Figure 1

```
   5'            11         21         31         41         51
+1 M  C  D   L  P  Q  T   H  S  L   G  N  R   R  A  L  I   L  L  A
      1 ATGTGCGACC TGCCGCAGAC CCACTCCCTG GGTAACCGTC GTGCTCTGAT CCTGCTGGCT
        TACACGCTGG ACGGCGTCTG GGTGAGGGAC CCATTGGCAG CACGAGACTA GGACGACCGA

5'           71         81         91         101        111
+1 Q  M  R   R  I  S  P   F  S  C   L  K  D   R  H  D  F   G  F  P
     61 CAGATGCGTC GTATCTCCCC GTTCTCCTGC CTGAAAGACC GTCACGACTT CGGTTTCCCG
        GTCTACGCAG CATAGAGGGG CAAGAGGACG GACTTTCTGG CAGTGCTGAA GCCAAAGGGC

5'       131      141        151        161        171
+1 Q  E  E   F  D  G  N   Q  F  Q   K  A  Q   A  I  S  V   L  H  E
    121 CAGGAAGAAT TCGACGGTAA CCAGTTCCAG AAAGCTCAGG CTATCTCCGT TCTGCACGAA
        GTCCTTCTTA AGCTGCCATT GGTCAAGGTC TTTCGAGTCC GATAGAGGCA AGACGTGCTT

5'           191        201        211        221        231
+1 M  I  Q   Q  T  F  N   L  F  S   T  K  D   S  S  A  A   W  D  E
    181 ATGATCCAGC AGACCTTCAA CCTGTTCTCC ACCAAAGACT CCTCCGCTGC TTGGGACGAA
        TACTAGGTCG TCTGGAAGTT GGACAAGAGG TGGTTTCTGA GGAGGCGACG AACCCTGCTT

5'           251        261        271        281        291
+1 S  L  L   E  K  F  Y   T  E  L   Y  Q  Q   L  N  D  L   E  A  C
    241 TCCCTGCTGG AAAAATTCTA CACCGAACTG TACCAGCAGC TGAACGACCT GGAAGCTTGC
        AGGGACGACC TTTTTAAGAT GTGGCTTGAC ATGGTCGTCG ACTTGCTGGA CCTTCGAACG

5'           311        321        331        341        351
+1 V  I  Q   E  V  G  V   E  E  T   P  L  M   N  V  D  S   I  L  A
    301 GTTATCCAGG AAGTTGGTGT TGAAGAAACC CCGCTGATGA ACGTTGACTC CATCCTGGCT
        CAATAGGTCC TTCAACCACA ACTTCTTTGG GGCGACTACT TGCAACTGAG GTAGGACCGA

5'           371        381        391        401        411
+1 V  K  K   Y  F  Q  R   I  T  L   Y  L  T   E  K  K  Y   S  P  C
    361 GTTAAAAAAT ACTTCCAGCG TATCACCCTG TACCTGACCG AAAAAAAATA CTCCCCGTGC
        CAATTTTTTA TGAAGGTCGC ATAGTGGGAC ATGGACTGGC TTTTTTTTAT GAGGGGCACG

5'           431        441        451        461        471
+1 A  W  E   V  V  R  A   E  I  M   R  S  F   S  L  S  T   N  L  Q
```



```
  421 GCTTGGGAAG TTGTTCGTGC TGAAATCATG CGTTCCTTCT CCCTGTCCAC CAACCTGCAG
        CGAACCCTTC AACAAGCACG ACTTTAGTAC GCAAGGAAGA GGGACAGGTG GTTGGACGTC

5'           491        501
+1 E  R  L   R  R  K  E   #
    481 GAACGTCTGC GTCGTAAAGA ATAA
        CTTGCAGACG CAGCATTTCT TATT
```

Figure 2-A

```
5'          11         21         31         41         51
+1 M C D  L P Q T  H S L  G N R  R A L I  L L A
 1 ATGTGTGATT TACCTCAAAC TCATTCTCTT GGTAACCGTC GCGCTCTGAT TCTGCTGGCA
   TACACACTAA ATGGAGTTTG AGTAAGAGAA CCATTGGCAG CGCGAGACTA AGACGACCGT

5'          71         81         91         1          11
+1 Q M R  R I S P  F S C  L K D  R H D F  G F P
61 CAGATGCGTC GTATTTCCCC GTTTAGCTGC CTGAAAGACC GTCACGACTT CGGCTTTCCG
   GTCTACGCAG CATAAAGGGG CAAATCGACG GACTTTCTGG CAGTGCTGAA GCCGAAAGGC

5'          31         41         51         61         71
+1 Q E E  F D G N  Q F Q  K A Q  A I S V  L H E
121 CAAGAAGAGT TCGATGGCAA CCAATTCCAG AAAGCTCAGG CAATCTCTGT ACTGCACGAA
    GTTCTTCTCA AGCTACCGTT GGTTAAGGTC TTTCGAGTCC GTTAGAGACA TGACGTGCTT

5'          91         1          11         21         31
+1 M I Q  Q T F N  L F S  T K D  S S A A  W D E
181 ATGATCCAAC AGACCTTCAA CCTGTTTTCC ACTAAAGACA GCTCTGCTGC TTGGGACGAA
    TACTAGGTTG TCTGGAAGTT GGACAAAAGG TGATTTCTGT CGAGACGACG AACCCTGCTT

5'          51         61         71         81         91
+1 S L L  E K F Y  T E L  Y Q Q  L N D L  E A C
241 AGCTTGCTGG AGAAGTTCTA CACTGAACTG TATCAGCAGC TGAACGACCT GGAAGCATGC
    TCGAACGACC TCTTCAAGAT GTGACTTGAC ATAGTCGTCG ACTTGCTGGA CCTTCGTACG

5'          11         21         31         41         51
+1 V I Q  E V G V  E E T  P L M  N V D S  I L A
301 GTAATCCAGG AAGTTGGTGT AGAAGAGACT CCGCTGATGA ACGTCGACTC TATTCTGGCA
    CATTAGGTCC TTCAACCACA TCTTCTCTGA GGCGACTACT TGCAGCTGAG ATAAGACCGT
```

Figure 2-B

```
 5'            11          21          31          41          51
+1 M  C  D   L  P  Q  T   H  S  L   G  N  R   R  A  L  I   L  L  A
 1 ATGTGTGATT TACCTCAAAC TCATTCTCTT GGTAACCGTC GCGCTCTGAT TCTGCTGGCA
   TACACACTAA ATGGAGTTTG AGTAAGAGAA CCATTGGCAG CGCGAGACTA AGACGACCGT

 5'            71          81          91          1           11
+1 Q  M  R   R  I  S  P   F  S  C   L  K  D   R  H  D  F   G  F  P
61 CAGATGCGTC GTATTTCCCC GTTTAGCTGC CTGAAAGACC GTCACGACTT CGGCTTTCCG
   GTCTACGCAG CATAAAGGGG CAAATCGACG GACTTTCTGG CAGTGCTGAA GCCGAAAGGC

 5'            31          41          51          61          71
+1 Q  E  E   F  D  G  N   Q  F  Q   K  A  Q   A  I  S  V   L  H  E
121 CAAGAAGAGT TCGATGGCAA CCAATTCCAG AAAGCTCAGG CAATCTCTGT ACTGCACGAA
    GTTCTTCTCA AGCTACCGTT GGTTAAGGTC TTTCGAGTCC GTTAGAGACA TGACGTGCTT

 5'            91          1           11          21          31
+1 M  I  Q   Q  T  F  N   L  F  S   T  K  D   S  S  A  A   W  D  E
181 ATGATCCAAC AGACCTTCAA CCTGTTTTCC ACTAAAGACA GCTCTGCTGC TTGGGACGAA
    TACTAGGTTG TCTGGAAGTT GGACAAAAGG TGATTTCTGT CGAGACGACG AACCCTGCTT

 5'            51          61          71          81          91
+1 S  L  L   E  K  F  Y   T  E  L   Y  Q  Q   L  N  D  L   E  A  C
241 AGCTTGCTGG AGAAGTTCTA CACTGAACTG TATCAGCAGC TGAACGACCT GGAAGCATGC
    TCGAACGACC TCTTCAAGAT GTGACTTGAC ATAGTCGTCG ACTTGCTGGA CCTTCGTACG

 5'            11          21          31          41          51
+1 V  I  Q   E  V  G  V   E  E  T   P  L  M   N  V  D  S   I  L  A
301 GTAATCCAGG AAGTTGGTGT AGAAGAGACT CCGCTGATGA ACGTCGACTC TATTCTGGCA
    CATTAGGTCC TTCAACCACA TCTTCTCTGA GGCGACTACT TGCAGCTGAG ATAAGACCGT

 5'            71          81          91          1           11
+1 V  K  K   Y  F  Q  R   I  T  L   Y  L  T   E  K  K  Y   S  P  C
361 GTTAAAAAGT ACTTCCAGCG TATCACTCTG TACCTGACCG AAAAGAAATA TTCTCCGTGC
    CAATTTTTCA TGAAGGTCGC ATAGTGAGAC ATGGACTGGC TTTTCTTTAT AAGAGGCACG

 5'            31          41          51          61          71
+1 A  W  E   V  V  R  A   E  I  M   R  S  F   S  L  S  T   N  L  Q
421 GCTTGGGAAG TAGTTCGCGC TGAAATTATG CGTTCTTTCT CTCTGTCTAC TAACCTGCAG
    CGAACCCTTC ATCAAGCGCG ACTTTAATAC GCAAGAAAGA GAGACAGATG ATTGGACGTC

 5'            91          1
+1 E  R  L   R  R  K  E   #  @
81 GAGCGTCTGC GCCGTAAAGA ATAATAG
   CTCGCAGACG CGGCATTTCT TATTATC
```

Figure 3

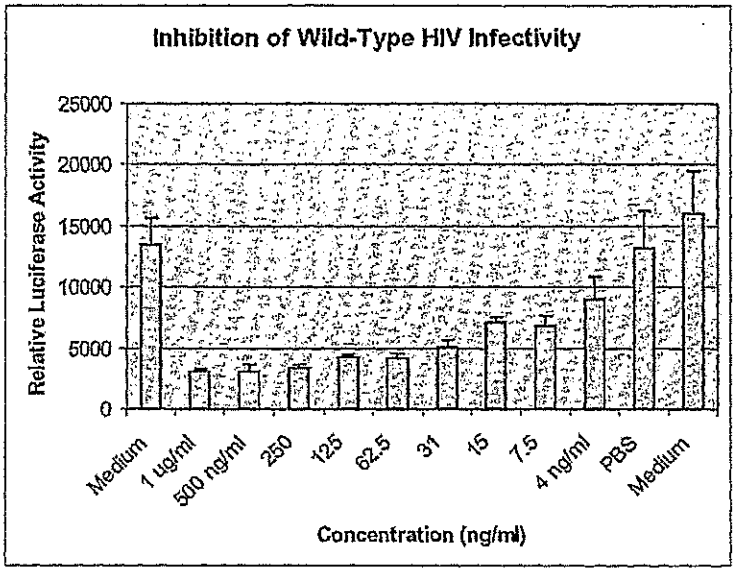

Inhibition of Wild-Type HIV Infectivity
Relative Luciferase Activity
25000
20000
15000
10000
5000
0
Medium
1 ug/ml
500 ng/ml
250
125
62.5
31
15
7.5
4 ng/ml
PBS
Medium
Concentration (ng/ml)

Figure 4

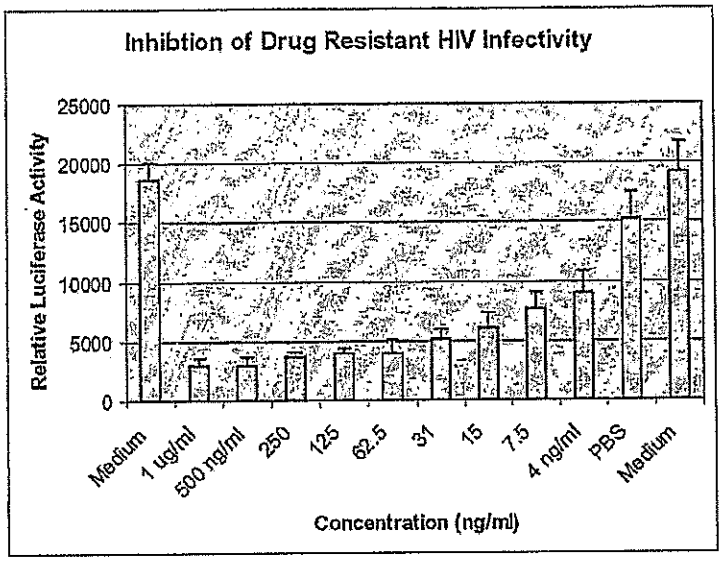
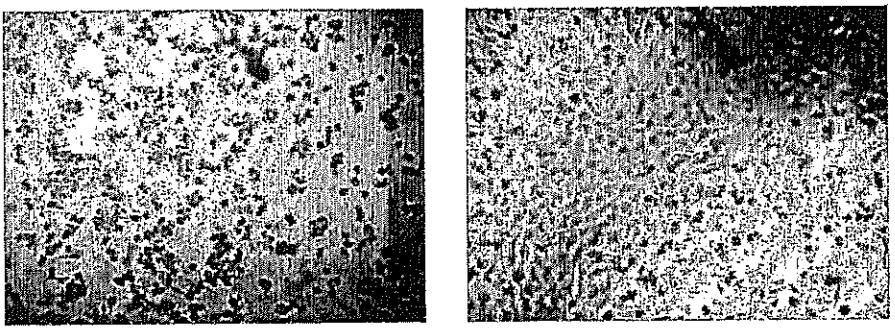

Inhibtion of Drug Resistant HIV Infectivity
Relative Luciferase Activity
25000
20000
15000
10000
5000
0
Medium
1 ug/ml
500 ng/ml
250
125
62.5
31
15
7.5
4 ng/ml
PBS
Medium
Concentration (ng/ml)

Figure 5

Inhibition of Influenza Infection (24 Hours)



Untreated 10 ng/ml