y A G I A G R T M Q

AgeI

541 GGTTATTCATAGCCATCGTAGCTTTACCGGTGCAATTATGCCGCTGGTTCAGGCCGAAGG
-----+-----+-----+-----+-----+-----+
CCAATAAGTATCGGTAGCATCGAAATGGCCACGTTAATACGGCGACCAAGTCCGGCTTCC
V I H S H R S F T G A I M P L V Q A E G

BstEII

PflMI

601 TATTAATGCAAATGATGTTAGCCTGGTTACCGTTCCGCTGACCCATGTTCTGGGTCTGGA
-----+-----+-----+-----+-----+-----+
ATAATTACGTTTACTACAATCGGACCAATGGCAAGGCGACTGGGTACAAGACCCAGACCT
I N A N D V S L V T V P L T H V L G L D

661 TGCAGCACTGCTGAGCGCACTGGTTAGCGGTGCAACCGCACTGCTGCTGAAAAAGTTCAA
-----+-----+-----+-----+-----+-----+
ACGTCGTGACGACTCGCGTGACCAATCGCCACGTTGGCGTGACGACGACTTTTTCAAGTT
A A L L S A L V S G A T A L L L K K F N

TATGGATAAAATCAAAGAGATGGTTGCACGTCGTAGCCCGACCTATCTGGTTGCAGTTCC
 721 -----+-----+-----+-----+-----+-----+
 ATACCTATTTTAGTCTTCTACCAACGTGCAGCATCGGGCTGGATAGACCAACGTCAAGG
M D K I K E M V A R R S P T Y L V A V P

GCTGGTTTTTCAGACCCTGATGAAAGAAGATGAAGAATTTGTAAAAGCCTGGGTCAGAG
 781 -----+-----+-----+-----+-----+-----+
 CGACCAAAAAAGTCTGGGACTACTTTCTTCTACTTCTTAAACAATTTTCGGACCCAGTCTC
L V F Q T L M K E D E E F V K S L G Q S

BclI

CCTGCGTTGGGCAATGAGCGGTGGTGCATATCTGCCTCCGGATGATCAGCGTCGTTGGGA
 841 -----+-----+-----+-----+-----+-----+
 GGACGCAACCCGTTACTCGCCACCACGTATAGACGGAGGCCTACTAGTCGCAGCAACCCCT
L R W A M S G G A Y L P P D D Q R R W E

PstI

AgeI *BspMI*

AGAACTGACCGGTAAACCGCTGCTGCAGGTTTATGGTATGACCGAAGCACCGCAGATTTT
 901 -----+-----+-----+-----+-----+-----+
 TCTTGACTGGCCATTTGGCGACGACGTCCAAATACCATACTGGCTTCGTGGCGTCTAAAA
E L T G K P L L Q V Y G M T E A P Q I F

TGCAACCACACCCGAAAAACATAAAATTGGTAGCCTGGGTTTTCCGCTGCCTGGTGTGGA
 961 -----+-----+-----+-----+-----+-----+
 ACGTTGGTGTGGGCTTTTTGTATTTTAACCATCGGACCCAAAAGGCGACGGACCACAAC
A T T P E K H K I G S L G F P L P G V E

AgeI

AGCACTGCTGGTTAATCCGGAAACCCTGGAACCGTTGAAGATCAGGGTGAACCTGCTGGT
 1021 -----+-----+-----+-----+-----+-----+
 TCGTGACGACCAATTAGGCCTTTGGGACCTTGGCCAACTTCTAGTCCCACTTGACGACCA
A L L V N P E T L E P V E D Q G E L L V

BspMI *BamHI*

TCGTGGTCCGCAGGTTATGAAATGTTATCCGGATCCTGAAGAAAACAGCAAAGCCTTTGT
 1081 -----+-----+-----+-----+-----+-----+
 AGCACCAGGCGTCCAATACTTTACAATAGGCCTAGGACTTCTTTTGTGCTTTTCGGAAACA
R G P Q V M K C Y P D P E E N S K A F V

AgeI

1141 TGAAGTGAATGGTAAAGTTTGGATGCGCACCGGTGATATTCTGGCAAAAGATGAAGAAGG
-----+-----+-----+-----+-----+-----+
ACTTCACTTACCATTTCAAACCTACGCGTGGCCACTATAAGACCGTTTTCTACTTCTTCC
_E_V_N_G_K_V_W_M_R_T_G_D_I_L_A_K_D_E_E_G_

1201 CTTCTATTATTTCCGTGGTGTTCGTAAACGTATGCTGAAATACAAAGGCTATCCGATCTT
-----+-----+-----+-----+-----+-----+
GAAGATAATAAAGGCACCACAAGCATTTGCATACGACTTTATGTTTCCGATAGGCTAGAA
_F_Y_Y_F_R_G_V_R_K_R_M_L_K_Y_K_G_Y_P_I_F_

1261 TCCGAAAGACCTGGAAGTCTGCTGAAACATCCGTGTGTTGCCGAAGCCGAAGTTGT
-----+-----+-----+-----+-----+-----+
AGGCTTTCTGGACCTTGACTAAGACGACTTTGTAGGCACACAACGGCTTCGGCTTCAACA
_P_K_D_L_E_L_I_L_L_K_H_P_C_V_A_E_A_E_V_V_

1321 TGGTGAACCGGCAGGCGAAGTTGGTCAGATTCCGGTTGCAAAAGTTAAACTGAAAGAAGG
-----+-----+-----+-----+-----+-----+
ACCACTTGGCCGTCCGCTTCAACCAGTCTAAGGCCAACGTTTTCAATTTGACTTTCTTCC
_G_E_P_A_G_E_V_G_Q_I_P_V_A_K_V_K_L_K_E_G_

1381 TTGTAAAGCCACACCGGAAGAAATCATGGATTTTGTGAATAAACGTGTGGCAGCCTACAA
-----+-----+-----+-----+-----+-----+
AACATTTCCGGTGTGGCCTTCTTTAGTACCTAAAACACTTATTTGCACACCGTCGGATGTT
_C_K_A_T_P_E_E_I_M_D_F_V_N_K_R_V_A_A_Y_K_

NcoI

1441 AAAAGTGCGCAAAGTTATTATCCTGGAATAACCATGGCTGGGCCTCATGGGCCTTCCTTT
-----+-----+-----+-----+-----+-----+
TTTTACGCGTTTCAATAATAGGACCTTATTGGTACCGACCGGAGTACCGGAAGGAAA
_K_V_R_K_V_I_I_L_E_*_

1501 CACTGCCCCGCTTTCCAG
-----+-----
GTGACGGGCGAAAGGTC