

RELAÇÃO DE CLONES ANTI-BOTRÓPICOS

KC329709 (Clone 9 - BthTX-I):

ATGGCCGACGTGCAGCTGCAGGCGTCTGGGGGAGGCTTGGTGCAGGCTGGGGGGTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAAACATCAATACTATCGATGTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCG
CGAGTTGGTCGCAGACATTACCAGACTTGCTAGCGCAAATATGCAGACTCCGTGAAGGGCCGATTACCC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAACCTGGAACCTAAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATCTTAAGTACTGATCACTCGTACATGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KC329718 (clone 82 - BthTX-I):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGAGGATTGGTGCAGGCTGGGGGGTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAGGCACCTTCAGTAATCCGTCTATGGGCTGGTCCGCCAGGCTCCAGGGAAGGAGCG
TGAGTTTGTAGCAGCTGTTAGCTGGAGTGCTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCC
ACCATCTCCAGAGACAACGCCAAGAACACGGTGGATCTGCGAATGACCAGCCTGAAACCTGAGGACACGG
CCGTTTATTATTGTTCTGCCACATACTATAACGGTGAATACTACTTACTGCGGGCAGATAGATATCAACA
CTGGGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

KC329717 (Clone 75 - BthTX-I):

ATGGCCGACGTCCAGCTGCAGGCGTCTGGGGGAGGCTTGGTGCAGGCTGGGGGGTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAAACATCGACACTATCGATGTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCG
CGAGTTGGTCGCAGACATTACCAGTCAGGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTACCC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAATCTGGAACCTGAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATACTAAGTACTGATCACTCGTACAAGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KC329716 (Clone 68 - BthTX-I):

ATGGCCGAGGTCCAGCTGCAGGCGTCTGGGGGAGGCTTGGTGCAGGCTGGGGGGTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAAACATCGACACTATCGATGTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCG
CGAGTTGGTCGCAGACATTACCAGTCAGGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTACCC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAATCTGGAACCTGAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATACTAAGTACTGATCACTCGTACAAGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KC329715 (Clone 67 - BthTX-I):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGAGGAGGCTTGGTGCAGGCTGGGGGGTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAAACATCAATACTATCGATGTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCG
CGAGTTGGTCGCAGACATTACCAGACTTGCTAGCGCAAATATGCAGACTCCGTGAAGGGCCGATTACCC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAACCTGGAACCTAAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATCTTAAGTACTGATCACTCGTACATGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KC329714 (Clone 66 - BthTX-I):

ATGGCCGACGTGCAGCTGCAGGCGTCTGGGGAGGATTGGTGCAGGCTGGGGGGTCTCTGAGACTCTCCT
GTGCAGCCTCTGGACCCATATATGAAAGTTATGGAATGGCCTGGTCCGCCAGGGTCCAGGGCAGGGACG
TGAGTTTGTAGCAGCGATCCACCTAAGTAGTAGTACCACATACTATGGAGACTCCGTGAAGGGCCGATTCC
ACCATCTCCAGAGACAACGCCCAGAACATGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGG
CCATTTATTTCTGTGCAATAGGTAACCTACGAATTGCGGTACCTCCCACTTCAGTCGGGTATGATTACTG
GGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

KC329713 (Clone 58 - BthTX-I):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGACGCACCGATAGTACGTATGCCATGGCCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAGTTTGTTCAGCTATAACCTATACTGGTGGTACCACACACTATGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACGTCGCCAAGGACATTATGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTGCAGAAAAACGTAGTAGCTGGTACAGGCCATTTGGTGTAGATGAGTTTGGCTCCTG
GGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

KC329712 (Clone 48 - BthTX-I):

ATGGCCGACGTGCAGCTGCAGGCGTCTGGGGGAGGCTTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAAACATCAATACTATCGATGTTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCG
CGAGTTGGTTCGACAGACATTACCAGACTTGCTAGCGCAAACCTATGCAGACTCCGTGAAGGGCCGATTTCACC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAACCTGGAACCTAAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATCTTAAGTACTGATCACTCGTACATGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KC329711.1 (Clone 32 - BthTX-I):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGGAGGCTTGGTGCAGGCTGGGGGCTCTCTGGGACTCTCCT
GTGCAGCCTCTGGAAACATCGACACTATCGATGTTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCG
CGAGTTGGTTCGACAGACATTACCAGTCAGGGTAGCACAAACCTATGCAGACTCCGTGAAGGGCCGATTTCACC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAATCTGGAACCTGAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATACTAAGTACTGATCACTCGTACAAGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KC329710 (Clone 23 - BthTX-I):

ATGGCCGACGTGCAGCTGCAGGCGTCTGGGGGAGGCTTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAAACATCGACACTATCGATGTTCATGGGCTGGTACCGCCAGGCTCCAGGGAGGCAGCG
CGAGTTGGTTCGACAGACATTACCAGTCAGGGTAGCACAAACCTATGCAGACTCCGTGAAGGGCCGATTTCACC
ATCTCCAGAGACAACGCCAAGAATACGGTGTATCTGCAAATGAACAATCTGGAACCTGAGGACACCGCCG
TCTATTATTGTGCGCAGTGGATACTAAGTACTGATCACTCGTACAAGCACTACTGGGGCCAGGGGACCCA
GGTCACCGTCACCGTCTCCTCA

KF498607 (Clone 20 - BthTX-II)

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGACGCACCTTCAGTGACCTGTCTATGGGCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAGTTTGTAGCAGCTGTTAGCTGGAGTGTAGGTACAACATACTATGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAACGCCAAGAACACGGTGGATCTCCAAATGATCAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTTTCAGCCACATACTATACGGGTGAATACTACTTACTACAGGCAGATAGATATCAACA
CTGGGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

KF498608 (Clone 30 – BthTX – II)

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGACGCACCTTCAGTGACCTGTCTATGGGCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAGTTTGTAGCAGCTGTTAGCTGGAGTGTAGGTACAACATACTATGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAACGCCAAGAACACGGTGGATCTCCAAATGATCAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTTTCAGCCACATACTATACGGGTGAATACTACTTACTACAGGCAGATAGATATCAACA
CTGGGGCCAGGTCACCGTCACCGTCTCCTCA

KF498609 (Clone 28 – BthTX – II)

ATGGCCGAGGTGCACCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGAAGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGACGCACCTTCAGTGACCTGTCTATGGGCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAGTTTGTAGCAGCTGTTAGCTGGACCCCTGGTACAACATACTATGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAACGCCAAGAACACGGTGGATCTCCAAATGATCAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTACAGCCACATACTATACGGGTGAATACTACTTAGTACAGGCAGATAGATATCAACA
CTGGGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

OL960540.1 (Clone 34 anti-metaloprotease):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGGAGGATTAGTGCAGGTTGGGGACTCTCTGAGACTCTCCT
GTACAGTCTCTGGAGGCACCTTCAATAGGTATACCATGGGCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAATGGGTAGGAGCTATAAACTGGAGTGGTGTAGCTCAGAAAGTATGCAGACTCCGTGCAGGGCCGATTC
ACCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGG
CCGTTTATACCTGTGCAACAGGGCCGTATGGTGGAAAGCCTGGGGGATCAAACAGGATATGAGTATGAATA
CTGGGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

OL960541.1 (Clone 47 anti-metaloprotease):

ATGGCCGAGGTCCAGCTGCAGGCGTCTGGAGGAGGATTGGTGCAGACTGGGGGCTCTCTGAGACTCTCCT
GTACAGCCTCTGGACGCACCTTCAGTAGCTATGTATAGGTTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TAGTTTTGTAGCGGCTATTAGAAAAGAGTGGTAGTCTCACATACTATACAGACTCCGTGAAGGGCCGGTTC
ACCATTTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTGCCGCAGACCCGACGACCCGTACGTTTATGTCTGACTATGAGGATGACTATGATTA
TTGGGGCCAGGTCACCGTCACCGTCTCCTCA

OL960542.1 (Clone 53 anti-metaloprotease):

ATGGCCGACGTGCAGCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGACGCTCTCCT
GTGCAGCCTCTGGAGGCACCTTTACAAACTATGCCATGGCCTGGTTCCGCCAGGCTCCAGCAAAGGATCG
TGAATTTGTAGCGGCTGTTAACTGGAGTGGTGGTCGGAAATTGTATGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACGACGCCAAGAATACGGTGTATCTCCAAATGAACAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTGCAGTGGGTATAGTAAGCGATTACGTTAGCGACTTTGACTATGACTATTGGGGCCA
GGGGACCCAGGTCACCGTCACCGTCTCCTCA

OL960543.1 (Clone 61 anti-metaloprotease):

ATGGCCGAGGTCCAGCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGTAGCCTCTGGAGGCACCTTCGATCGGTACGCCATGGGCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAATTTGTAGCGACTATTAGCTGGAGTAGTTTTTCGCATACGTTATTTCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAACCTGAAACCTGAGGACACGG
CCGTTTATTACTGTGCAGCAGCATCAACTGGTAGCGACTATCTTCGTGAATATGACTATGACTATTGGGG
CCAGGGGATGCAGGTCACCGTCACCGTCTCCTCA

OL960544.1 (Clone 64 anti-metaloprotease):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGGAGGATTGGTGCAGGCTGGGGATTCTCTGAGACTCTCCT
GTGCAGGCTCTGGACGCACCGTCAGTACCGCTGCCATGGGCTGGTTCCGGCAGGCTCCAGGCAAGGAGCG
TGATTTTGTAGCGGCAATTAACTGGAGTGGTAGTAACACATACTATGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAGCGCCAAGAACACGGTGTATCTGCAAATGAACAACCTGAAACCTGAGGACACGG
CCGTTTATTACTGTGTAGCGGATAATATTGTCCGGTAGTGGTAGTTACTACAACAGTCGAGAGTATGACTA
CTGGGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA

OL960545.1 (Clone 78 anti-metaloprotease):

ATGGCCGAGGTCCAGCTGCAGGCGTCTGGGGAGGATTGGTGCAGCCTGGGGGCTCTCTGAGACTCTCCT
GTGCAGCCTCTGGAGGCCGCTTCAGTAATCACGCCATGGCCTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAGTTTGTAGCAGCTGTTAATTGGAGTGGTGAGAGGAAGTTCTATGCAGACGCCGTGAAGGGCCGATTC
ACCATCTCCAGAGAGGACGCCAAGAACACGTTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGG
CCGTTTATTACTGTGCAACGGGAATAGTAAGCGATTACATCAGCGACTTTGACTACACCTACTGGGGCCA
GGGAACCCAGGTCACCGTCACCGTCTCCTCA

OL960546.1 (Clone 79 anti-metaloprotease):

ATGGCCGAGGTGCAGCTGCAGGCGTCTGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTCTCCT
GTGCGGCCTCCGGACACTCTGTCAATACCTATGCCATAAGTTGGTTCCGCCAGGCTCCAGGGAAGGAGCG
TGAATTTGTAGCAGGTATTAGTTGGAGTGGTAGTAATGCATACTATGGAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATGACAAGAACACGGCGTATCTGCAGATGAACAGCCTGAAACCTGACGACACGG
CCGTTTATTACTGTGCAGCAGATCGGATCTCGGGTTGGGAAAGAGGTAATCCCAGGGACTATGACTACTG
GGGCCAGGGGACCCAGGTCACCGTCACCGTCTCCTCA