

Figura 1

SEQ ID NO: 1

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MAAASISAAT TIPKPSSHIS SSSRSSIFIS RFTLPLSLNP QKAIPHRSLH 50
ISNSVSKPTT PAPSSSTTLT IPQASPPRFS PDEARKGADI LVEALERQGV 100
TDVFAYPGGA SMEIHQALTR SPIIRNVLP RHEQGGVFAAE GYARASGKPG 150
VCIATSGPGA TNLVSGGLADA LLDSVPIVAI TGQVPRRMIG TDAFQETPIV 200
EVTRISITKHN YLVLDVDDIP RIVSEAFFLA TSGRPGPVLI DVPKDIQQQL 250
AVPNWNTPIK LPGYMSRLPK VPNEHLEQI VRLIFESKKP VLYVGGGCLN 300
SSEELRKFEV LTGIPVASTL MGLGAFPVGH ELSLQMLGMH GTVYANYSDV 350
KSDLLLAFGV RFDDRVTGKL EAFASRAKIV HIDIDSAEIG KNKQPHVSV 400
ADVKFALQGM NKILESRC AKSKLDFKAWRE ELNEQKSKYP LKYKTFGDAI 450
PPQYAIQVLD ELTDGNAIIS TGVGQHQMWA AQFYKYKRPR QWLTSGGLGA 500
MGFGLPAAIG AAVANPGAVV VDIDGDGSFI MNVQELATIR VENLPIKIML 550
LNNQHLGMVV QWEDRFYKAN RAHTYLGDP KESEIFPNML KFAEACGIPA 600
ARVTRKEGLR MAIQKMLDTP GPYLLDVIVP HQEHVLPMP SGGAFKDVIT 650
EGDGRTKY
```

Figura 2

SEQ ID NO: 2

ATGGCGGGCGGCTCTACCTCTGCGGCTACCACTATCCCTAAACCTCTTCTCACATTCT
TCCTCCTCCAGATCTTCAATCTTCAATTTCCAGATTACCCCTCCCATTTGTCTCTCAACCCC
CAAAAGGCCATTCTCACCCTCTCTCCACATATCAAACCTCTGTCTCTAAACCTACAACC
CCTGCCCCCTCATCTCCACCACCTTAACCATTCCTCAAGCGTCTCCTCCCAGGTTTTCT
CCTGATGAAGCTCGAAAAGGCCGCGACATCCTCGTTGAAGCGCTGGAACGCCAAGGGGTC
ACTGATGTATTTGCTTATCCAGGCGGCGCATCCATGGAGATCCATCAAGCCCTGACTCGC
TCACCTATAATTGCAATGTCTCTCCGCGCCATGAGCAAGGTGGGGTCTTTGCGGCTGAG
GGATATGCTCGCGCTTCTGGCAAGCCTGGCGTCTGTATCGCAACCTCGGGACCCGCGCT
ACAAATCTCGTAAGTGGCTTGGCAGACGCTCTCCTTGACAGCGTCCCCATTGTGGCTATC
ACCGGCCAAGTTCTCGCCGCGATGATTGGCACCAGCGCATTCGAAGAACTCCCATTGTT
GAGGTAACCTCGGTCAATACTAAGCACAATTACCTGGTCTTGATGTTGATGATATTCTT
AGAATTGTAAGTGAAGCTTTCTTTTTGGCCACCTCGGGACGTCCTGGCCAGTTCTGATT
GATGTACCAAAAGATATACAACAACAATTAGCTGTTCCAAATTGGAATACACCTATTAAA
TTGCCCTGGTTACATGTCGAGGTTGCCTAAAGTGCCCAACGAATCACATTTGGAGCAGATT
GTGAGGCTAATTTTGTAGTCAAAGAAACCGGTTTTATACGTGGGAGGTGGGTGTTTAAAT
TCAAGTGAGGAGTTGAGAAAGTTTGTGAGTTAACTGGGATCCCAGTGGCTAGTACTTTG
ATGGGGCTCGGAGCATTCCCAGTTGGCCACGAATTGTCAATACAAATGCTTGGGAATGCAT
GGAATGTTTATGCTAACTACTCGGTGGATAAGAGTGATTTGTTGCTTGGCTTTGGGGTG
AGGTTTGATGACAGGGTGACAGGCAAGCTTGAGGCCTTTGCAAGCAGAGCTAAGATTGTT
CACATTGATATTGATTCCGCTGAGATTGGGAAAAATAAGCAGCCCCATGTGTCTGTTTGT
GCAGATGTGAAGTTTGCCTTGCAAGGGATGAACAAGATTTTGGAGAGCAGATGTGCTAAG
AGTAAGCTAGATTTTAAGGCTTGAGGGGAGGAGTTGAATGAGCAGAAAAGTAAATATCCA
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GAATTAACAGATGGGAATGCCATTATAAGTACTGGCGTTGGACAACATCAGATGTGGGCT
GCTCAATTTTACAAGTACAAGAGACCACGGCAATGGTTGACGTCAGGGGGATTAGGGGCT
ATGGGTTTTGGATTGCTGCCGCCATTGGGGCTGCTGTTGCTAATCCTGGTGCAGTTGTT
GTAGATATTGATGGTGATGAAGTTTTATCATGAATGTCCAGGAGTTGGCAACAATTCGT
GTGGAGAATCTGCCAATTAATAATGCTTTTGAATAATCAGCATTTGGGAATGGTGGTA
CAATGGGAGGACCGATTCTACAAGGCTAATAGAGCTCATACTTATTTGGGGGATCCATCA

Figura 2, continuación

AAGGAGTCTGAGATTTTCCCAATATGTTGAAGTTTGCAGAAGCTTGTGGAATACCTGCT
GCTCGCGTGACAAGAAAAGAGGGTCTTAGAATGGCGATTCAGAAAATGCTAGATACTCCA
GGGCCATACTTGTGGATGTGATTGTGCCCCATCAAGAACATGTGCTGCCCATGATCCCA
AGTGGGGGAGCTTTTAAGGATGTGATAACTGAGGGTGATGGAAGAACGAAGTATTGA

Figura 3A

SEQ ID NO: 5

MAAASTSAAT TIPKPSSHIS SSSRSSIFIS RFTLPLSLNP QKAIPHRSLH
ISNSVSKPTT PAPSSSTLT IPQASPPRFS PDEARKGADI LVEALERQGV
TDVFAYPGGA SMEIHQALTR SPIIRNVLP R HEQGGVFAAE GYARASGKPG
VCIATSGPGA TNLVSGLADA LLDSVPIVAI TGQVPRRMIG TDAFQETPIV
EVTRSITKHN YLVLDVDDIP RIVSEAFFLA TSGRPGPVLI DVPKDIQQQL
AVPNWNTPIK LPGYMSRLPK VPNESHLEQI VRLIFESKKP VLYVGGGCLN
SSEELRKFEV LTGIPVASTL MGLGAFFVGH ELSLQMLGMH GTVYANYSD
KSDLLAFGV RFDARVTGKL EAFASRAKIV HIDIDSAEIG KNKQPHVSVC
ADVKFALQGM NKILESRCAL SKLDFKAWRE ELNEQKSKYP LKYKTFGDAI
PPQYAIQVLD ELTDGNAIIS TGVGQHQMWA AQFYKYKRPR QWLTSGGLGA
MGFGLPAAIG AAVANPGAVV VDIDGDGSFI MNVQELATIR VENLPIKIML
LNNQHLGMVV QSEDRFYKAN RAHTYLGDPK KESEIFPNML KFAEACGIPA
ARVTRKEGLR MAIQKMLDTP GPYLLDVIVP HQEHVLPMP SGGAFKDVIT
EGDGRTKY

Figura 3B

SEQ ID NO: 3

MAAASTSAAT TIPKPSSHIS SSSRSSIFIS RFTLPLSLNP QKAIPHRSLH
ISNSVSKPTT PAPSSSTILT IPQASPPRFS PDEARKGADI LVEALERQGV
TDVFAYPGGA SMEIHQALTR SPIIRNVLP RHEQGGVF AAE GYARASGKPG
VCIATSGPGA TNLVSGGLADA LLDSVPIVAI TGQVPRRMIG TDAFQETPIV
EVTRSITKHN YLVLDVDDIP RIVSEAFFLA TSGRPGPVLI DVPKDIQQQL
AVPNWNTPIK LPGYMSRLPK VPNESHLEQI VRLIFESKKP VLYVGGGCLN
SSEELRKFVE LTGIPVASTL MGLGAFFVGH ELSLQMLGMH GTVYANYSD
KSDLLAFGV RFDDRVTGKL EAFASRAKIV HIDIDSAEIG KNKQPHVSVC
ADVKFALQGM NKILESRCAL SKLDFKAWRE ELNEQKSKYP LKYKTFGDAI
PPQYAIQVLD ELTDGNAIIS TGVGQHQMWA AQFYKYKRPR QWLTSGGLGA
MGFGLPAAIG AAVANPGAVV VDIDGDGSFI MNVQELATIR VENLPIKIML
LNNQHLGMVV QSEDIFYKAN RAHTYLGDPK KESEIFPNML KFAEACGIPA
ARVTRKEGLR MAIQKMLDTP GPYLLDVIVP HQEHVLPMP SGGAFKDVIT
EGDGRTKY

Figura 4

SEQ ID NO: 4

Met Ala Ala Ala Thr Thr Thr Thr Thr Thr Ser Ser Ser Ile Ser Phe
Ser Thr Lys Pro Ser Pro Ser Ser Ser Lys Ser Pro Leu Pro Ile Ser
Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro Asn Lys Ser Ser Ser Ser
Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala
Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys
Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro
Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val
Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His Gln
Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu
Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys
Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Leu Val Ala Ile
Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln Glu
Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr Leu
Val Met Asp Val Glu Asp Ile Pro Arg Ile Ile Glu Glu Ala Phe Phe
Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys
Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Glu Gln Ala Met Arg
Leu Pro Gly Tyr Met Ser Arg Met Pro Lys Pro Pro Glu Asp Ser His
Leu Glu Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Lys Pro Val Leu
Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser Asp Glu Leu Gly Arg Phe
Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly
Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His
Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu
Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala

Figura 4, continuación

Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu
Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys
Leu Ala Leu Cln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu
Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys
Cln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro
Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile
Ile Ser Thr Gly Val Gly Cln His Cln Met Trp Ala Ala Cln Phe Tyr
Asn Tyr Lys Lys Pro Arg Cln Trp Leu Ser Ser Gly Gly Leu Gly Ala
Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro
Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn
Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val
Leu Leu Leu Asn Asn Cln His Leu Gly Met Val Met Cln Trp Glu Asp
Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala
Cln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys
Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala
Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile
Cys Pro His Cln Glu His Val Leu Pro Met Ile Pro Ser Gly Gly Thr
Phe Asn Asp Val Ile Thr Glu Gly Asp Gly Arg Ile Lys Tyr

Figura 5

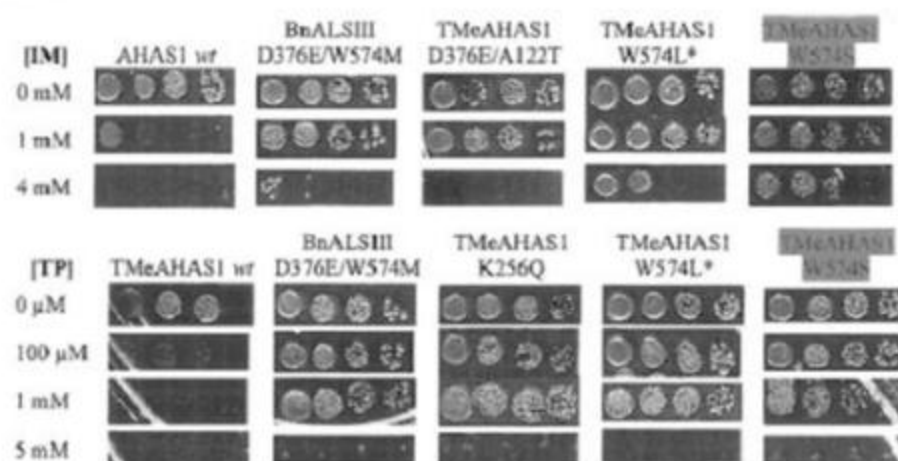


Figura 6A

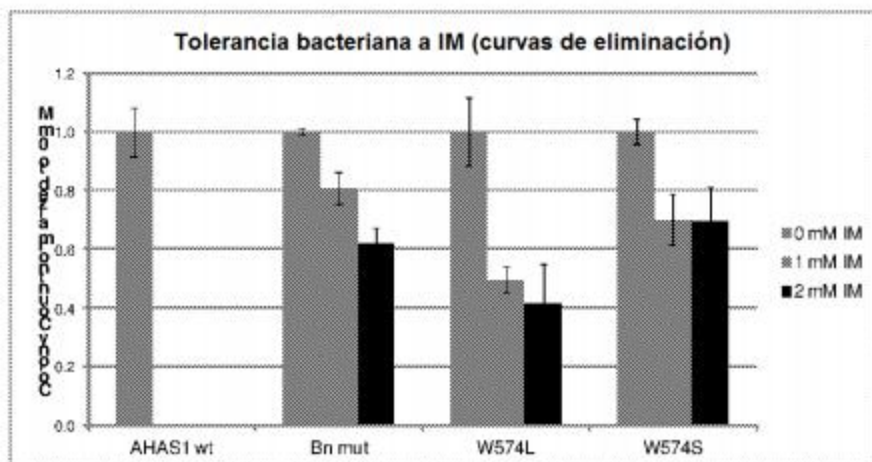


Figura 6B

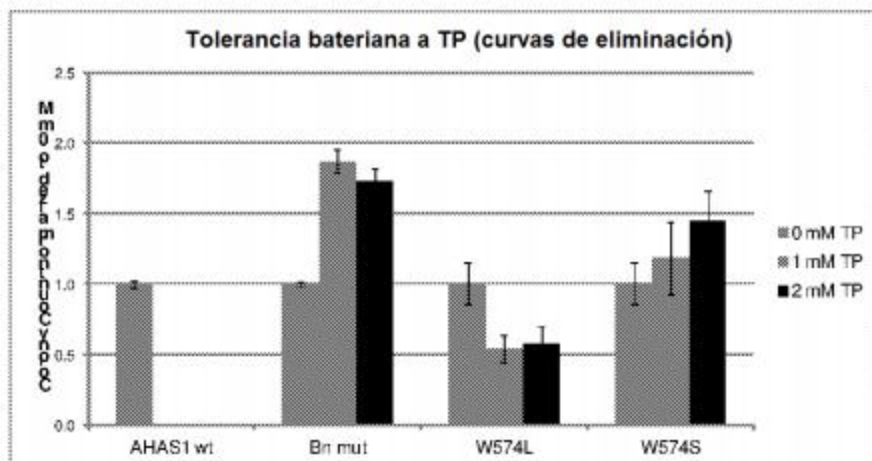


Figura 7

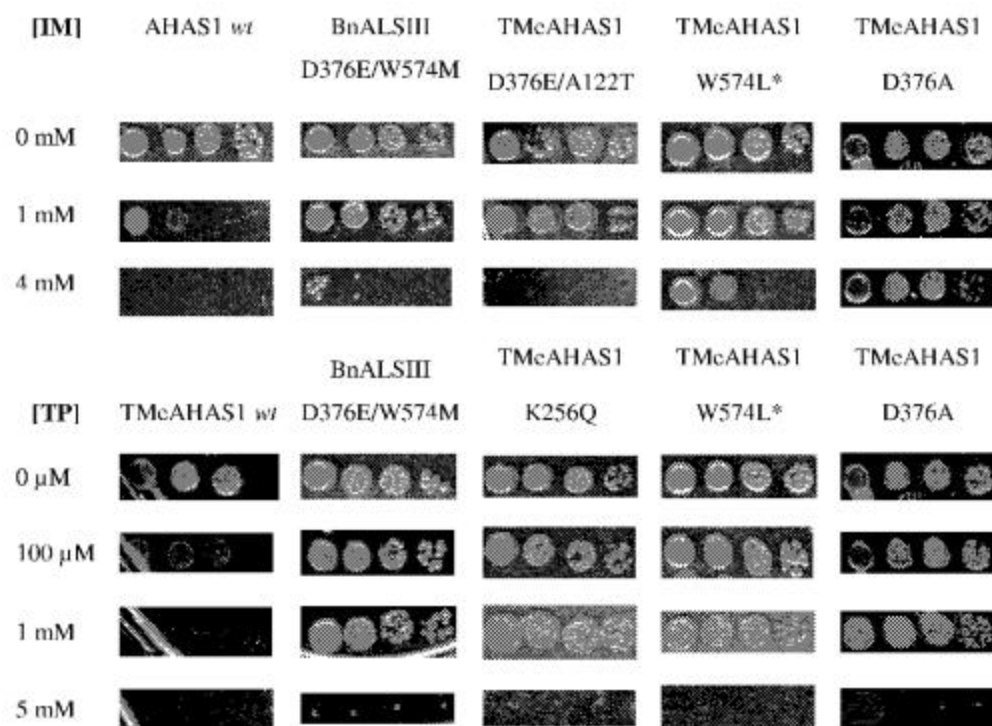


Figura 8A

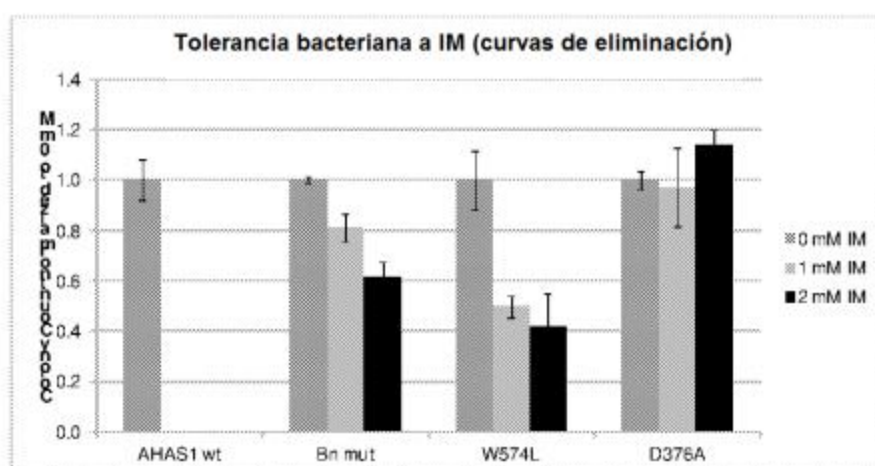


Figura 8B

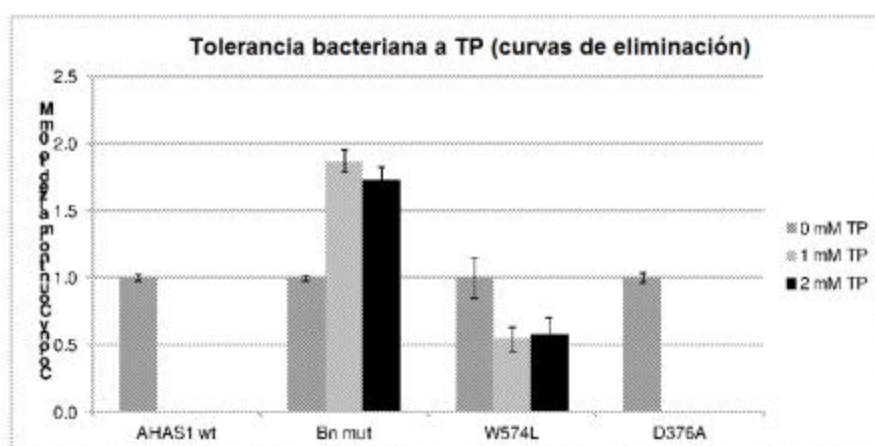


Figura 9A

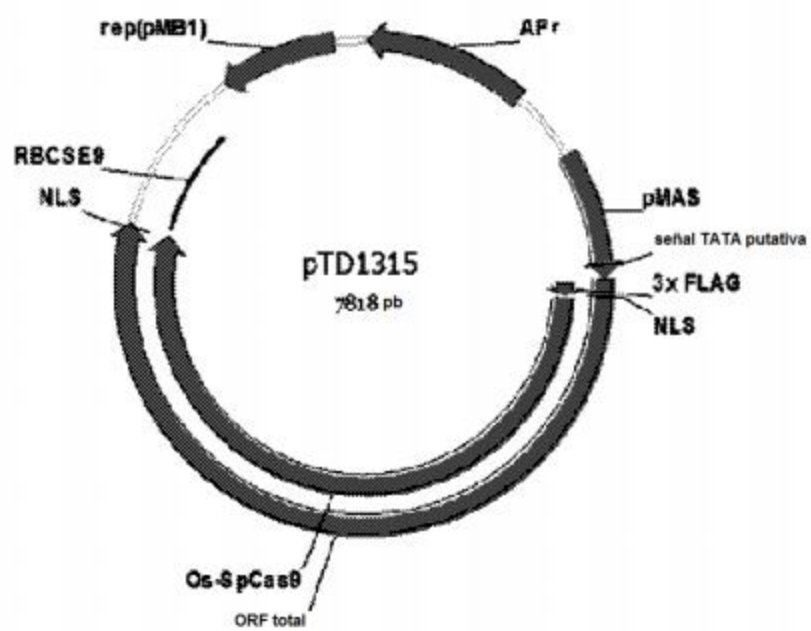


Figura 9B

