

ID Construct **13ABGMZC**
 Customer **UNIVERSITÄT REGENSBURG, Jennifer Flechsler**
 Name of the gene **Igni_0132**
 optimized for **Escherichia coli**
 Upper sequence: as provided
 Lower sequence: as sequenced

13.07.2013 11:07:28

Sequence identity: 100%

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                                     GCTAGCGTGTATAATCCGTTTGGTG
                                     |||||
1  TCGGGGTTCTCATCATCATCATCATGGTATGGCTAGCGTGTATAATCCGTTTGGTG
   -----+-----+-----+-----+-----+-----+
                                     ATTATGTTTGGGAATTTTCGTAGTCCGCGTAGCAAATTTGGTCCGGGTGCACTGAATGAAC
                                     |||||
61 ATTATGTTTGGGAATTTTCGTAGTCCGCGTAGCAAATTTGGTCCGGGTGCACTGAATGAAC
   -----+-----+-----+-----+-----+-----+
                                     TGAAAGTTGATCTGGAACGTCTGCGTGTTGAAAAACCGTTTCTGATTACCACCAAAGGTT
                                     |||||
121 TGAAAGTTGATCTGGAACGTCTGCGTGTTGAAAAACCGTTTCTGATTACCACCAAAGGTT
   -----+-----+-----+-----+-----+-----+
                                     GGGTTAAACGTGGTATTGTTGATCGTCTGCGTGAAATTCTGGGTAAAGATGTTCCGTATT
                                     |||||
181 GGGTTAAACGTGGTATTGTTGATCGTCTGCGTGAAATTCTGGGTAAAGATGTTCCGTATT
   -----+-----+-----+-----+-----+-----+
                                     GGGATGGTGTGTAACCGGAACCGAGCGCAGAAAGCGTTGAAGAAGCAGCAAAAGCACTGG
                                     |||||
241 GGGATGGTGTGTAACCGGAACCGAGCGCAGAAAGCGTTGAAGAAGCAGCAAAAGCACTGG
   -----+-----+-----+-----+-----+-----+

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CAGAAAGCGGTGCAGATAGCGTTATTGCAATTGGTGGTGGTAGCGCACTGGATACCGCAA
 |||||
 CAGAAAGCGGTGCAGATAGCGTTATTGCAATTGGTGGTGGTAGCGCACTGGATACCGCAA
 301 -----+-----+-----+-----+-----+-----+

AAATTGCAAATCTGCTGGCAACCTATGGTGGTCGTGTTTCGTGATTATGTTGCACCGCCTT
 |||||
 AAATTGCAAATCTGCTGGCAACCTATGGTGGTCGTGTTTCGTGATTATGTTGCACCGCCTT
 361 -----+-----+-----+-----+-----+-----+

ATGGTGAAGGTAAACCGGTTCCGGGTCCGGTTAAACCGATGGTTGCAGTTCCGACCACCG
 |||||
 ATGGTGAAGGTAAACCGGTTCCGGGTCCGGTTAAACCGATGGTTGCAGTTCCGACCACCG
 421 -----+-----+-----+-----+-----+-----+

CAGGCACCGGTAGCGAAGTTACCAGCGTTGCAGTTGTTACCCTGAAAGATGTTGGTGTTA
 |||||
 CAGGCACCGGTAGCGAAGTTACCAGCGTTGCAGTTGTTACCCTGAAAGATGTTGGTGTTA
 481 -----+-----+-----+-----+-----+-----+

AAGTTGGTATCAGCAGCGATTTTCTGCGTCCGAGCCTGGCACTGCTGGACCCGGAAGTGA
 |||||
 AAGTTGGTATCAGCAGCGATTTTCTGCGTCCGAGCCTGGCACTGCTGGACCCGGAAGTGA
 541 -----+-----+-----+-----+-----+-----+

CCATGACCGTTCCGCCTAAAGTTACCGCAGATACCGGTATGGATGCACTGACCCATGCAG
 |||||
 CCATGACCGTTCCGCCTAAAGTTACCGCAGATACCGGTATGGATGCACTGACCCATGCAG
 601 -----+-----+-----+-----+-----+-----+

TTGAAAGCTATATCGCAAAACCGTATTGGGCACGTGAACGTCCGGAAGATCCGGCAAAAC
 |||||
 TTGAAAGCTATATCGCAAAACCGTATTGGGCACGTGAACGTCCGGAAGATCCGGCAAAAC
 661 -----+-----+-----+-----+-----+-----+

GTCCGGTTTATGTTGGTAGCTTTACCGTTACCGATGCACTGGCCGAACGTGCAATTGAAC
 ||
 GTCCGGTTTATGTTGGTAGCTTTACCGTTACCGATGCACTGGCCGAACGTGCAATTGAAC
 721 -----+-----+-----+-----+-----+-----+

TGATTGGTAAATATCTGCGTCGTGCAGTTTATCAGGGTCGTACCGATCTGGAAGCACGTA
 ||
 TGATTGGTAAATATCTGCGTCGTGCAGTTTATCAGGGTCGTACCGATCTGGAAGCACGTA
 781 -----+-----+-----+-----+-----+-----+

GCGGTATGCTGATTGCAAGCTATCTGGCAGGTCTGGCATTGTTGGTAATGCCGGTGTTGGTC
 ||
 GCGGTATGCTGATTGCAAGCTATCTGGCAGGTCTGGCATTGTTGGTAATGCCGGTGTTGGTC
 841 -----+-----+-----+-----+-----+-----+

TGGCACATGCAGCAAGCTATCCGCTGGGTGGTCGTTATAAAGTTACACATGGTGAAGCAG
 ||
 TGGCACATGCAGCAAGCTATCCGCTGGGTGGTCGTTATAAAGTTACACATGGTGAAGCAG
 901 -----+-----+-----+-----+-----+-----+

TTGGTATTCTGCTGCCTGCAGTTCTGGAATTTAATGCACCGGCAAATTATGAAAAAGCCA
 ||
 TTGGTATTCTGCTGCCTGCAGTTCTGGAATTTAATGCACCGGCAAATTATGAAAAAGCCA
 961 -----+-----+-----+-----+-----+-----+

AACGTGTTGGCGAACTGCTGACCGGTGAAAAATGTCCGGAACGTGATCCTGCAAAATGTG
 ||
 AACGTGTTGGCGAACTGCTGACCGGTGAAAAATGTCCGGAACGTGATCCTGCAAAATGTG
 1021 -----+-----+-----+-----+-----+-----+

CAGAATGGGCAGCAAATGCAATTCGTGAACTGCAGCGTGATATCAAATTTACACCGGGTC
 ||
 CAGAATGGGCAGCAAATGCAATTCGTGAACTGCAGCGTGATATCAAATTTACACCGGGTC
 1081 -----+-----+-----+-----+-----+-----+

TGGAAGCAGTGGGTGTTAAAGAAGAGGATCTGATGGAAATGGCAAAGAAACCCTGAATC
||
TGGAAGCAGTGGGTGTTAAAGAAGAGGATCTGATGGAAATGGCAAAGAAACCCTGAATC
1141 -----+-----+-----+-----+-----+-----+

AGAAACGTCTGCTGGCCACCAATCCGCGTCCGGTTACCGAAGAAGATGTTTATTGGGTTT
||
AGAAACGTCTGCTGGCCACCAATCCGCGTCCGGTTACCGAAGAAGATGTTTATTGGGTTT
1201 -----+-----+-----+-----+-----+-----+

ATAAACGTAGCATGCGCAACTATTAACCATGG
||||||||||||||||||||||||||||||
ATAAACGTAGCATGCGCAACTATTAACCATGGAATTCTGAAGCTTGATCCGGCTGCTAACA
1261 -----+-----+-----+-----+-----+-----+

AAGCCCG
1321 -----