FIG. 1

1434A08 (SEQ ID NO:216)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCATCGTACTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1437G04 (SEQ ID NO:217)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTACTACCATTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1437A09(SEQ ID NO:218)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTAAACAGCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1438E05(SEQ ID NO:219)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTAACGTTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1438D01(SEQ ID NO:220)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTAACCGTGCTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1438B02(SEQ ID NO:221)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTAAAACTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1438A09(SEQ ID NO:222)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTAAACAGCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

FIG. 1 (continued)

1486G03(SEQ ID NO:223)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTCGTTACTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1486C04(SEQ ID NO:224)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCCGCATCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1486D04(SEQ ID NO:225)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTTCTACTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1486B05(SEQ ID NO:226)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTCGTATCTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1486D05(SEQ ID NO:227)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCATCAGCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1487C03(SEQ ID NO:228)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTAAACAGGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1487G03(SEQ ID NO:229)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTGCTCATCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

FIG. 1 (continued)

1487D09(SEQ ID NO:230)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATATTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTTCTCGTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1487H04(SEQ ID NO:231)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTGCTCGTCAGTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACCAGGAATACGAATACCGTTACATACCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490E02(SEQ ID NO:232)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTACTCAGTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490G02(SEQ ID NO:233)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCCGCGTTACCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACATGGAAGAAAAATACGCTGTTATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490H05(SEQ ID NO:234)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTATGCGTCAGCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490B03(SEQ ID NO:235)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTCGTAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAAAGAAGCTAACTATCGTGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490H06(SEQ ID NO:236)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTCAGAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

FIG. 1 (continued)

1490A07(SEQ ID NO:237)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCATGCTAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490C07(SEQ ID NO:238)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTAACCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1490H08(SEQ ID NO:239)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTAACACTTCTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACGGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1491A05(SEQ ID NO:240)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTCAGGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1571H03(SEQ ID NO:241)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTAACCGTGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAGAATACCATATCATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1571G04(SEQ ID NO:242)
ATGGGAGTTTCTGATGTGCCSCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCCGCGTTCTCACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1571G06(SEQ ID NO:243)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCACCTGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTACTAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAAAGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

FIG. 1 (continued)

1571F10(SEQ ID NO:244)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTCGTTACCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGAACAGGTTGAATACCGTGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1572D04(SEQ ID NO:245)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCCGCGTCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGAACAGCCGATCTACGCCACTATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1572F05(SEQ ID NO:246)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTCAGAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1572G06(SEQ ID NO:247)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTTACAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1572B10(SEQ ID NO:248)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTGTTCCGCGTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1572C09(SEQ ID NO:249)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTACTCCGAAACATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1572H05(SEQ ID NO:250)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTTCTAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGAACAGGTTGAATACCGTGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

FIG. 1 (continued)

1572H08(SEQ ID NO:251)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTTCTCGTAAATACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1550A07(SEQ ID NO:252)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTGTTCCGCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1550C05(SEQ ID NO:253)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCCGCGTCGTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1550E03(SEQ ID NO:254)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATATCCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTATGCGTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACTCCGAAGAACTGTACAAATACATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1550E06(SEQ ID NO:255)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGATGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCCGCCGCGTCATACCGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACGCTCAGGAAAACTACAAAGAAATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

1550H05(SEQ ID NO:256)
ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG
CTGGGGTCATTACCCGCTGCATGTTCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCC
CTGTCCAGGAGTTCACTGTGCCTCGTCAGATCTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTT
GATTATACCATCACTGTGTATGCTGTCACTTACTACAACGAAGCTGACTACTCTCAGATCCCAATTTC
CATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA

FIG. 2

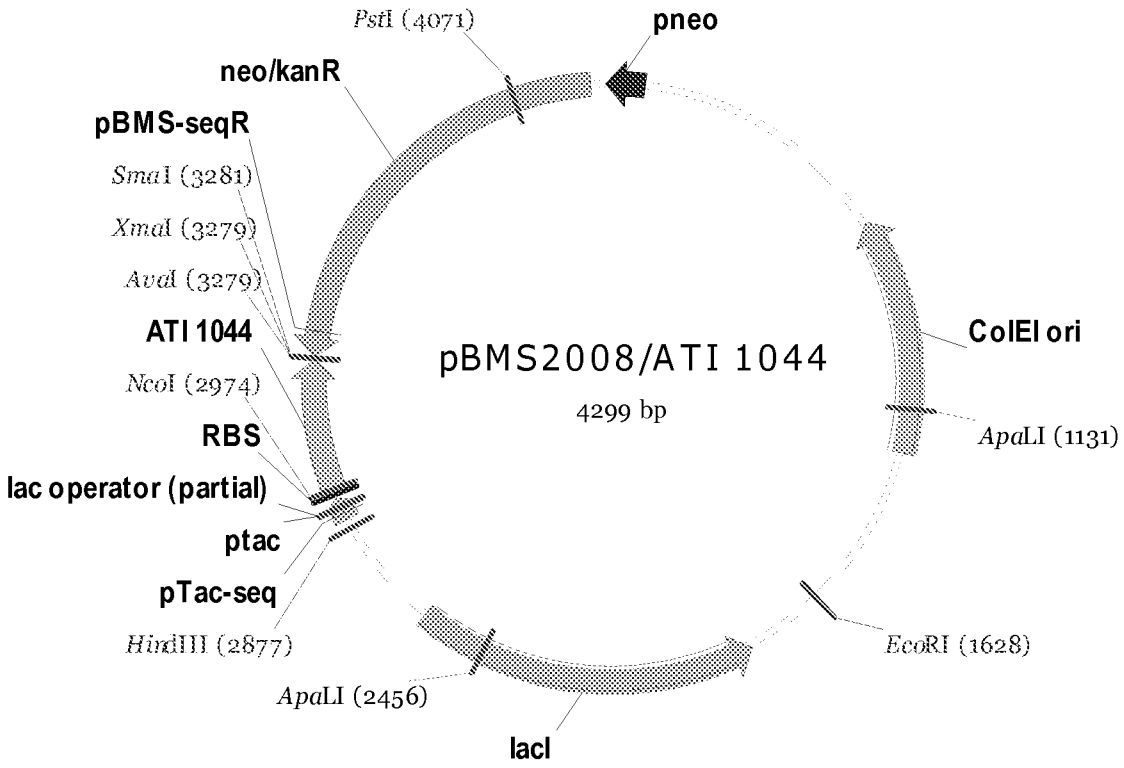

PstI (4071)
pneo
neo/kanR
pBMS-seqR
SmaI (3281)
XmaI (3279)
AvaI (3279)
ATI 1044
NcoI (2974)
RBS
lac operator (partial)
ptac
pTac-seq
HindIII (2877)
ApaLI (2456)
lacI
pBMS2008/ATI 1044
4299 bp
ColEI ori
ApaLI (1131)
EcoRI (1628)

FIG. 3

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Wildtype VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRT
1434A08  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPHRTHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1437G04  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPYYHYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1437A09  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPSKQHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1438E05  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPSNVHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1438D01  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPNRAHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1438B02  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPRKTYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1438A09  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPRSRYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1486G03  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPSRYYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1486C04  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPPHRYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1486D04  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPRSTHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1486B05  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPSRIYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1486D05  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPHQRYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1487C03  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPKQVYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1487G03  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPAHRYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1487D09  VSDVPRDLEVVAATPTSLLISWGHYPMHIRYYRITYGETGGNSPVQEFTVPRSRHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1487H04  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPARQYTATISGLKPGVDYTITVYAVTYYQEYEYRYIPISINYRT
1490E02  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPRTQYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1490G02  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPPRYHTATISGLKPGVDYTITVYAVTYYMEKYAVIPISINYRT
1490H05  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPMRQHTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1490B03  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPSRKYTATISGLKPGVDYTITVYAVTYYKEANYREIPISINYRT
1490H06  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPRQKYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1490A07  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPHAKYTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1490C07  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPSNRYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1490H08  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPNTSHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1491A05  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPSQVYTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1571H03  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPNRVYTATISGLKPGVDYTITVYAVTYYAQEEYHIIPISINYRT
1571G04  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPPRSHTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1571G06  VSDVPRDLEVVAATPTSLLISWGHYPLHLRYYRITYGETGGNSPVQEFTVPRTKYTATISGLKPGVDYTITVYAVTYYKEADYSQIPISINYRT
1571F10  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPSRYHTATISGLKPGVDYTITVYAVTYYEQVEYREIPISINYRT
```

FIG. 3 (continued)

```
1572D04  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPPRRYTATISGLKPGVDYTITVYAVTYYEQPIYATIPISINYRT
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1572G06  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPRYKYTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1572B10  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPVPRHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1572C09  VSDVPRDLEVVAATPTSLLISWGHYPMHIRYYRITYGETGGNSPVQEFTVPTPKHTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1572H05  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPRSKYTATISGLKPGVDYTITVYAVTYYEQVEYREIPISINYRT
1572H08  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPSRKYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1550A07  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPVPRYTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1550C05  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPPRRYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
1550E03  VSDVPRDLEVVAATPTSLLISWGHYPLHIRYYRITYGETGGNSPVQEFTVPRMRHTATISGLKPGVDYTITVYAVTYYSEELYKYIPISINYRT
1550E06  VSDVPRDLEVVAATPTSLLISWGHYPMHVRYYRITYGETGGNSPVQEFTVPPPRHTATISGLKPGVDYTITVYAVTYYAQENYKEIPISINYRT
1550H05  VSDVPRDLEVVAATPTSLLISWGHYPLHVRYYRITYGETGGNSPVQEFTVPRQIYTATISGLKPGVDYTITVYAVTYYNEADYSQIPISINYRT
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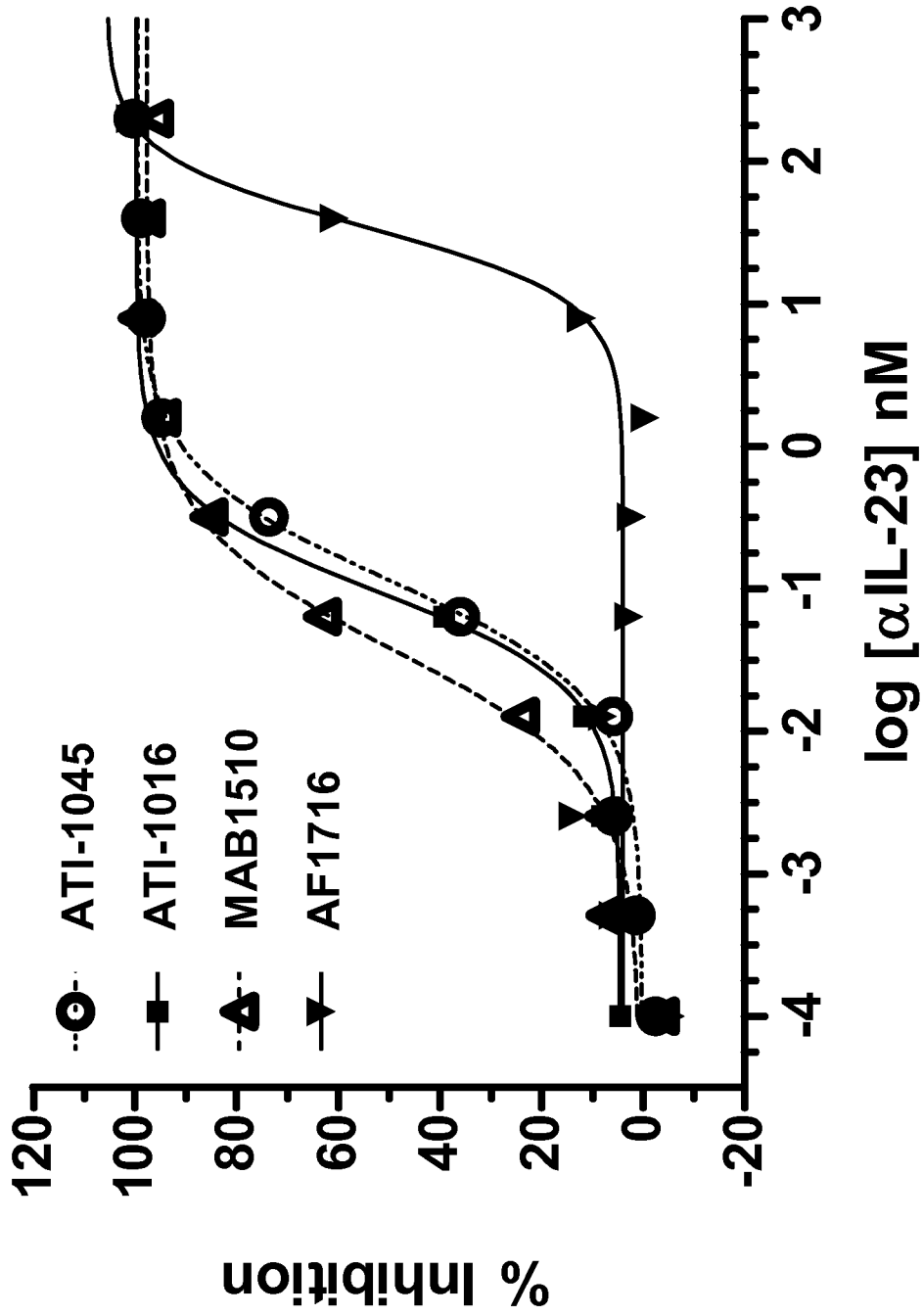

% Inhibition
120
100
80
60
40
20
0
-20
-4
-3
-2
-1
0
1
2
3
log [αIL-23] nM
ATI-1045
ATI-1016
MAB1510
AF1716

FIG. 4

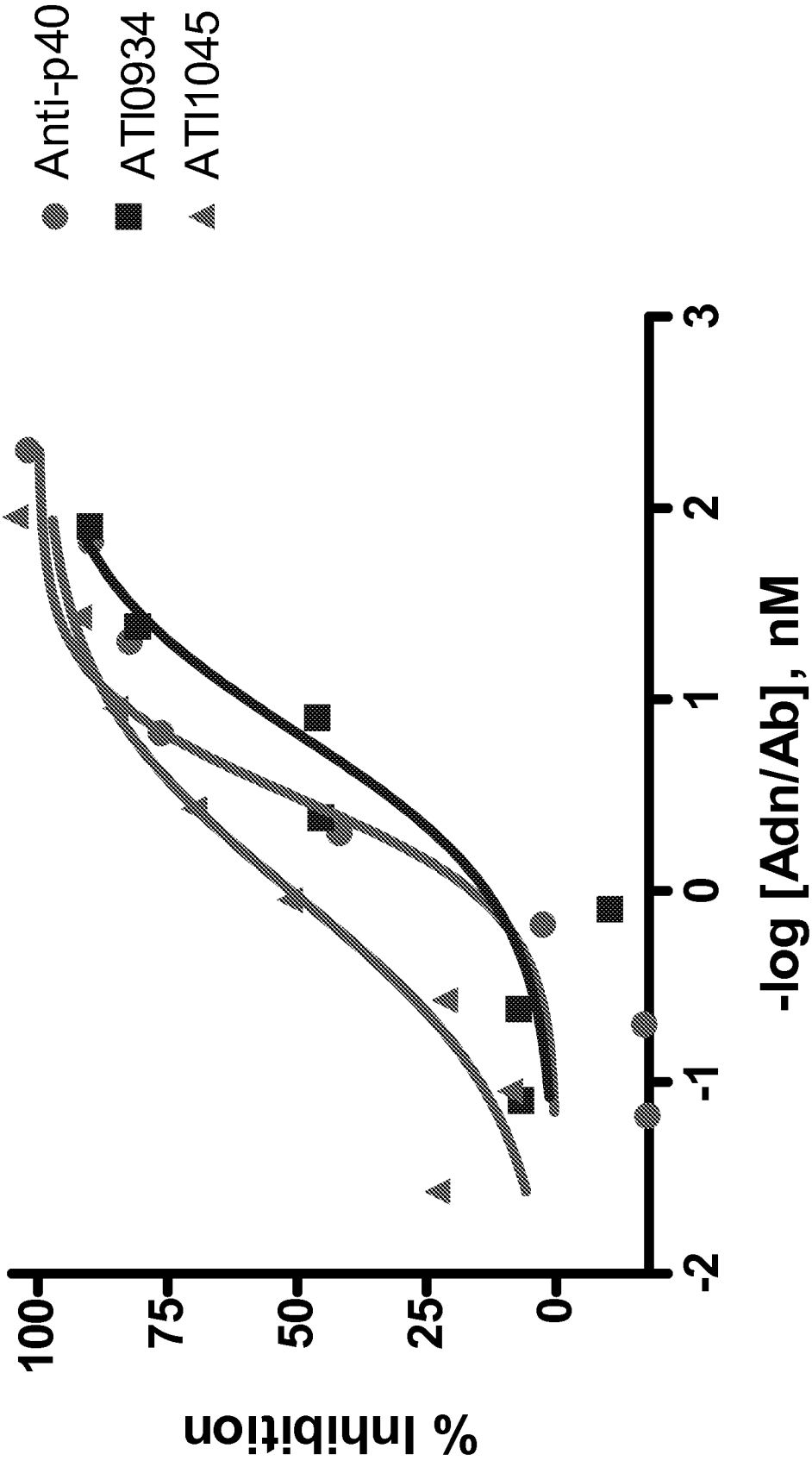

Anti-p40
ATI0934
ATI1045
% Inhibition
100
75
50
25
0
-2
-1
0
1
2
3
-log [Adn/Ab], nM

FIG. 5

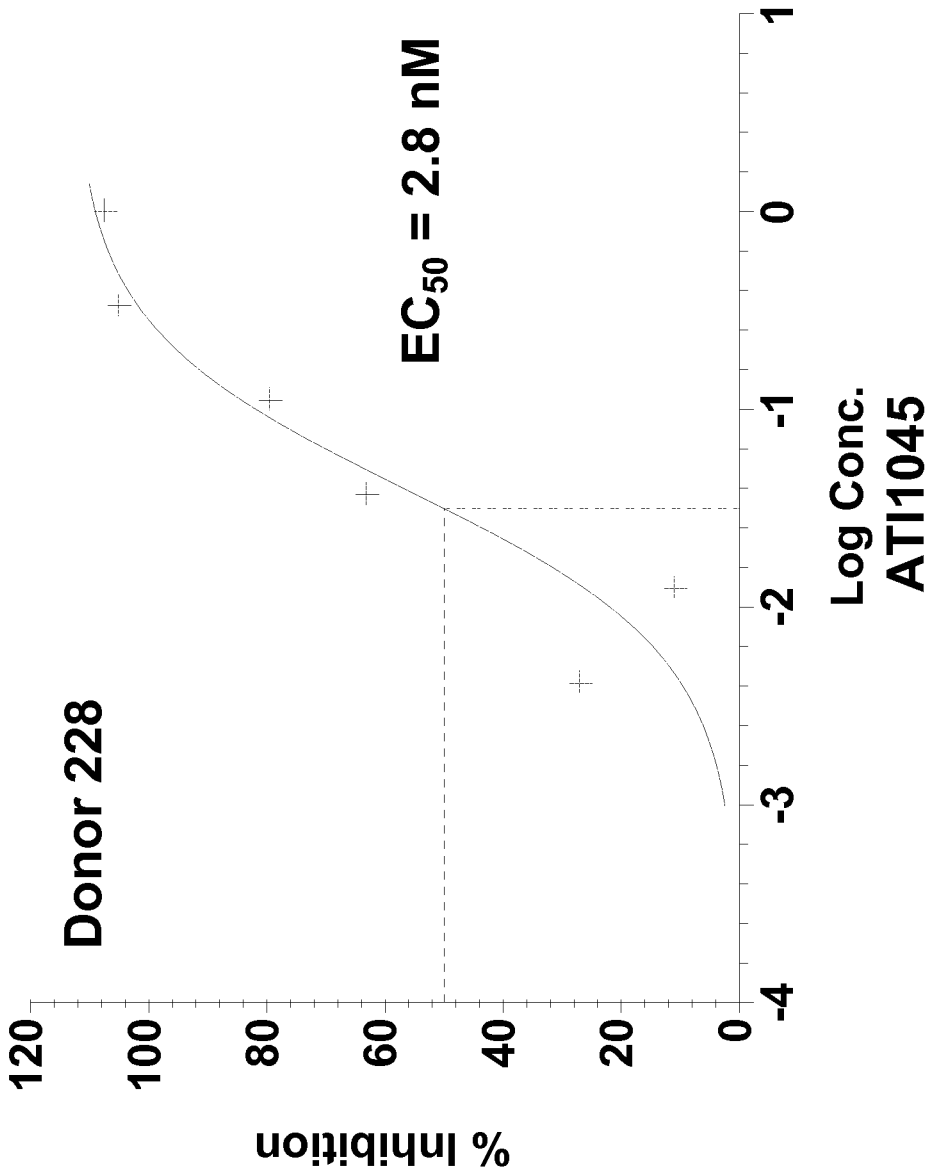

Donor 228
EC50 = 2.8 nM
% Inhibition
120
100
80
60
40
20
0
-4
-3
-2
-1
0
1
Log Conc.
ATI1045

FIG. 6

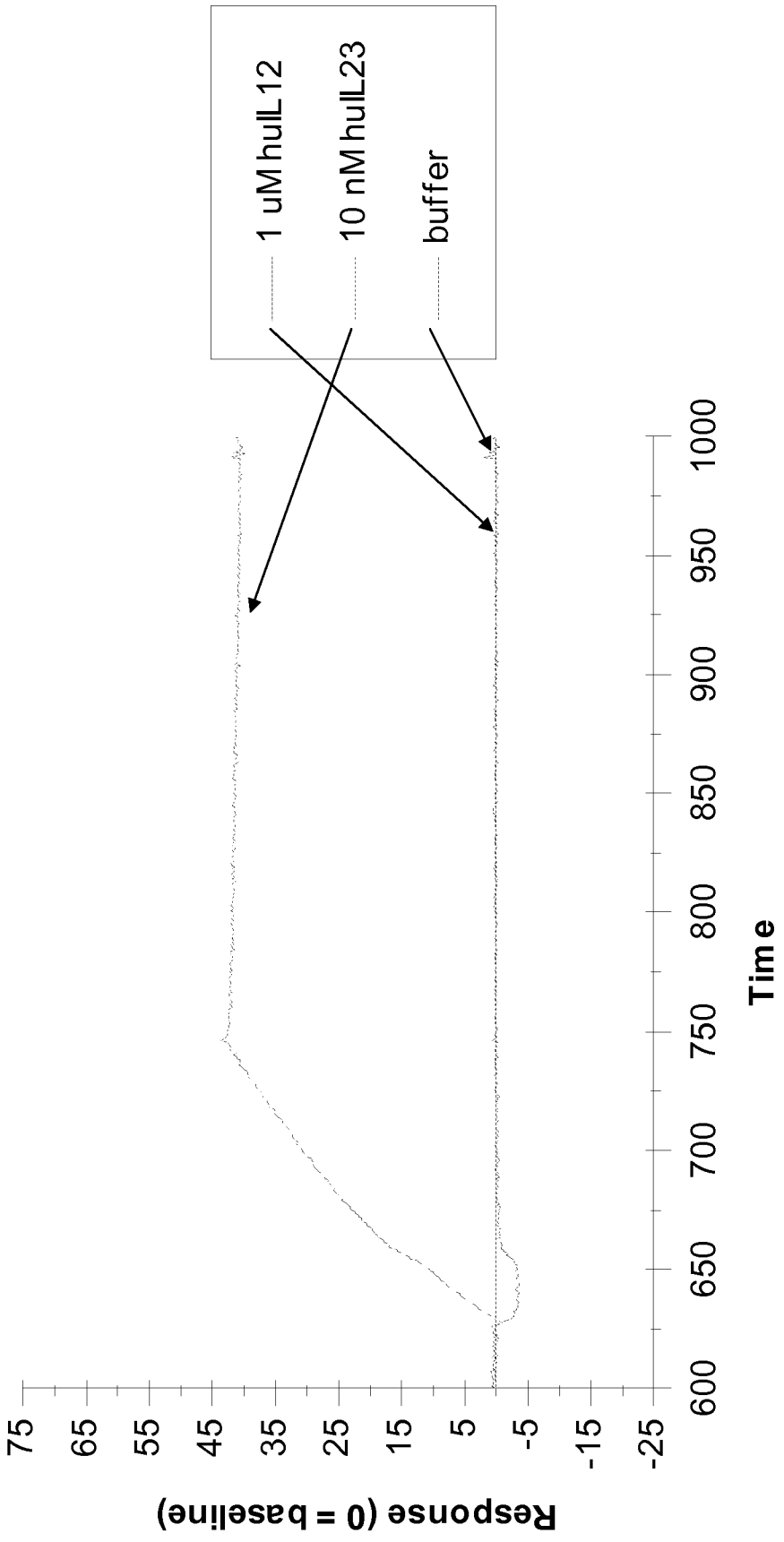

1 uM huIL12
10 nM huIL23
buffer
Response (0 = baseline)
75
65
55
45
35
25
15
5
-5
-15
-25
600
650
700
750
800
850
900
950
1000
Time

FIG. 7

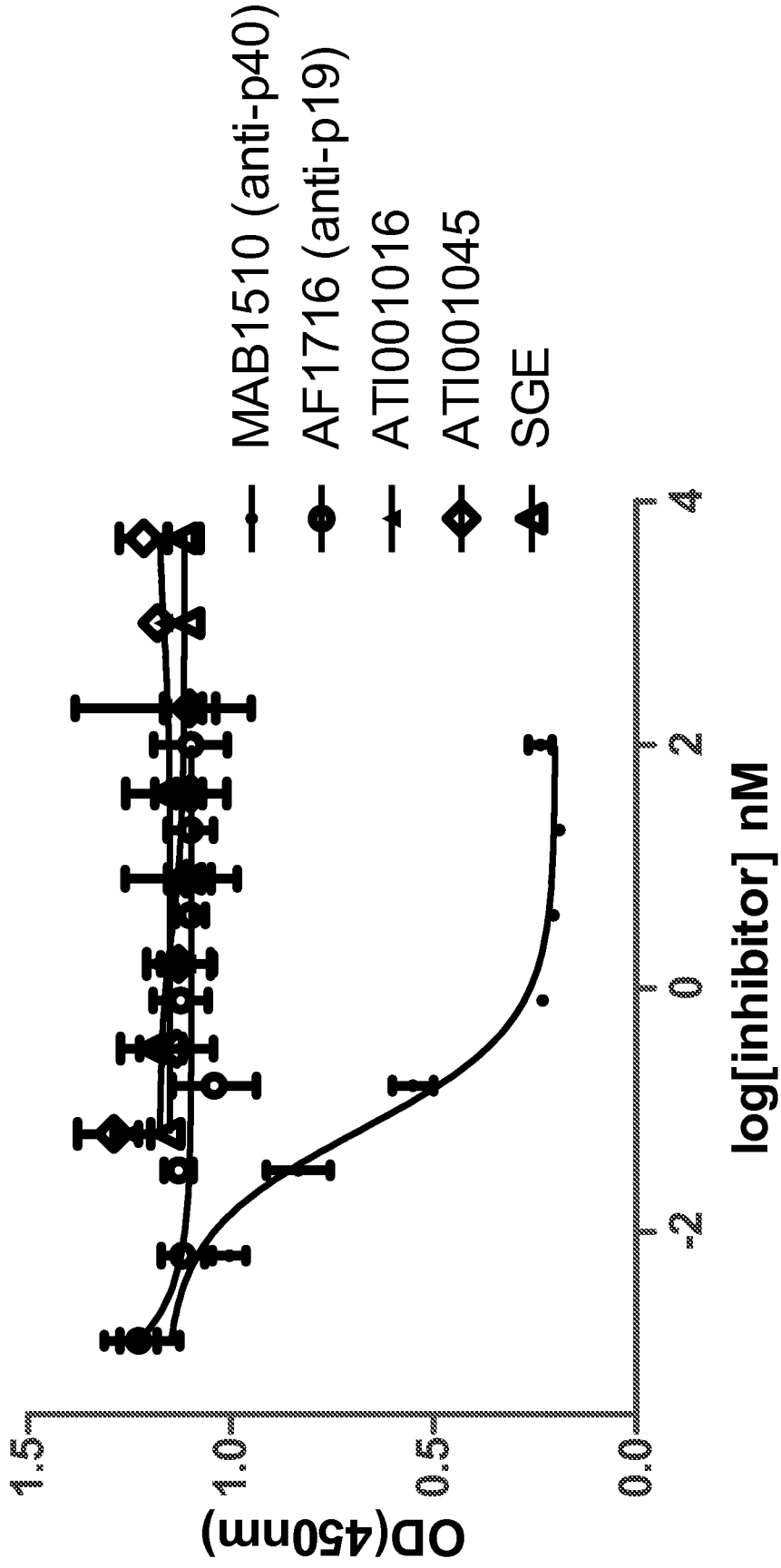

MAB1510 (anti-p40)
AF1716 (anti-p19)
ATI001016
ATI001045
SGE
OD(450nm)
1.5
1.0
0.5
0.0
-2
0
2
4
log[inhibitor] nM

FIG. 8

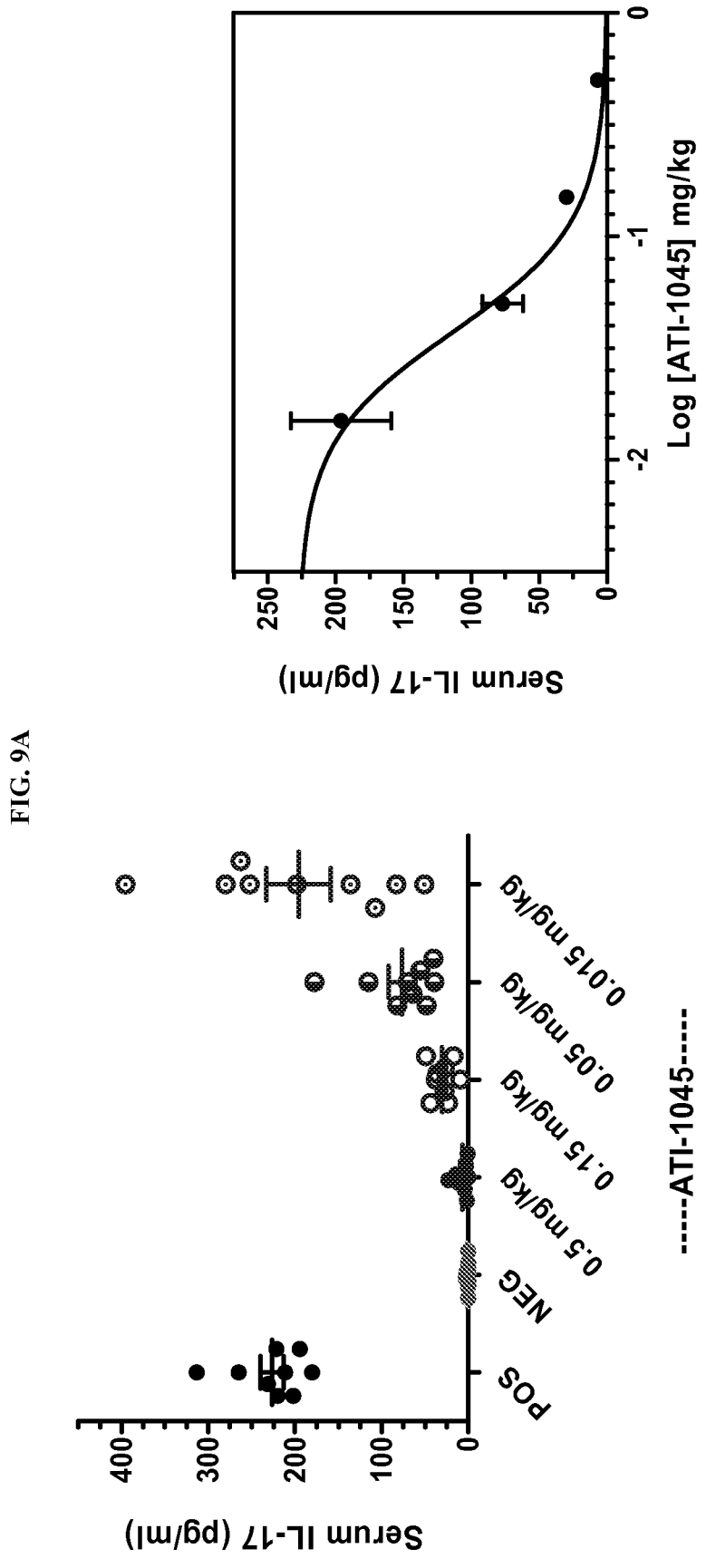
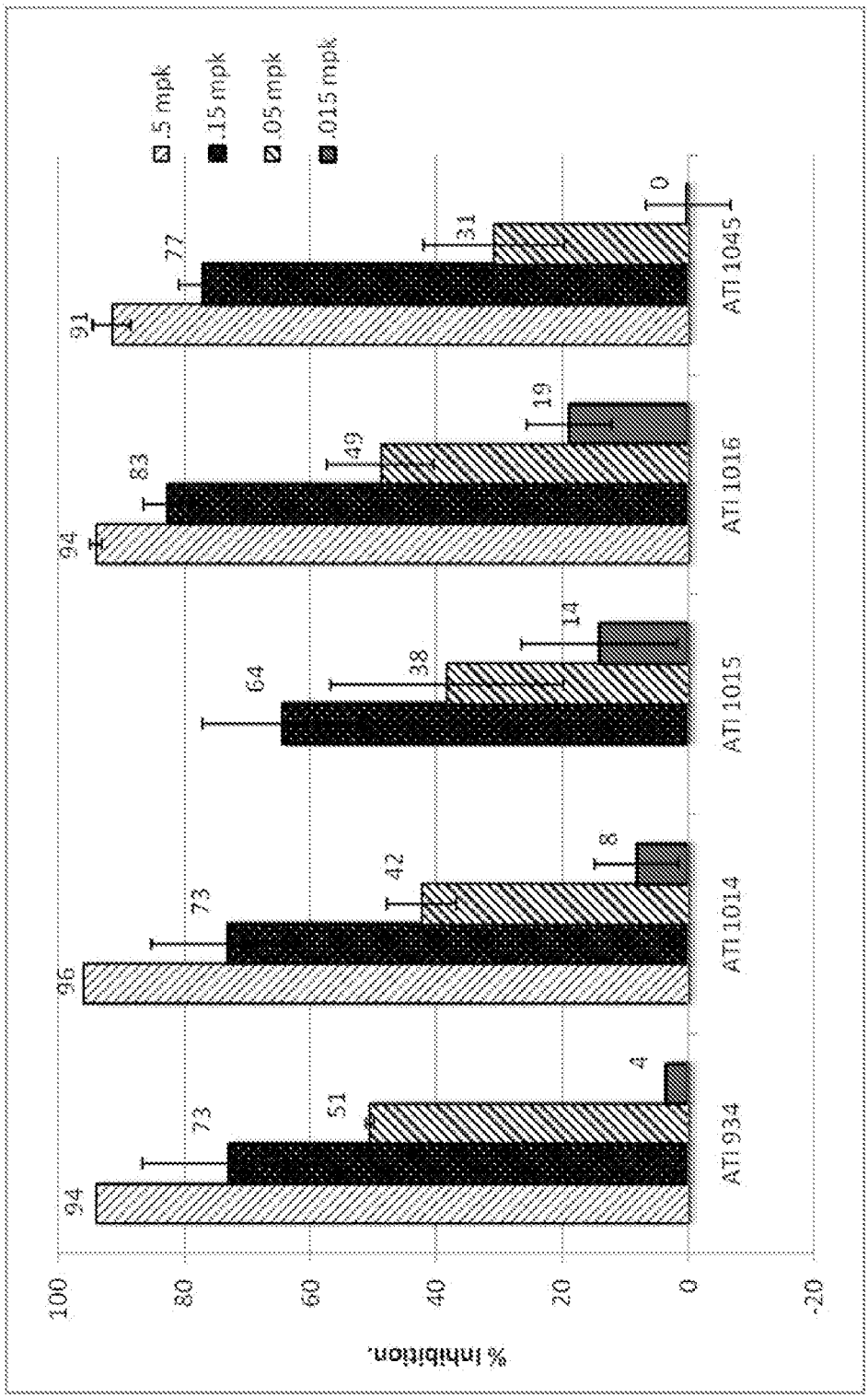

Serum IL-17 (pg/ml)
0
100
200
300
400
POS
NEG
0.5 mg/kg
0.15 mg/kg
0.05 mg/kg
0.015 mg/kg
-----ATI-1045-----
Serum IL-17 (pg/ml)
0
50
100
150
200
250
0
-1
-2
Log [ATI-1045] mg/kg

FIG. 9A

FIG. 9B


.5 mpk
.15 mpk
.05 mpk
.015 mpk
% Inhibition
100
80
60
40
20
0
-20
ATI 934
ATI 1014
ATI 1015
ATI 1016
ATI 1045
94
73
51
4
96
73
42
8
64
38
14
94
83
49
19
91
77
31
0

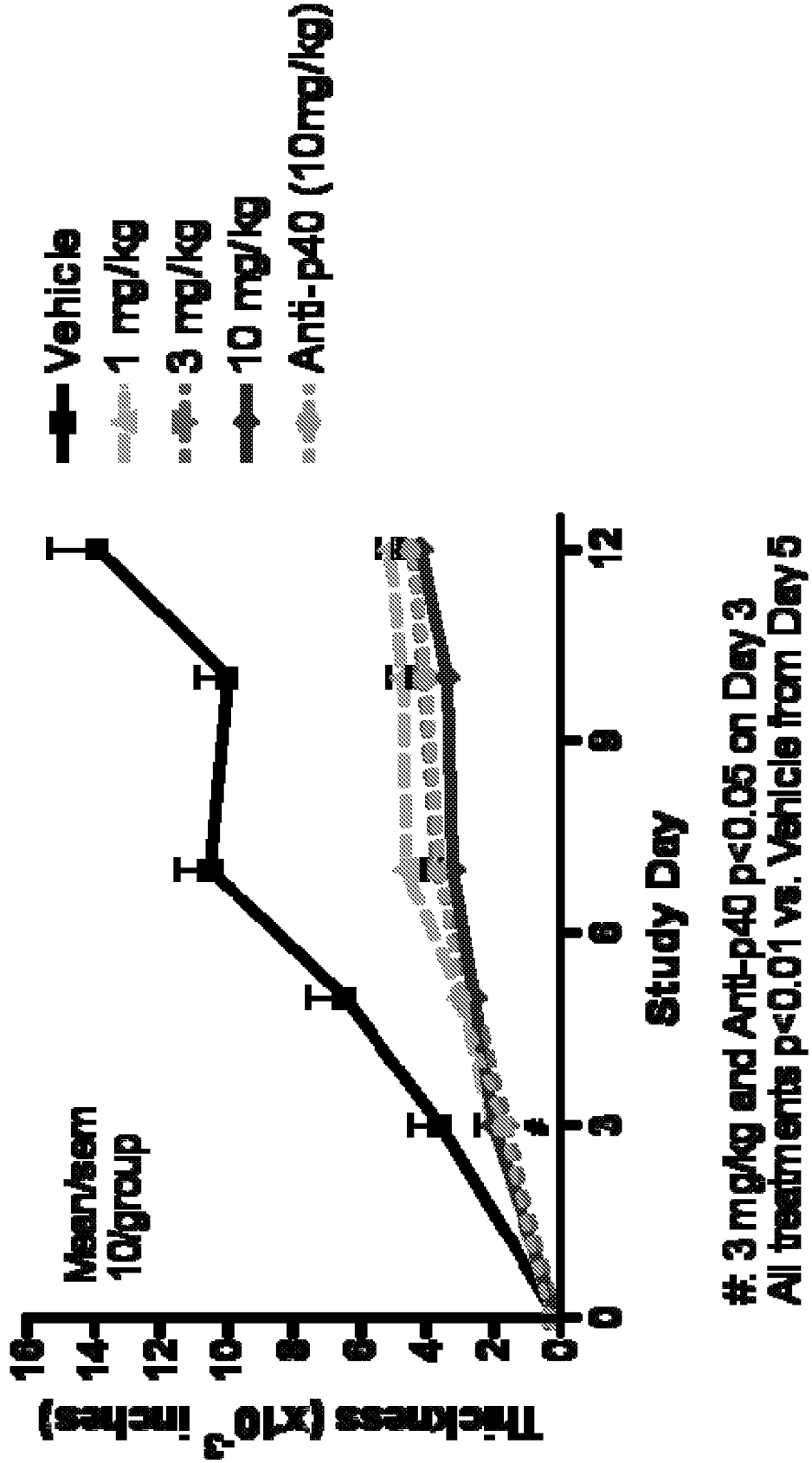

Vehicle
1 mg/kg
3 mg/kg
10 mg/kg
Anti-p40 (10mg/kg)
Mean/sem
10/group
Thickness (x10⁻³ inches)
Study Day
#: 3 mg/kg and Anti-p40 p<0.05 on Day 3
All treatments p<0.01 vs. Vehicle from Day 5

FIG. 10A

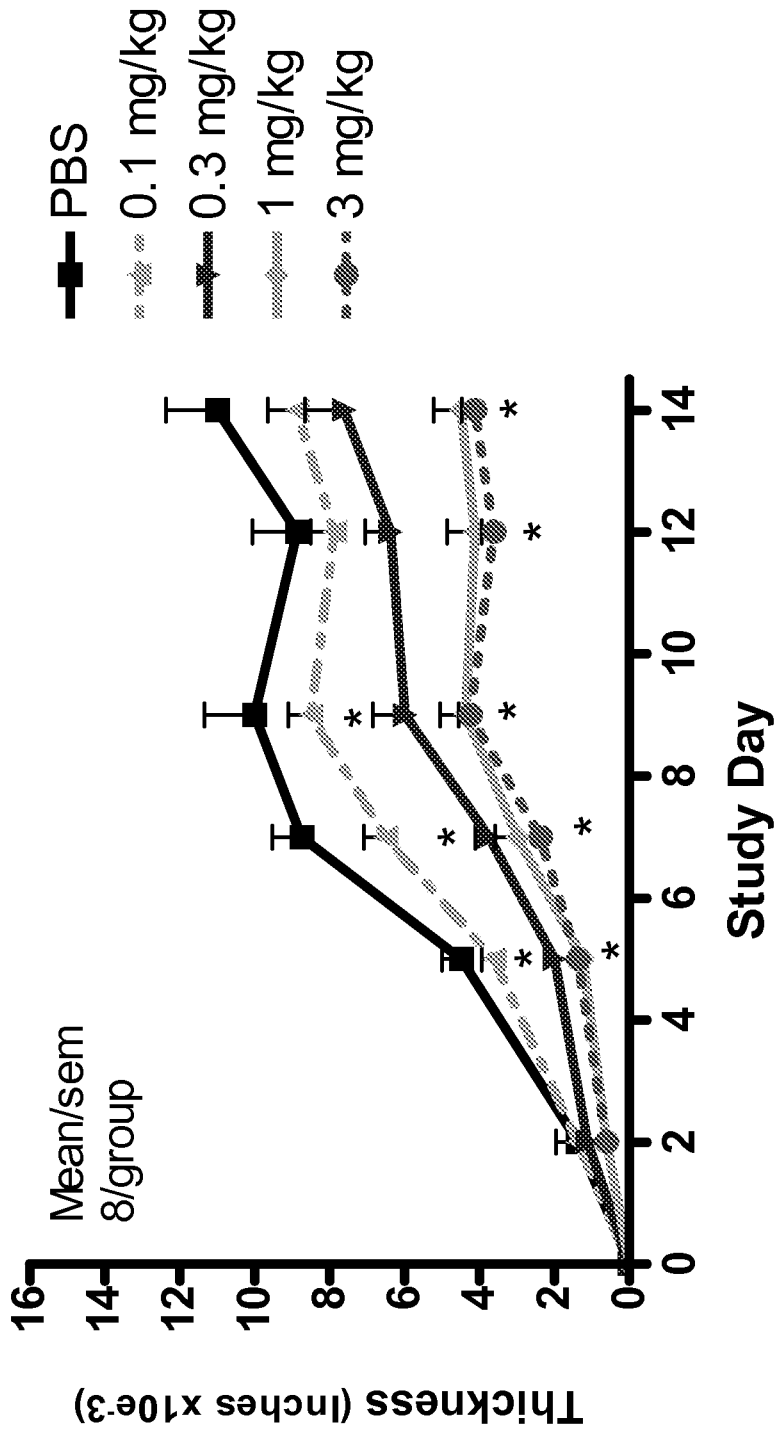

PBS
0.1 mg/kg
0.3 mg/kg
1 mg/kg
3 mg/kg
Mean/sem
8/group
Thickness (Inches x10e-3)
Study Day
0
2
4
6
8
10
12
14
16
0.1 NS all days
Day 5, 7, 9: 0.3, 1, 3 p<0.01
Day 12, 14:1, 3 p<0.01

FIG. 10B

FIG. 11A

Determination of HSA *in vivo* half-life in mice

20 mg/kg

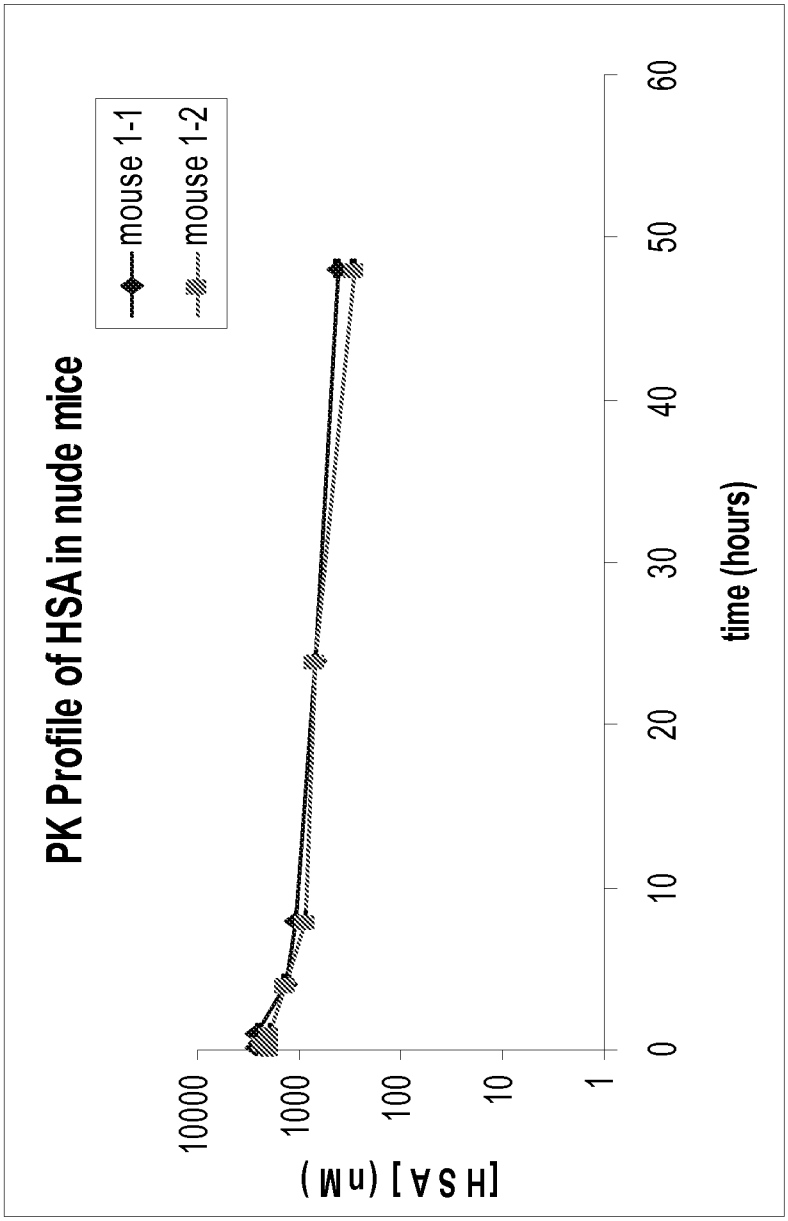


FIG. 11B

50 mg/kg

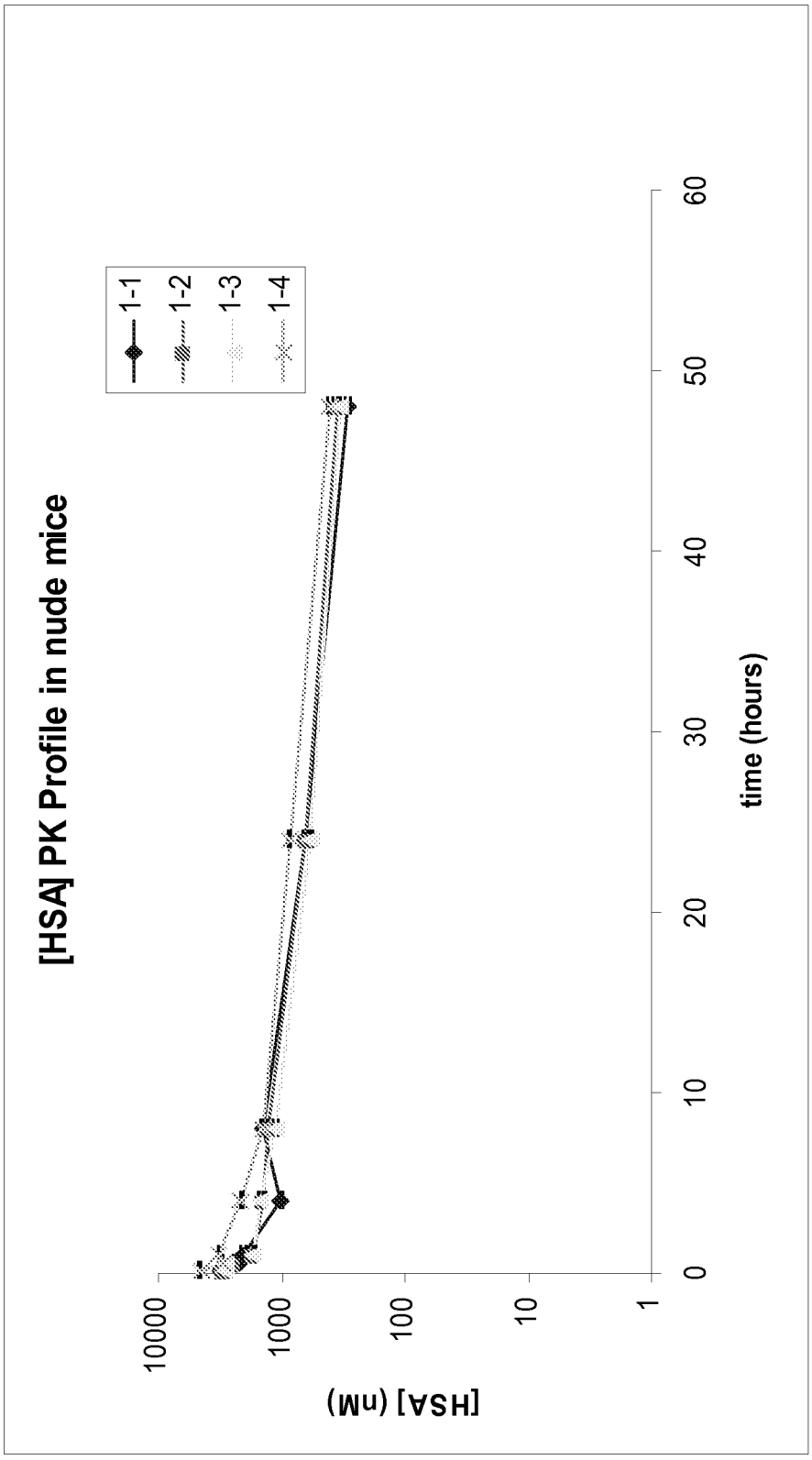


FIG. 12A

Half-life determination of SABA1-4 in mice

SABA1.1

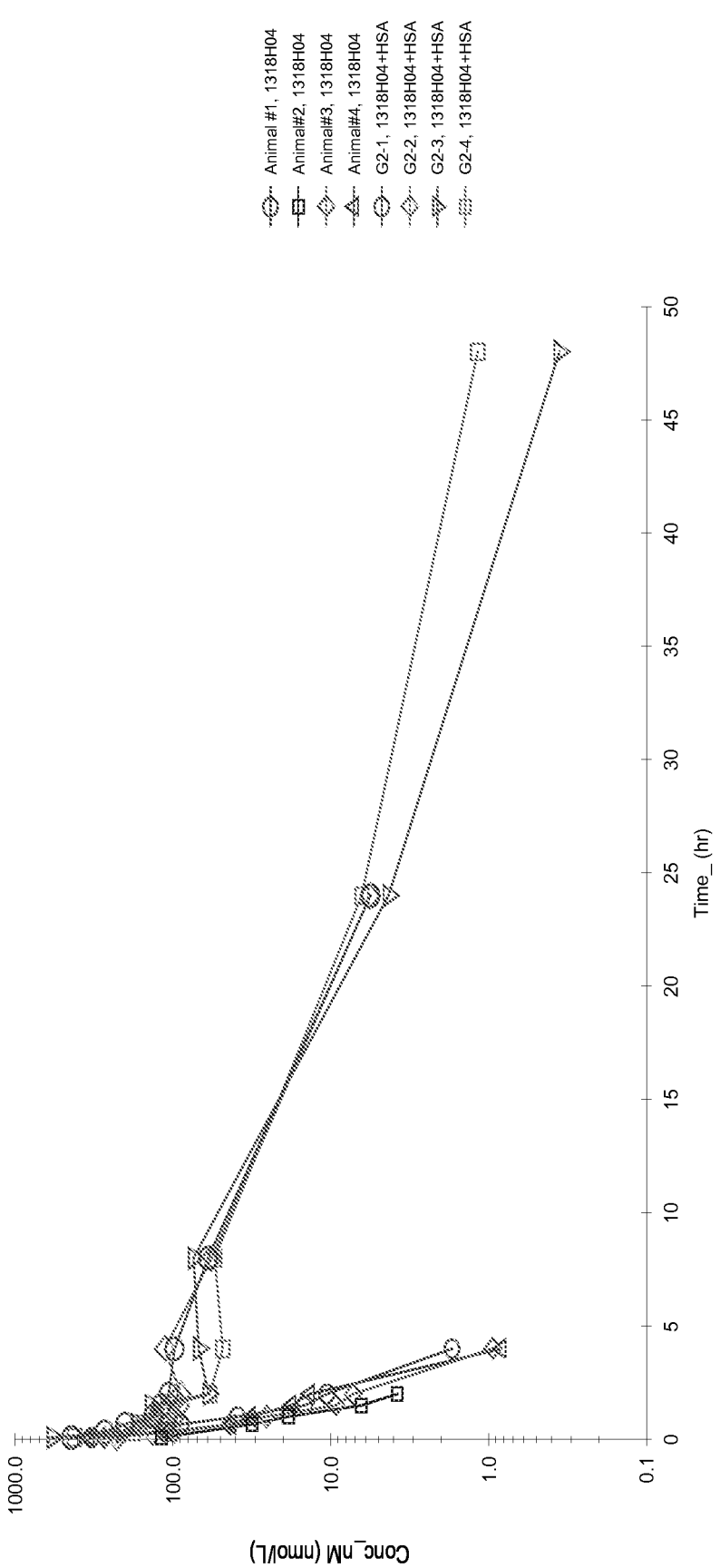


FIG. 12B

SABA2.1

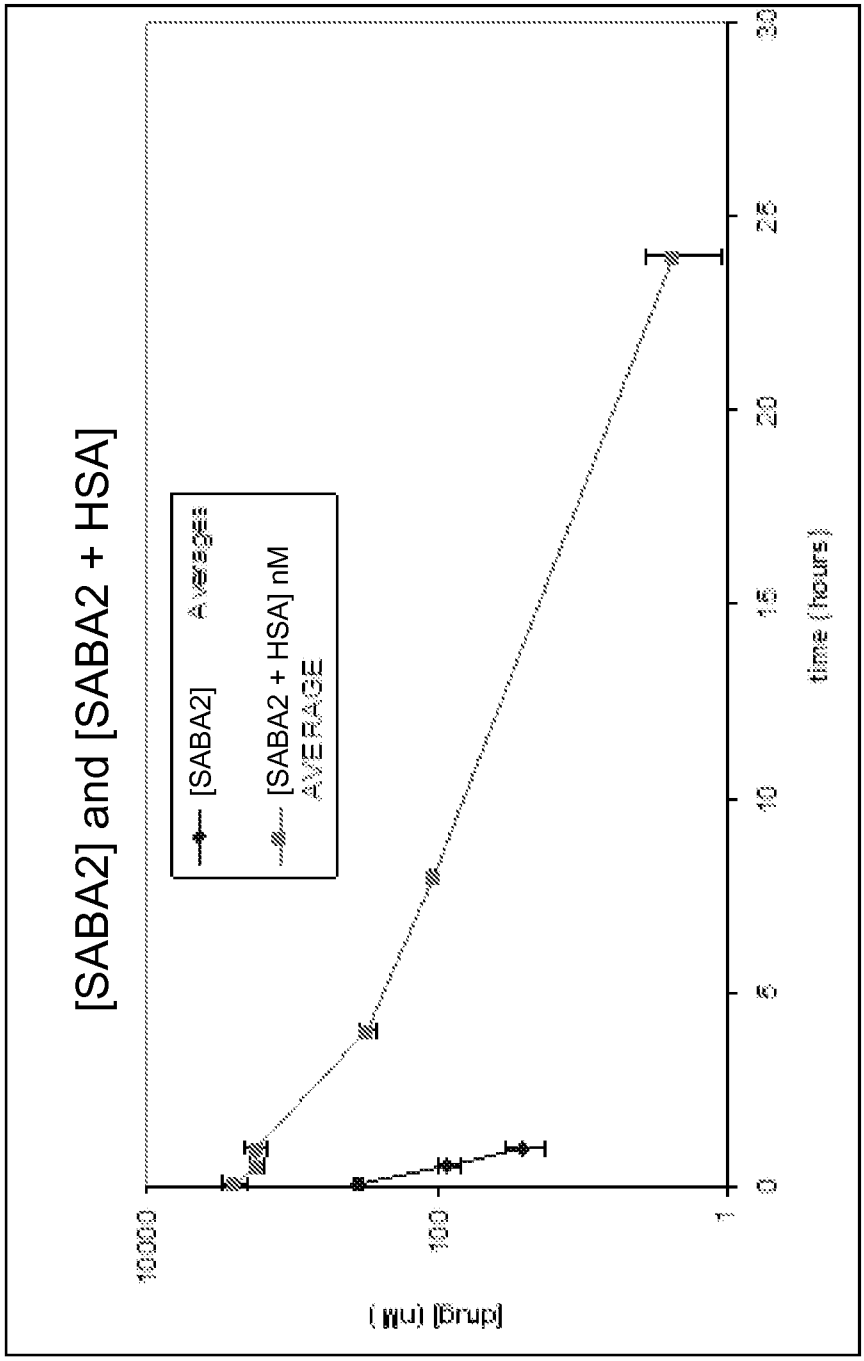


FIG. 12C

SABA3.1

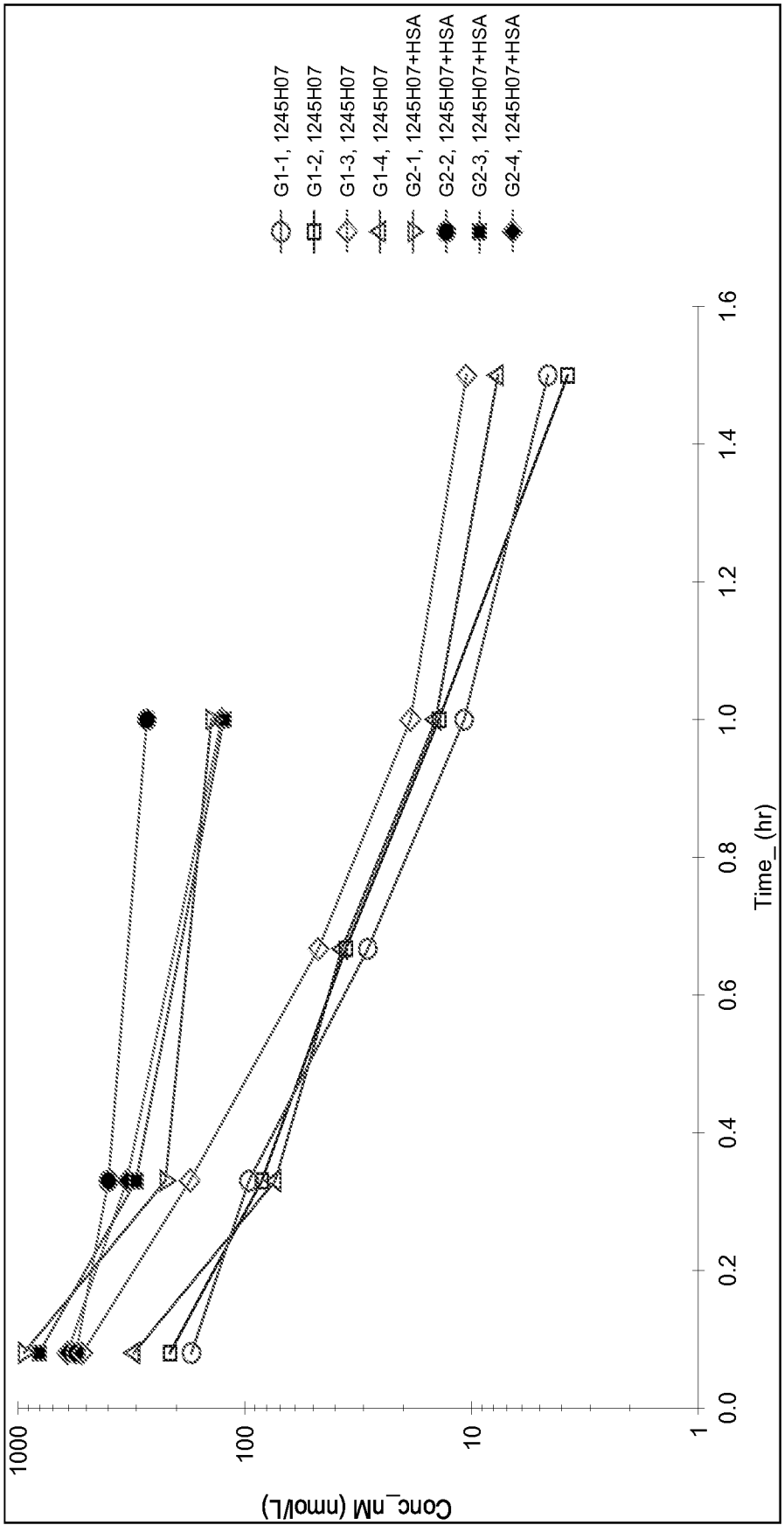


FIG. 12D

SABA4.1

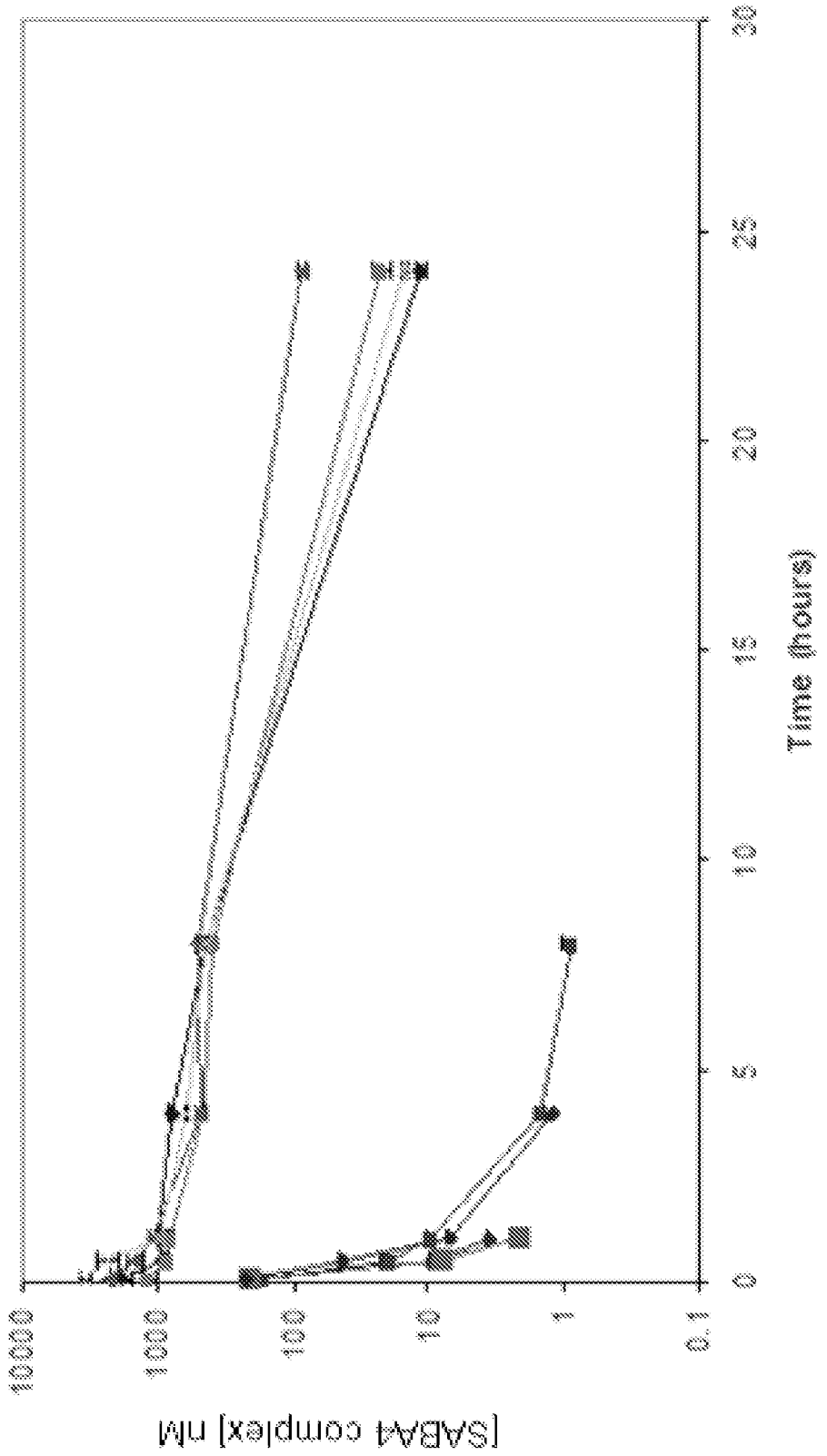


FIG. 13A

Summary of half-life enhancement in mice of SABA1-4 when co-injected with HSA

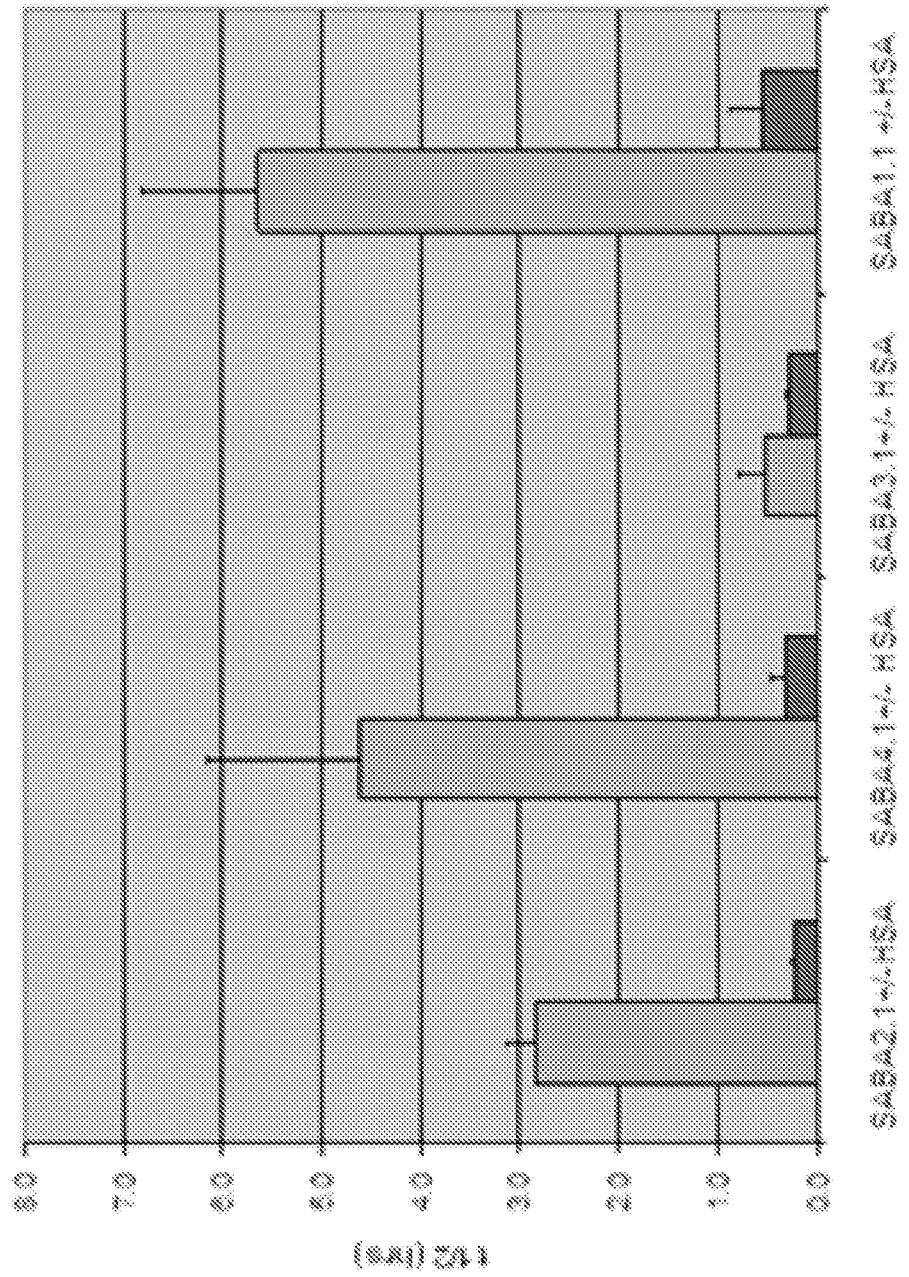


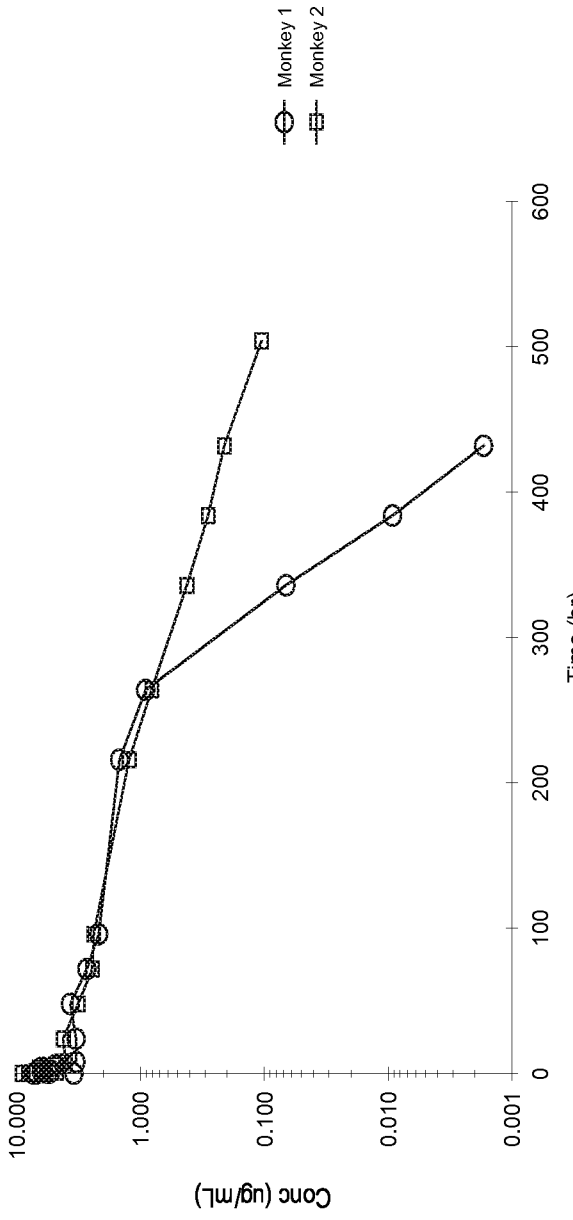
FIG. 13B

CLONE	PK (T1/2)		Comments
	Mice	Cyno	
SABA1.1	5.6hrs	96-137hrs	T1/2 = 96-137hrs
SABA5.1	4.6hrs	12hrs	Poor binding affinity for RhSA. 2-fold decrease in KD observed at pH<6.0
SABA2.1	2.8hrs	NA	Loss of binding at pH <6.5
SABA3.1	32min	NA	Poor T1/2 observed in mice

FIG. 14A

SABA1.1 and SABA5.1 $t_{1/2}$ in Cynomolgus monkey

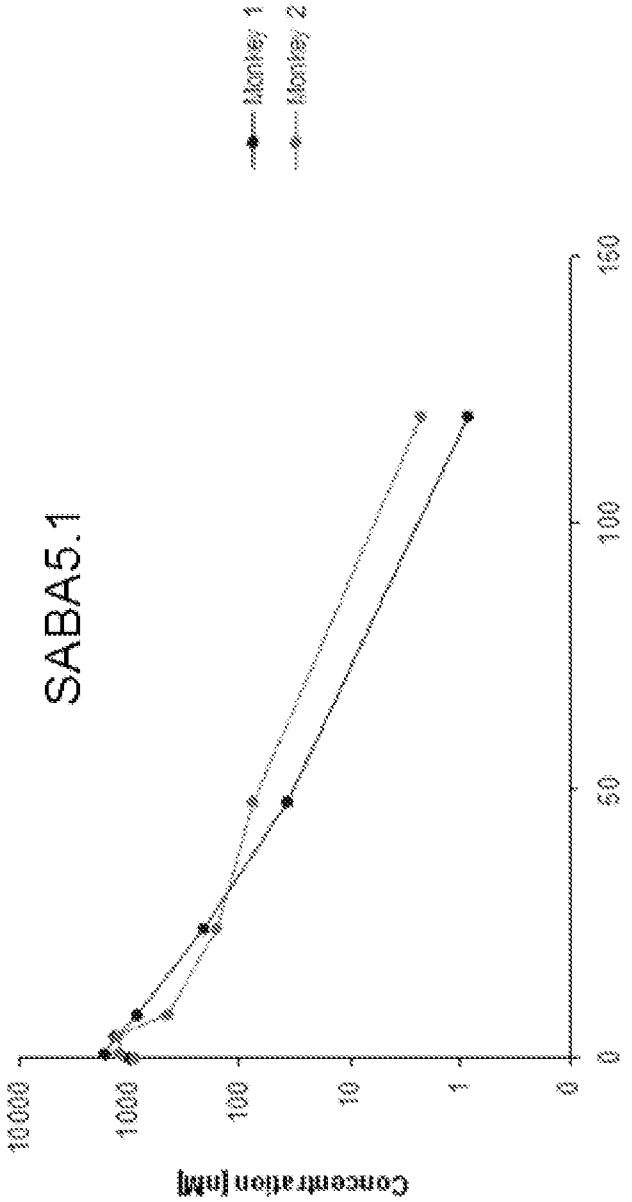
SABA1.1



Monkey	t1/2 (hrs)	Cmax (µg/mL)	AUCall (hr*µg/mL)	Cl_obs (mL/hr/kg)	Vz_obs (mL/kg)
#1	95.8	9.03	673.7	1.45	200.8
#2	136.6	7.24	625.1	1.60	315.2

FIG. 14B

SABA5.1



	HL_Lambda_z (hr)	Cmax (ug/mL)	AUCall (hr*ug/mL)	Cl_obs (mL/hr/kg)	Vz_obs (mL/kg)
N	2	2	2	2	2
Mean	12.186	17.358	246.882	4.089	72.507
SD	1.451	3.08	36.245	0.596	19.045
Min	11.16	15.18	221.25	3.67	59.04
Max	13.21	19.54	272.51	4.51	85.97
CV%	11.9	17.7	14.7	14.6	26.3

FIG. 15

SABA1.2 binding to albumins from human, mouse and rat by direct binding ELISA assay

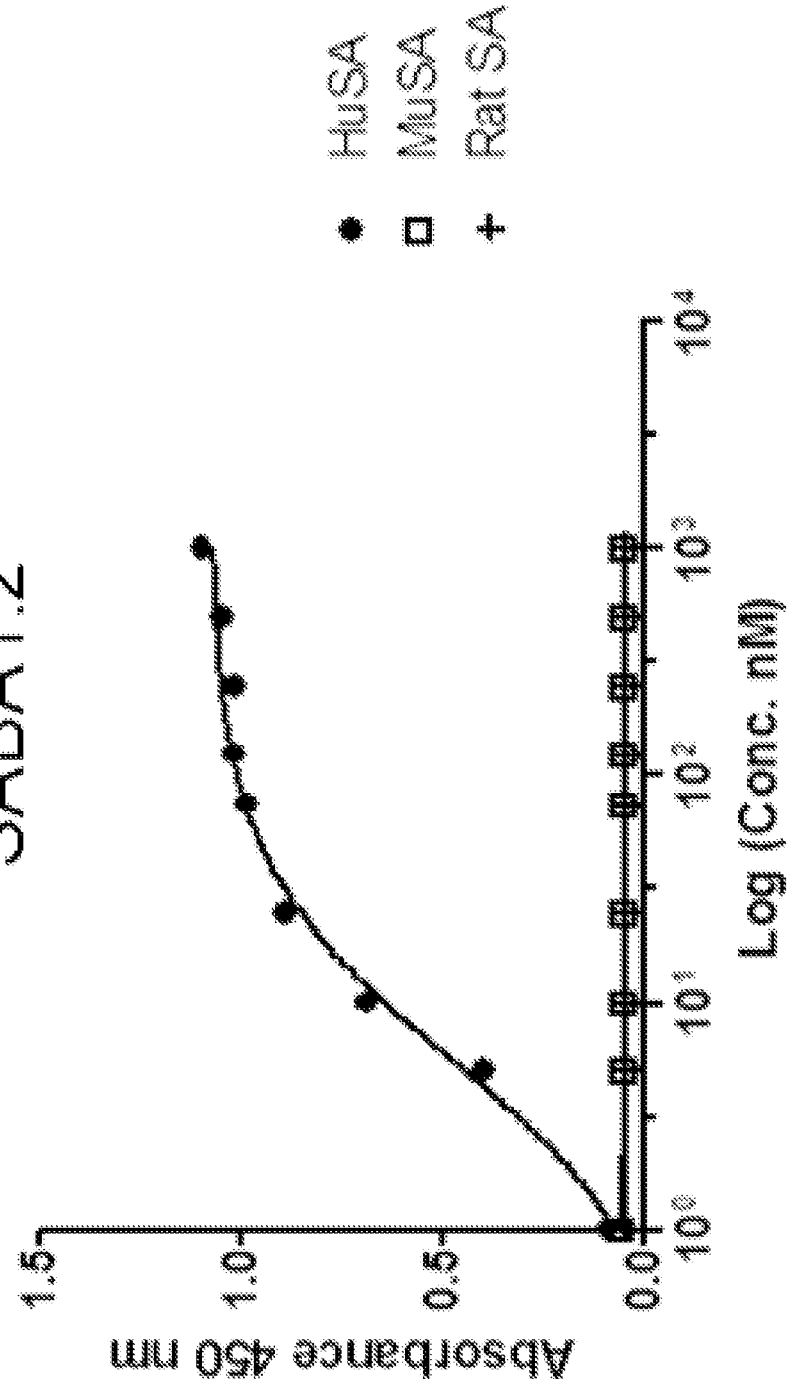


FIG. 16

SABA1.1 binds to HSA with 1:1 stoichiometry

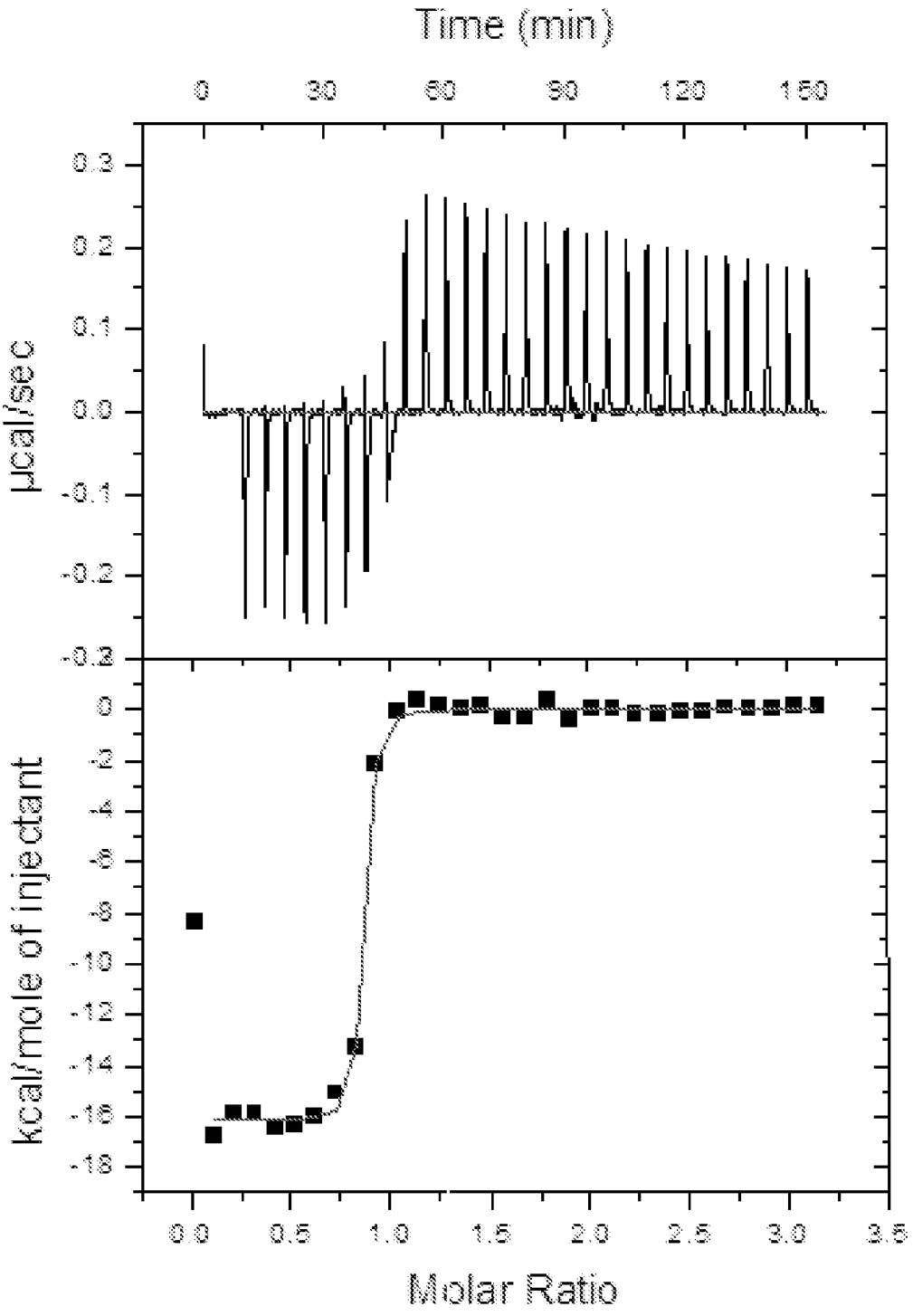


FIG. 17

Biacore Analysis of SABA1.2 Binding to Recombinant Domain Fragments of HSA

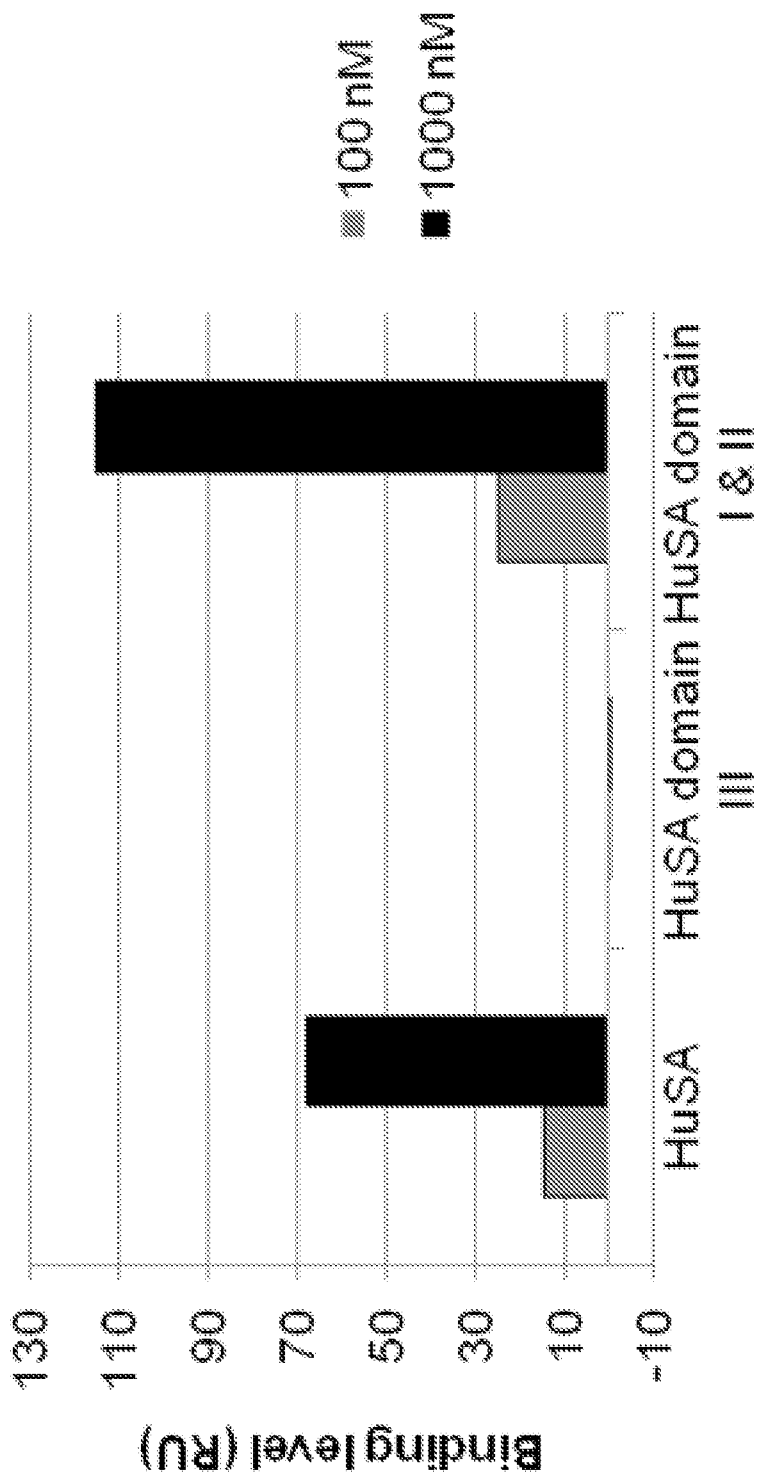


FIG. 18

Pharmacokinetic Profile for SABA1.2 in Monkeys Dosed at 1mpk and 10mpk

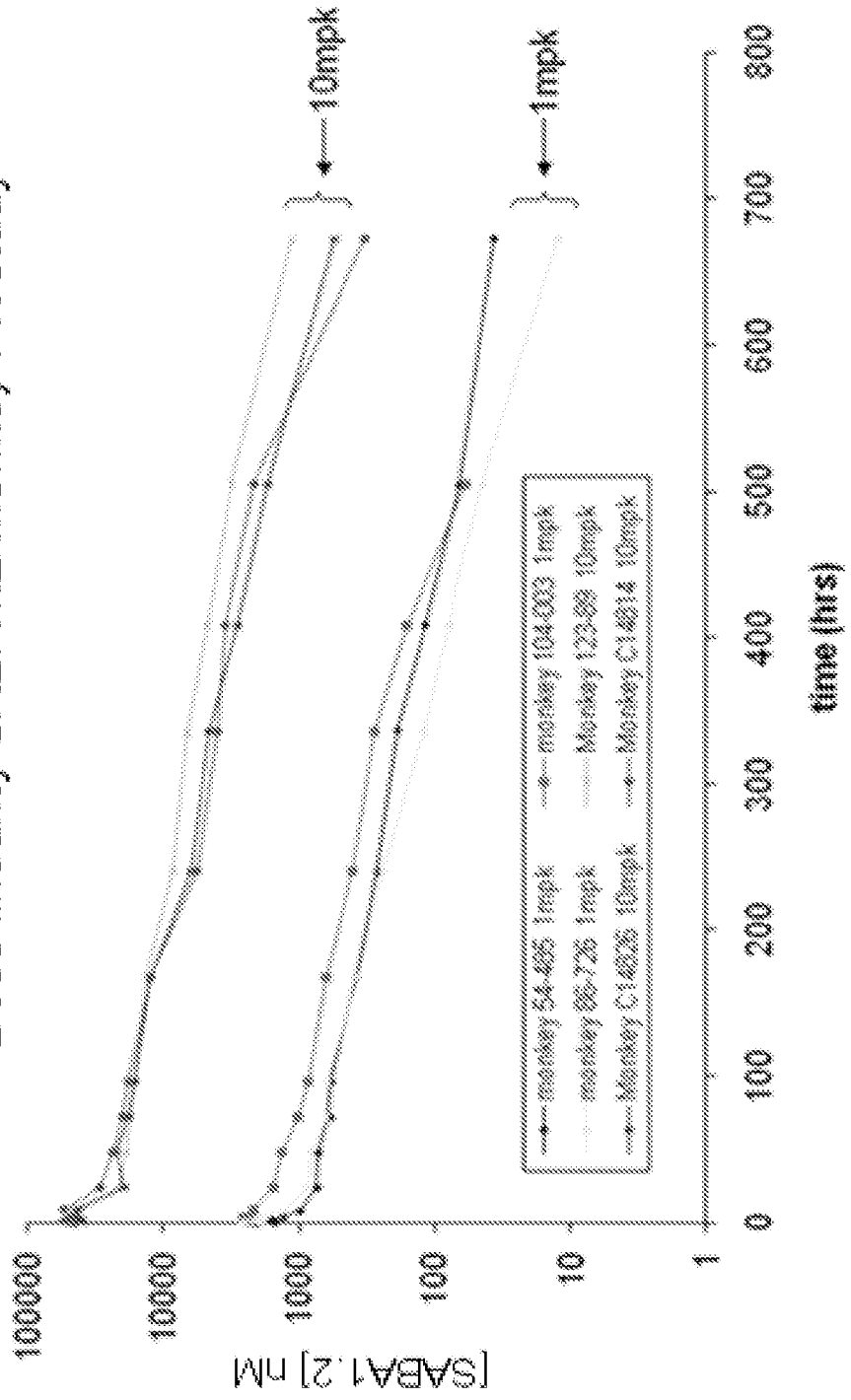


FIG. 19

Pharmacokinetic Profile for SABA1.2 in Monkeys Dosed Intravenously or Subcutaneously at 1mpk

