

ID Construct           **11AAJH3P**           **Map**  
 Customer               **ETH HOENGERBERG,Matthias Heinemann**  
 Name of the gene       **Ateam103**  
 optimized for           **Saccharomyces cerevisiae**

29.06.2011 13:38:06

*NcoI*

*SpeI BamHI*

CACTATAGGGCGAATTGAAGGAAGGCCGTCAAGGCCGCATACTAGTGGATCCATGGTTTC  
 1 -----+-----+-----+-----+-----+-----+  
 GTGATATCCCGCTTAACTTCCCTCCGGCAGTTCGGCGTATGATCACCTAGGTACCAAAG  
M V S

*HincII*

TAAGGGTGAAGAATTATTCACCTGGTGTGTTCCAATCTTGGTTGAATTGGATGGTGATGT  
 61 -----+-----+-----+-----+-----+-----+  
 ATTCCCCTTCTTAATAAGTGACCACAACAAGGTTAGAACCAACTTAACCTACCACTACA  
K G E E L F T G V V P I L V E L D G D V

TAACGGTCACAGATTTTCTGTTTCTGGTGAAGGTGAAGGTGATGCTACTTATGGTAAATT  
 121 -----+-----+-----+-----+-----+-----+  
 ATTGCCAGTGTCTAAAAGACAAAGACCACTTCCACTTCCACTACGATGAATACCATTAA  
N G H R F S V S G E G E G D A T Y G K L

*NcoI*

GACCTTGAAGTTCATCTGTACCACAGGTAATTTGCCAGTTCATGGCCAACCTTGGTTAC  
 181 -----+-----+-----+-----+-----+-----+  
 CTGGAACCTCAAGTAGACATGGTGTCCATTTAACGGTCAAGGTACCGGTTGAAACCAATG  
T L K F I C T T G K L P V P W P T L V T

*NdeI*

TACTTTGACTTGGGGTGTTCATGTTTGTCTAGATACCCAGATCATATGAAGCAACACGA  
 241 -----+-----+-----+-----+-----+-----+  
 ATGAAACTGAACCCCAAGTTACAAAACGATCTATGGGTCTAGTATACTTCGTTGTGCT  
T L T W G V Q C F A R Y P D H M K Q H D

TTTCTTCAAATCCGCTATGCCAGAAGGTTACGTTCAAGAAAGAACCATCTTCTTCAAGGA  
301 -----+-----+-----+-----+-----+-----+  
AAAGAAGTTTAGGCGATACGGTCTTCCAATGCAAGTTCTTTCTTGGTAGAAGAAGTTCCT  
F F K S A M P E G Y V Q E R T I F F K D

*BstBI* *HincII*

TGACGGTAACTACAAAAGTATAGAGCCGAAGTTAAGTTCGAAGGTGATACCTTGGTTAACAG  
361 -----+-----+-----+-----+-----+-----+  
ACTGCCATTGATGTTTTGATCTCGGCTTCAATTCAAGCTTCCACTATGGAACCAATTGTC  
D G N Y K T R A E V K F E G D T L V N R

AATCGAATTGAAGGGTATCGACTTCAAAGAAGATGGTAACATCTTGGGTCACAAGTTGGA  
421 -----+-----+-----+-----+-----+-----+  
TTAGCTTAACTTCCCATAGCTGAAGTTTCTTCTACCATTGTAGAACCCAGTGTTC AACCT  
I E L K G I D F K E D G N I L G H K L E

ATACAACACTACATCTCCATAACGTTTACATTACCGCCGATAAGCAAAAGAACGGTATTAA  
481 -----+-----+-----+-----+-----+-----+  
TATGTTGATGTAGAGGGTATTGCAAATGTAATGGCGGCTATTCGTTTTCTTGCCATAATT  
Y N Y I S H N V Y I T A D K Q K N G I K

*BclI*

GGCTCATTTCAAGATCAGACACAACATCGAAGATGGTGGTGTACAATTGGCTGATCATT  
541 -----+-----+-----+-----+-----+-----+  
CCGAGTAAAGTTCTAGTCTGTGTTGTAGCTTCTACCACCACATGTTAACCGACTAGTAAT  
A H F K I R H N I E D G G V Q L A D H Y

*AccI*

CCAACAAAACACTCCAATTGGTGATGGTCCAGTTTTTGTGTCAGATAACCATTACTTGTC  
601 -----+-----+-----+-----+-----+-----+  
GGTTGTTTTGTGAGGTTAACCACTACCAGGTCAAAACAACGGTCTATTGGTAATGAACAG  
Q Q N T P I G D G P V L L P D N H Y L S

TACCCAATCCAAATTGTCTAAGGACCCAAACGAAAAAAGAGATCACATGGTCTTGTGGA  
661 -----+-----+-----+-----+-----+-----+  
ATGGGTTAGGTTTAAACAGATTCCCTGGGTTTGTCTTTTTTCTCTAGTGTACCAGAACAACCT  
T Q S K L S K D P N E K R D H M V L L E

*ClaI*      *BbsI*                  *HincII*

721 -----+-----+-----+-----+-----+-----+  
ATTTGTTACTGCTGCTATCGATATGAAGACCGTTAAGGTTAACATTACTACTCCAGATGG  
TAAACAATGACGACGATAGCTATACTTCTGGCAATTCCAATTGTAATGATGAGGTCTACC  
F V T A A I D M K T V K V N I T T P D G

781 -----+-----+-----+-----+-----+-----+  
TCCTGTTTACGATGCCGATATTGAAATGGTTTCTGTCAGAGCTGAATCTGGTGATTTGGG  
AGGACAAATGCTACGGCTATAACTTTACCAAAGACAGTCTCGACTTAGACCACTAAACCC  
P V Y D A D I E M V S V R A E S G D L G

841 -----+-----+-----+-----+-----+-----+  
TATTTTGCCAGGTCATATTCCTACAAAAGCCCCATTGAAAATTGGTGCCGTTAGATTGAA  
ATAAAACGGTCCAGTATAAGGATGTTTTCGGGGTAACTTTTAACCACGGCAATCTAACTT  
I L P G H I P T K A P L K I G A V R L K

901 -----+-----+-----+-----+-----+-----+  
AAAGGACGGTCAAACAGAAATGGTTGCAGTTTCAGGTGGTACTGTTGAAGTTAGACCAGA  
TTTCTGCCAGTTTGTCTTTACCAACGTCAAAGTCCACCATGACAACCTCAATCTGGTCT  
K D G Q T E M V A V S G G T V E V R P D

*PvuII*

961 -----+-----+-----+-----+-----+-----+  
TCATGTTACTATTAACGCTCAAGCTGCTGAAACAGCTGAAGGTATTGACAAAGAAAGAGC  
AGTACAATGATAATTGCGAGTTCGACGACTTTGTGCGACTTCCATAACTGTTTCTTTCTCG  
H V T I N A Q A A E T A E G I D K E R A

*EcoRV*

1021 -----+-----+-----+-----+-----+-----+  
TGAAGCTGCTAGACAAAAGAGCCCAAGAAAGATTGAACTCTCAATCTGATGATACCGATAT  
ACTTCGACGATCTGTTTCTCGGGTCTTTCTAACTTGAGAGTTAGACTACTATGGCTATA  
E A A R Q R A Q E R L N S Q S D D T D I

1081 -----+-----+-----+-----+-----+-----+  
CAGAAGAGCAGAAATGGCTTTACAAAGAGCTTTGAACAGATTGGATGTTGCTGGTAAGGC  
GTCTTCTCGTCTTAACCGAAATGTTTCTCGAACTTGTCTAACCTACAACGACCATTCGG  
R R A E L A L Q R A L N R L D V A G K A

*EcoRI*

1141 TAACGAATTCATGGACGGTGGTGTTC AATTAGCAGACCACTATCAACAAAACACACCTAT  
-----+-----+-----+-----+-----+-----+  
ATTGCTTAAGTACCTGCCACCACAAGTTAATCGTCTGGTGATAGTTGTTTTGTGTGGATA  
N E F M D G G V Q L A D H Y Q Q N T P I

CGGTGACGGTCCTGTATTATTACCTGATAATCACTATTTGTCCTACCAATCTAAGTTGTC  
1201 -----+-----+-----+-----+-----+-----+  
GCCACTGCCAGGACATAATAATGGACTATTAGTGATAAACAGGATGGTTAGATTCAACAG  
G D G P V L L P D N H Y L S Y Q S K L S

*NdeI*

CAAAGATCCTAACGAAAAAAGAGATCATATGGTTTTATTAGAAATTTGTCACCGCTGCCGG  
1261 -----+-----+-----+-----+-----+-----+  
GTTTCTAGGATTGCTTTTTTCTCTAGTATACCAAATAATCTTAAACAGTGGCGACGGCC  
K D P N E K R D H M V L L E F V T A A G

TATTACTTTGGGTATGGATGAATTATACAAGGGTGGTTCTGGTGGTATGGTTAGTAAAGG  
1321 -----+-----+-----+-----+-----+-----+  
ATAATGAAACCCATACCTACTTAATATGTTCCACCAAGACCACCATACCAATCATTTC  
I T L G M D E L Y K G G S G G M V S K G

*AatII*

TGAAGAATTATTCACAGGTGTCGTCCTATTTTAGTAGAATTAGACGGTGACGTCAATGG  
1381 -----+-----+-----+-----+-----+-----+  
ACTTCTTAATAAGTGTCACAGCAGGGATAAAAATCATCTTAATCTGCCACTGCAGTTACC  
E E L F T G V V P I L V E L D G D V N G

TCATAAGTTTTTCAGTTAGTGGTGAAGGTGAAGGTGACGCAACATACGGTAAATTGACTTT  
1441 -----+-----+-----+-----+-----+-----+  
AGTATTCAAAAAGTCAATCACCCTTCCACTTCCACTGCGTTGTATGCCATTTAACTGAAA  
H K F S V S G E G E G D A T Y G K L T L

*AgeI*

1501 -----+-----+-----+-----+-----+-----+  
GAAATTGATATGCACTACCGGTAAGTTACCTGTTCCCTTGGCCTACATTAGTTACAACATT  
CTTTAACTATACGTGATGGCCATTCATGGACAAGGAACCGGATGTAATCAATGTTGTAA  
K L I C T T G K L P V P W P T L V T T L

*EcoRV*

1561 -----+-----+-----+-----+-----+-----+  
GGGTTACGGTTTACAATGCTTCGCTAGATATCCTGACCACATGAAGCAACATGACTTTTT  
CCCAATGCCAAATGTTACGAAGCGATCTATAGGACTGGTGTACTTCGTTGTACTGAAAA  
G Y G L Q C F A R Y P D H M K Q H D F F

1621 -----+-----+-----+-----+-----+-----+  
TAAGTCTGCAATGCCTGAAGGTTATGTCCAAGAAAGAACTATTTTCTTTAAGGACGATGG  
ATTCAGACGTTACGGACTTCCAATACAGGTTCTTTCTTGATAAAAGAAATTCCTGCTACC  
K S A M P E G Y V Q E R T I F F K D D G

1681 -----+-----+-----+-----+-----+-----+  
TAATTACAAGACCAGAGCTGAAGTAAAATTTGAAGGTGACACTTTGGTCAATAGAATTGA  
ATTAATGTTCTGGTCTCGACTTCATTTTAACTTCCACTGTGAAACCAGTTATCTTAACT  
N Y K T R A E V K F E G D T L V N R I E

1741 -----+-----+-----+-----+-----+-----+  
ATTGAAAGGTATTGATTTTAAAGAAGATGGTAACATTTTAGGTCATAAGTTAGAATACAA  
TAACTTTCCATAACTAAAATTTCTTCTACCATTGTAAAATCCAGTATTCAATCTTATGTT  
L K G I D F K E D G N I L G H K L E Y N

*AccI*

1801 -----+-----+-----+-----+-----+-----+  
TTATAACTCTCACAAACGTCTACATCACTGCTGACAAACAAAAAATGGTATCAAGGCCAA  
AATATTGAGAGTGTTCAGATGTAGTGACGACTGTTTGTTTTTTTTACCATAGTTCCGGTT  
Y N S H N V Y I T A D K Q K N G I K A N

*SalI*

*HincII*

*XhoI AccI HindIII*

1861 CTTCAAAATTAGACATAACATTGAATGACTCGAGGTCGACAAGCTTCTGGGCCTCATGGG  
-----+-----+-----+-----+-----+-----+  
GAAGTTTAAATCTGTATTGTAAGTACTGAGCTCCAGCTGTTCTGAAGACCCGGAGTACCC  
F K I R H N I E \* \_

CCTTCCTTTCCTGCCCCGCTTTCAG  
1921 -----+-----+-----  
GGAAGGAAAAGTGACGGGCGAAAGGTC