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

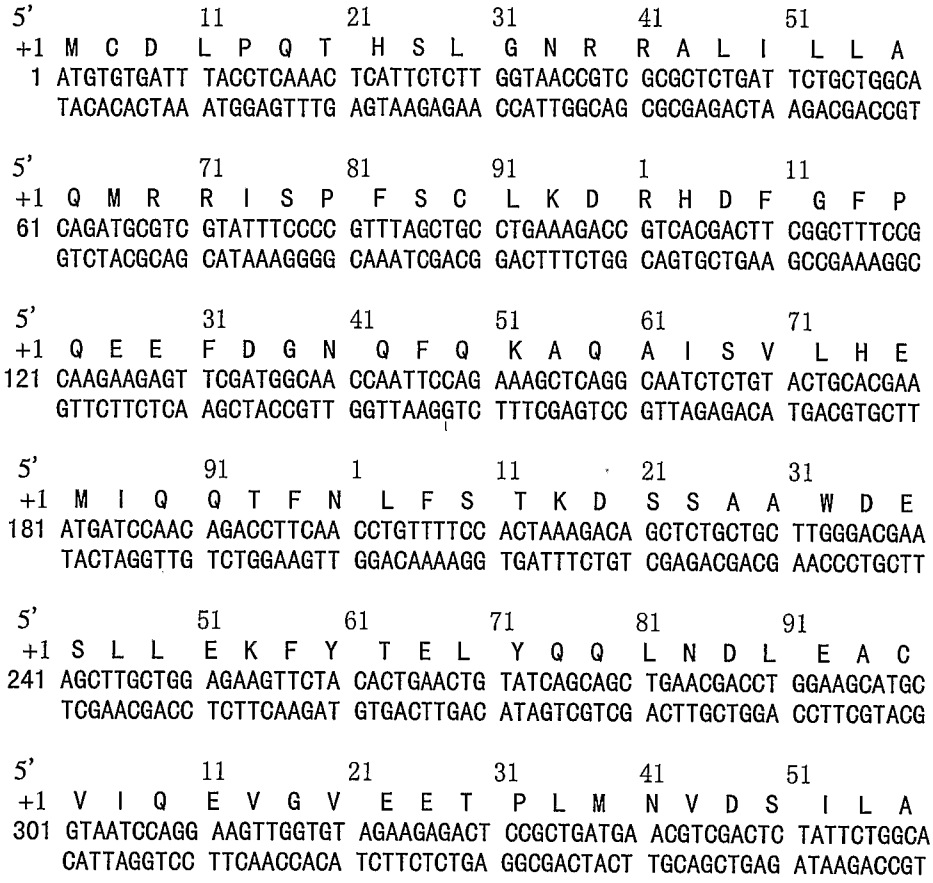

5' 11 21 31 41 51
+1 M C D L P Q T H S L G N R R A L I L L A
1 ATGTGTGATT TACCTCAAAC TCATTCTCTT GGTAACCGTC GCGCTCTGAT TCTGCTGGCA
TACACACTAA ATGGAGTTTG AGTAAGAGAA CCATTGGCAG CGCGAGACTA AGACGACCGT
5' 71 81 91 1 11
+1 Q M R R I S P F S C L K D R H D F G F P
61 CAGATGCGTC GTATTTCCCC GTTTAGCTGC CTGAAAGACC 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 3

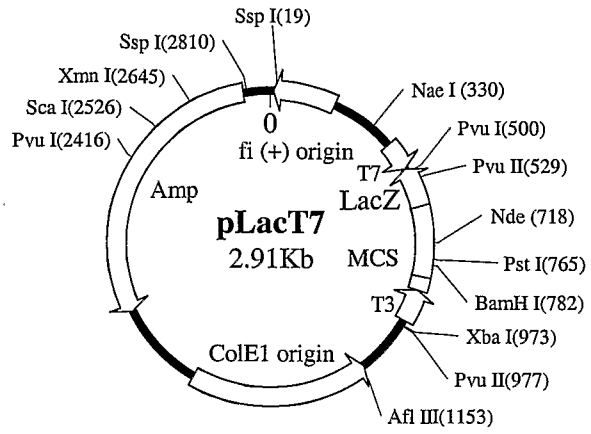

Ssp I(19)
Ssp I(2810)
Xmn I(2645)
Sca I(2526)
Pvu I(2416)
0
fi (+) origin
Nae I (330)
Pvu I(500)
Pvu II(529)
T7
LacZ
Amp
pLacT7
2.91Kb
MCS
Nde (718)
Pst I(765)
BamH I(782)
T3
Xba I(973)
ColE1 origin
Pvu II(977)
Afl III(1153)

Figure 4

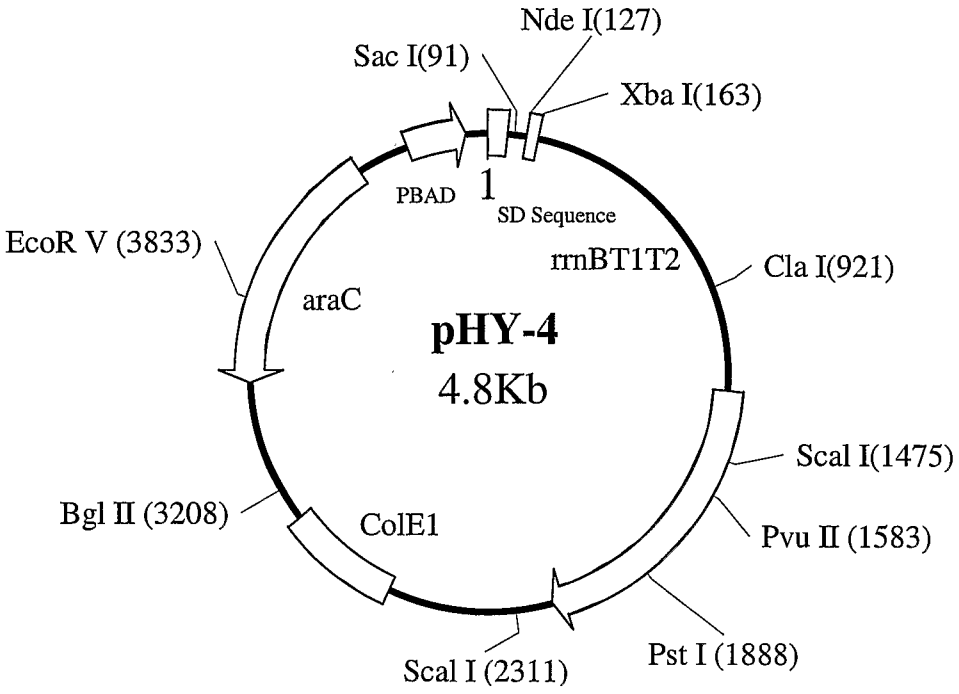

Nde I(127)
Sac I(91)
Xba I(163)
PBAD
1
SD Sequence
EcoR V (3833)
rrnBT1T2
Cla I(921)
araC
pHY-4
4.8Kb
ScaI I(1475)
Bgl II (3208)
ColE1
Pvu II (1583)
ScaI I (2311)
Pst I (1888)

Figure 5

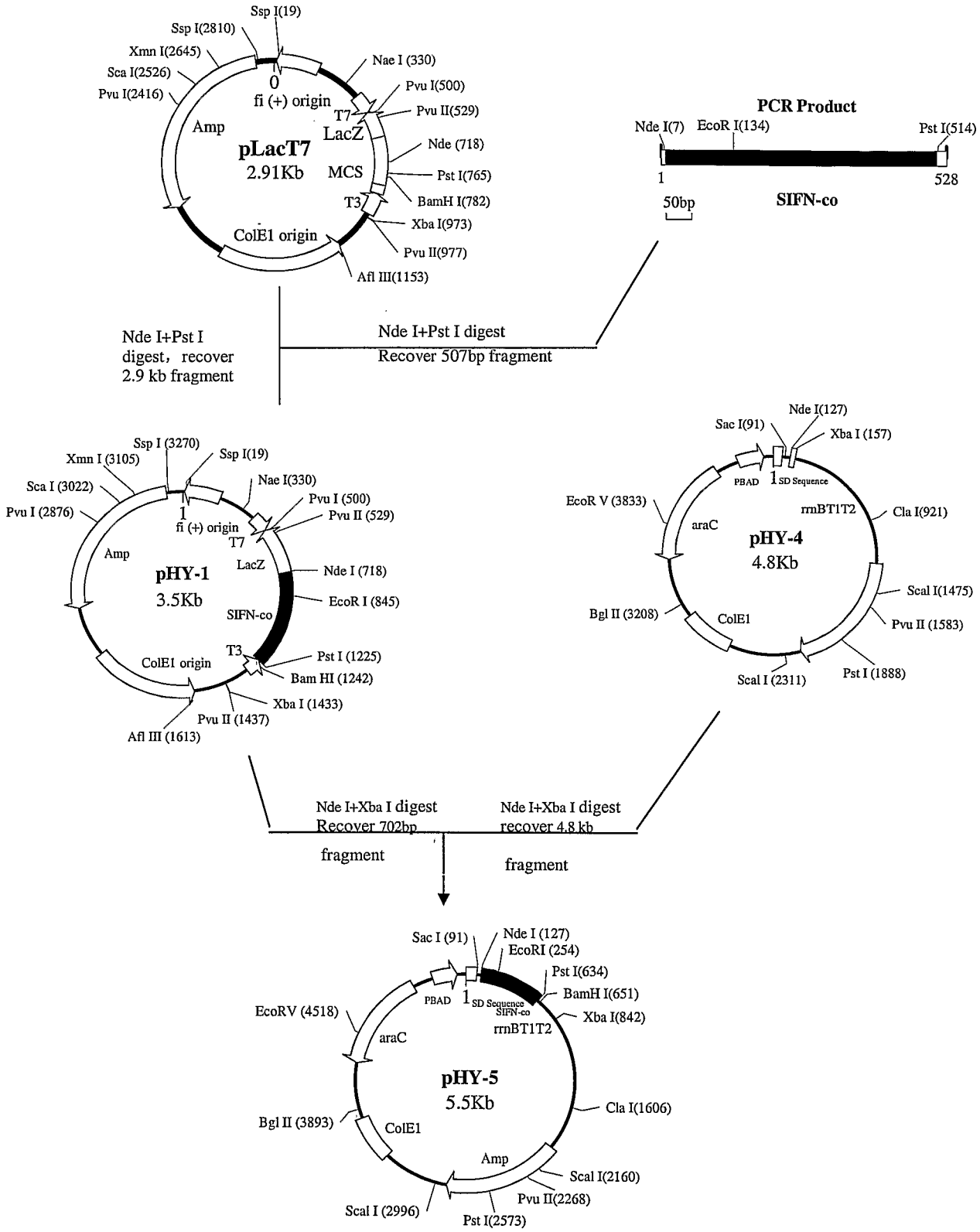

Ssp I(19)
Ssp I(2810)
Xmn I(2645)
Sca I(2526)
Pvu I(2416)
Nae I (330)
Pvu I(500)
Pvu II(529)
Nde (718)
Pst I(765)
BamH I(782)
Xba I(973)
Pvu II(977)
Afl III(1153)
0
fi (+) origin
T7
LacZ
Amp
pLacT7
2.91Kb
MCS
T3
ColE1 origin
PCR Product
Nde I(7)
EcoR I(134)
Pst I(514)
1
528
50bp
SIFN-co
Nde I+Pst I digest, recover 2.9 kb fragment
Nde I+Pst I digest
Recover 507bp fragment
Ssp I (3270)
Xmn I (3105)
Ssp I(19)
Sca I (3022)
Nae I(330)
Pvu I (2876)
Pvu I (500)
Pvu II (529)
1
fi (+) origin
T7
Amp
LacZ
pHY-1
3.5Kb
Nde I (718)
EcoR I (845)
SIFN-co
T3
Pst I (1225)
ColE1 origin
Bam HI (1242)
Xba I (1433)
Pvu II (1437)
Afl III (1613)
Nde I(127)
Sac I(91)
Xba I (157)
PBAD
1 SD Sequence
EcoR V (3833)
rrnBT1T2
Cla I(921)
araC
pHY-4
4.8Kb
ScaI I(1475)
Bgl II (3208)
ColE1
Pvu II (1583)
ScaI I (2311)
Pst I (1888)
Nde I+Xba I digest Recover 702bp fragment
Nde I+Xba I digest recover 4.8 kb fragment
Sac I (91)
Nde I (127)
EcoRI (254)
Pst I(634)
PBAD
1 SD Sequence
SIFN-co
BamH I(651)
Xba I(842)
EcoRV (4518)
rrnBT1T2
araC
pHY-5
5.5Kb
Cla I(1606)
Bgl II (3893)
ColE1
Amp
ScaI I(2160)
Pvu II(2268)
ScaI I (2996)
Pst I(2573)

Figure 6-A

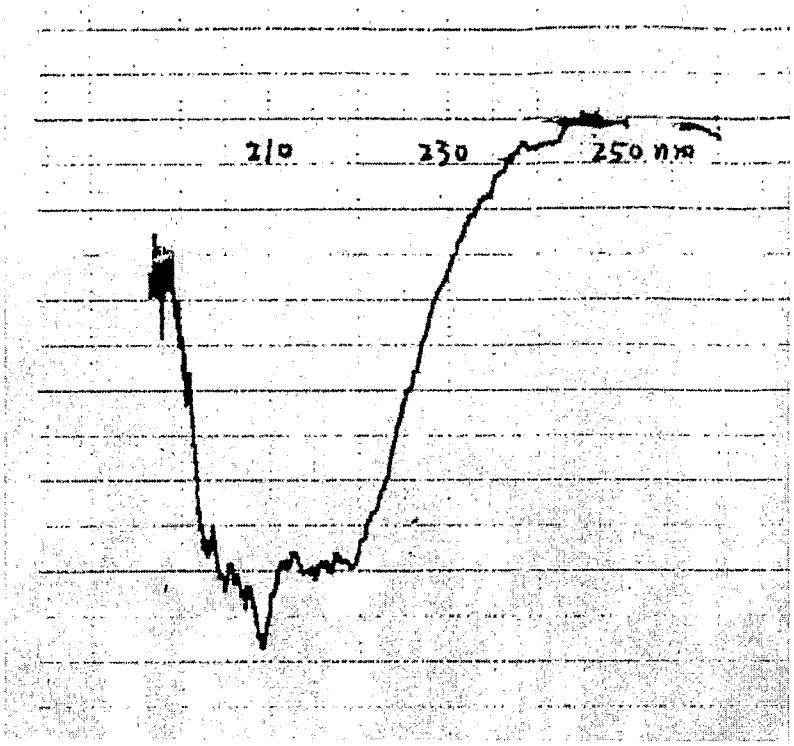


Figure 6-B

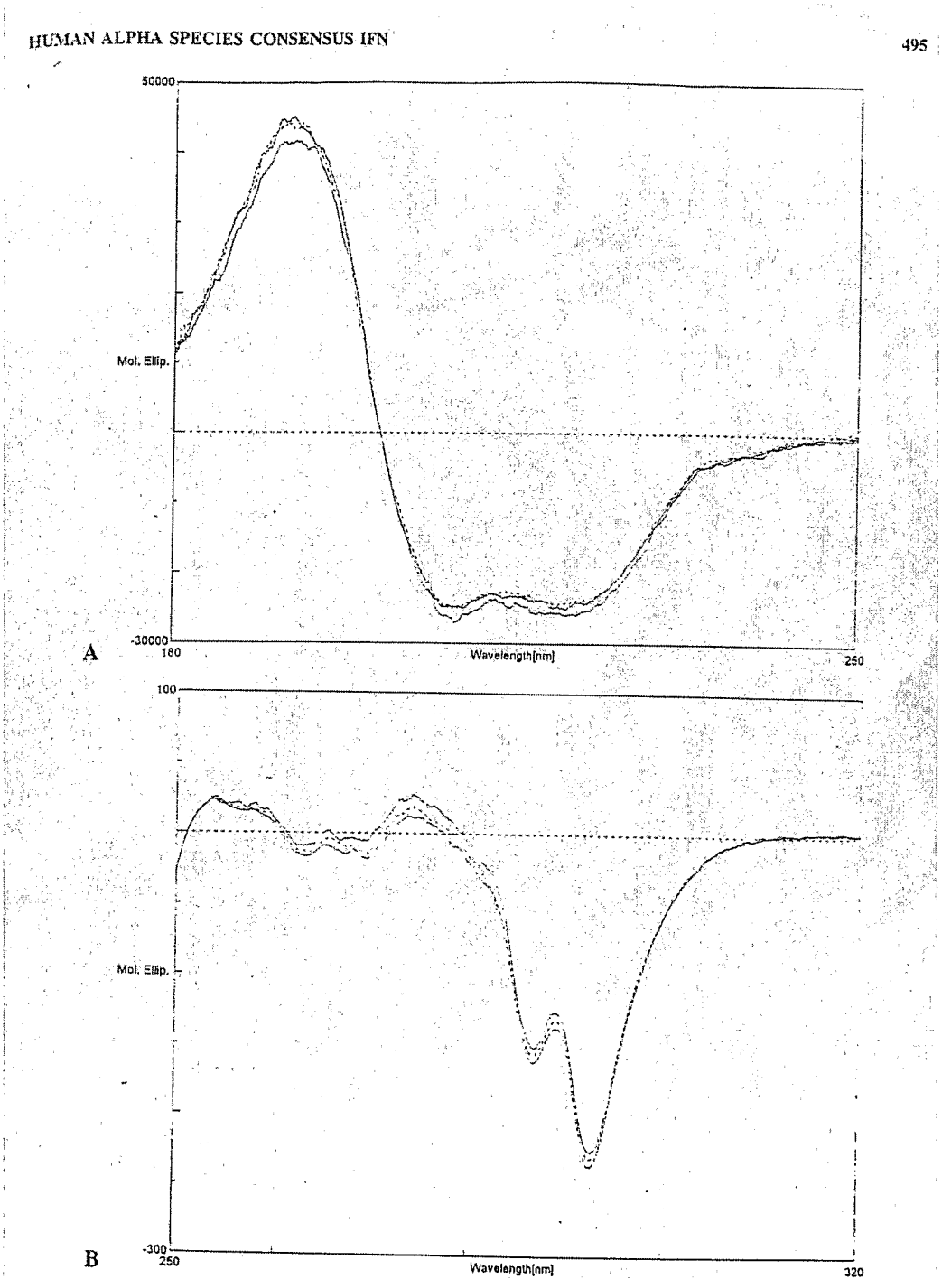

HUMAN ALPHA SPECIES CONSENSUS IFN
495
50000
Mol. Ellip.
-30000
180
Wavelength[nm]
250
A
100
Mol. Ellip.
-300
250
Wavelength[nm]
320
B

Figure 6-C

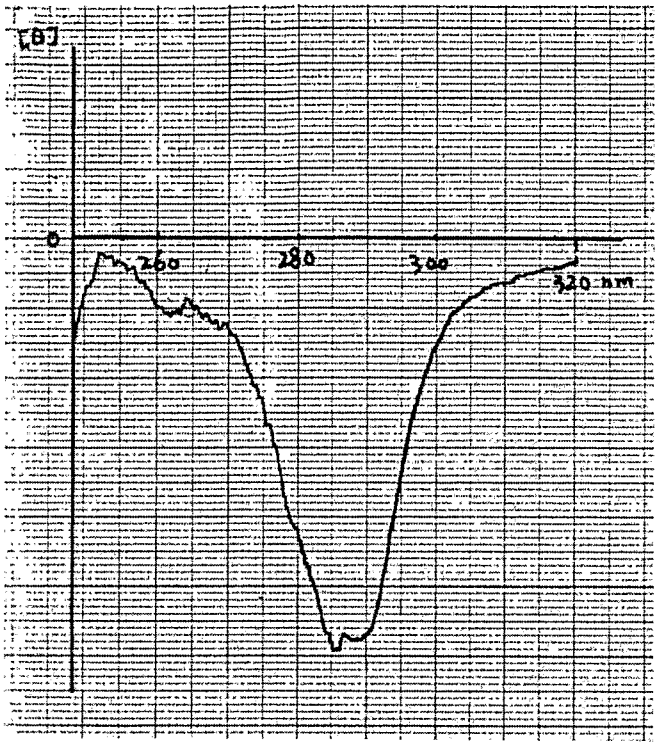


Figure 6-D

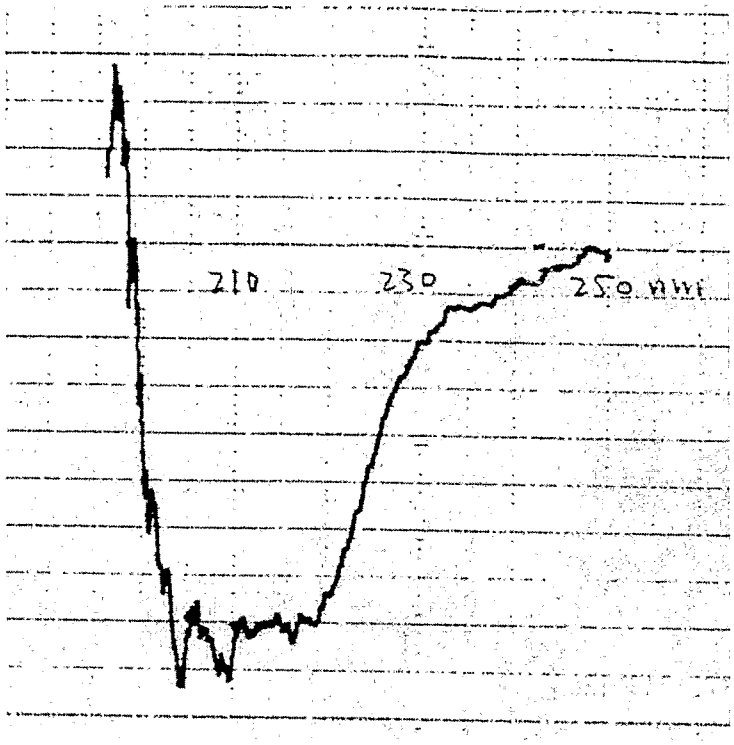


Figure 7A

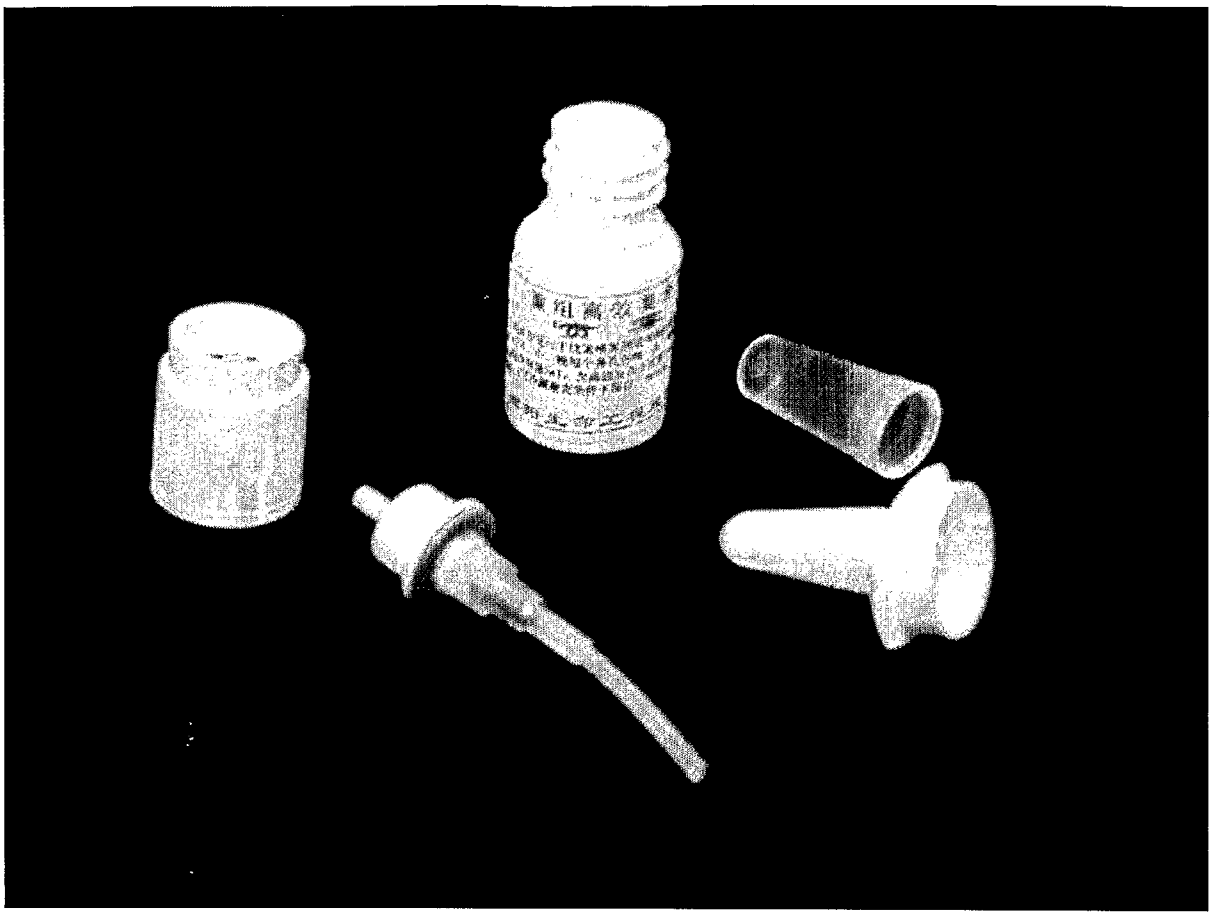


Figure 7B

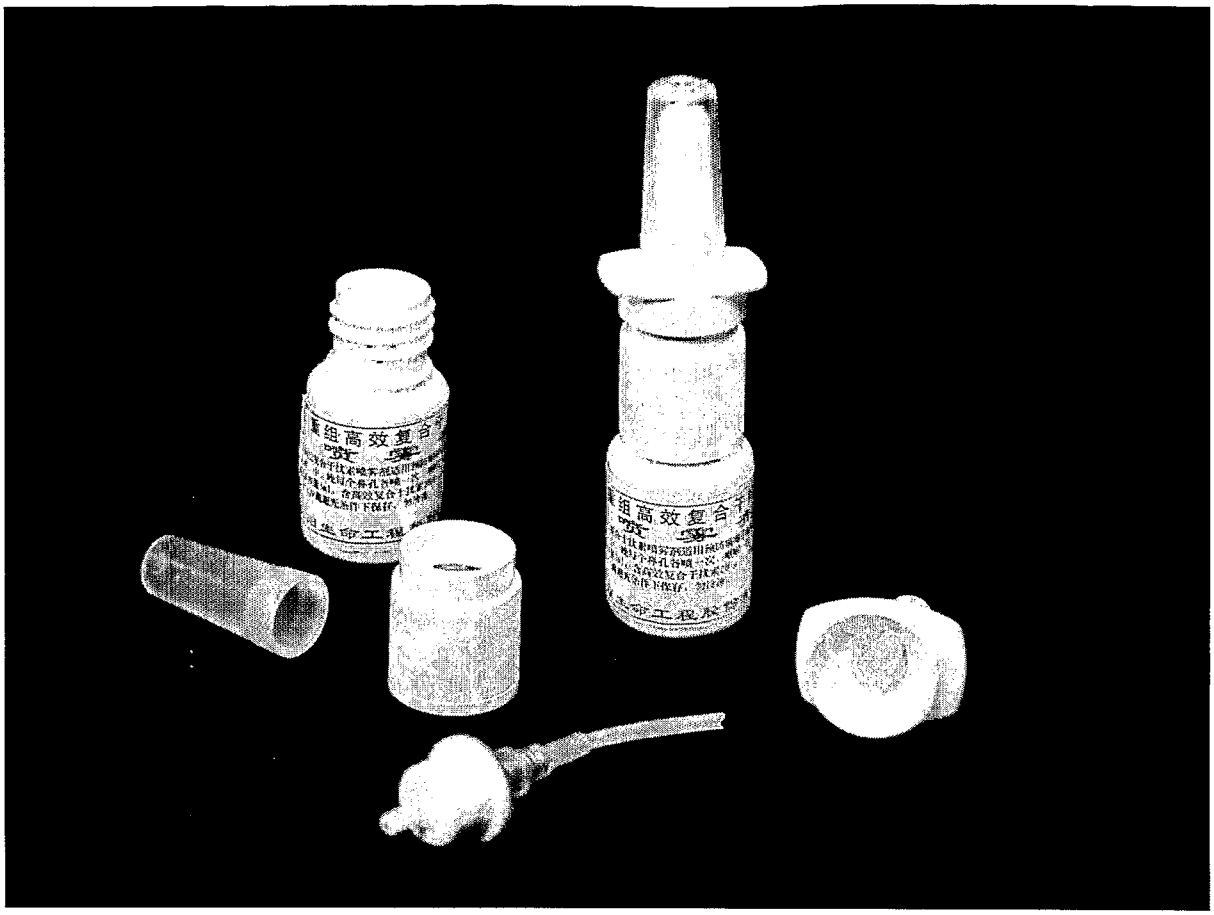
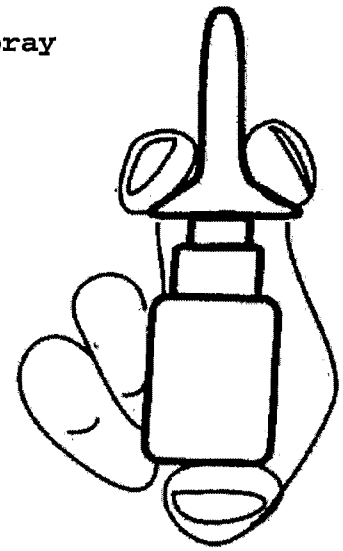


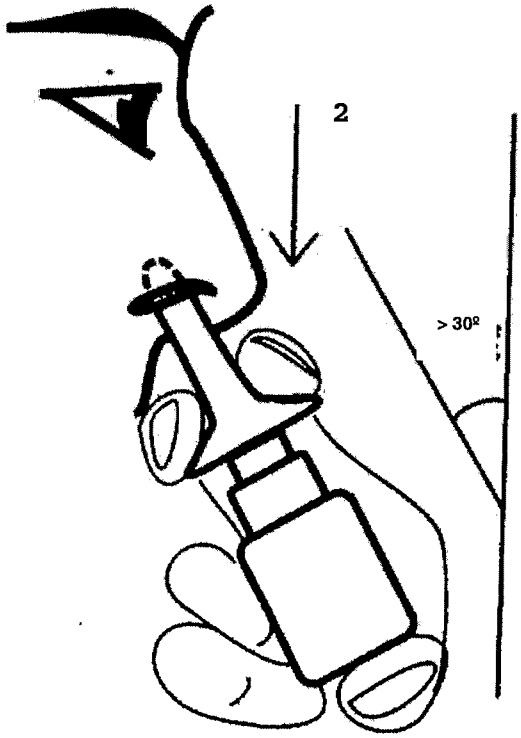
Figure 7C



Figure 7D

1. Pre-spray





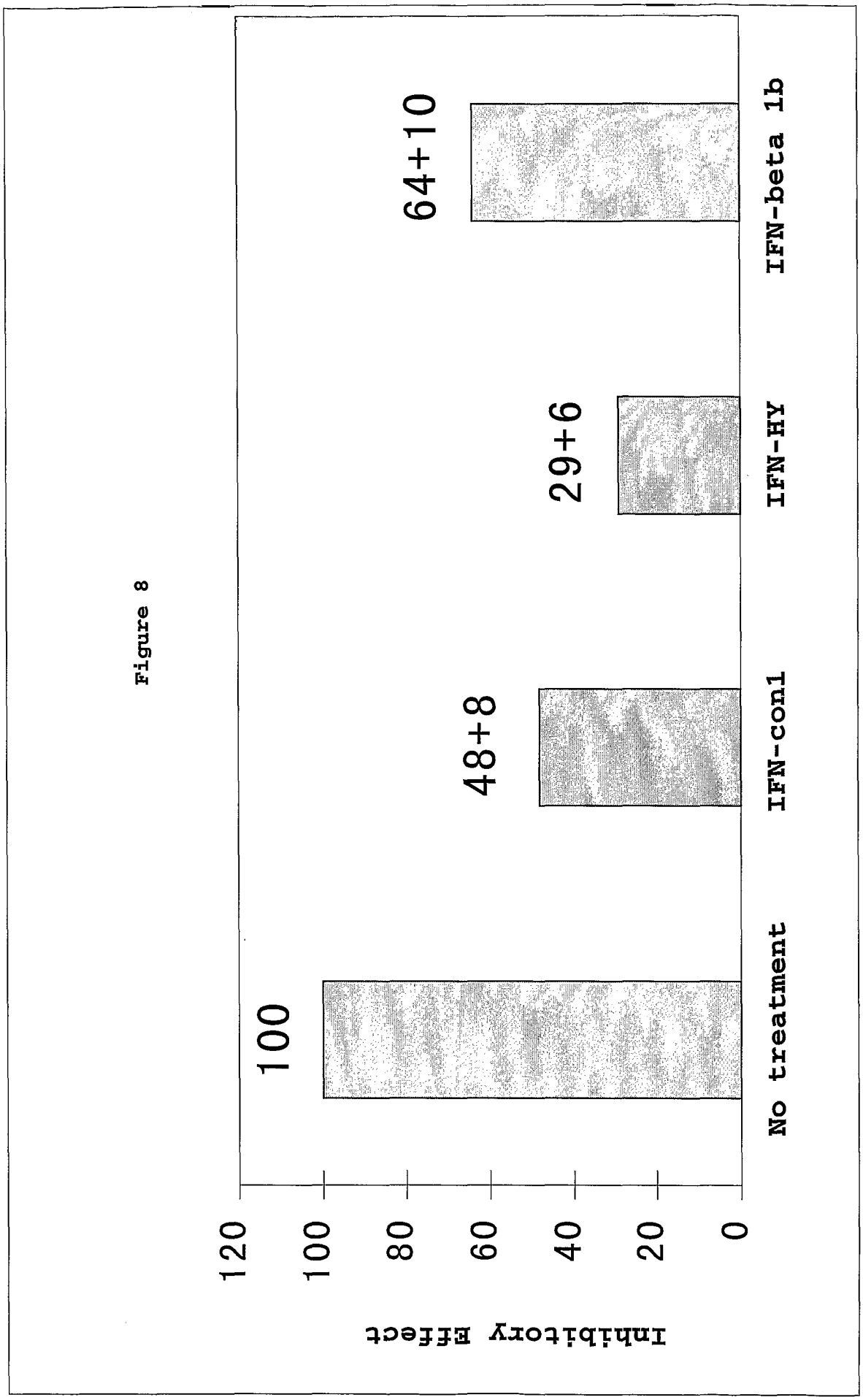
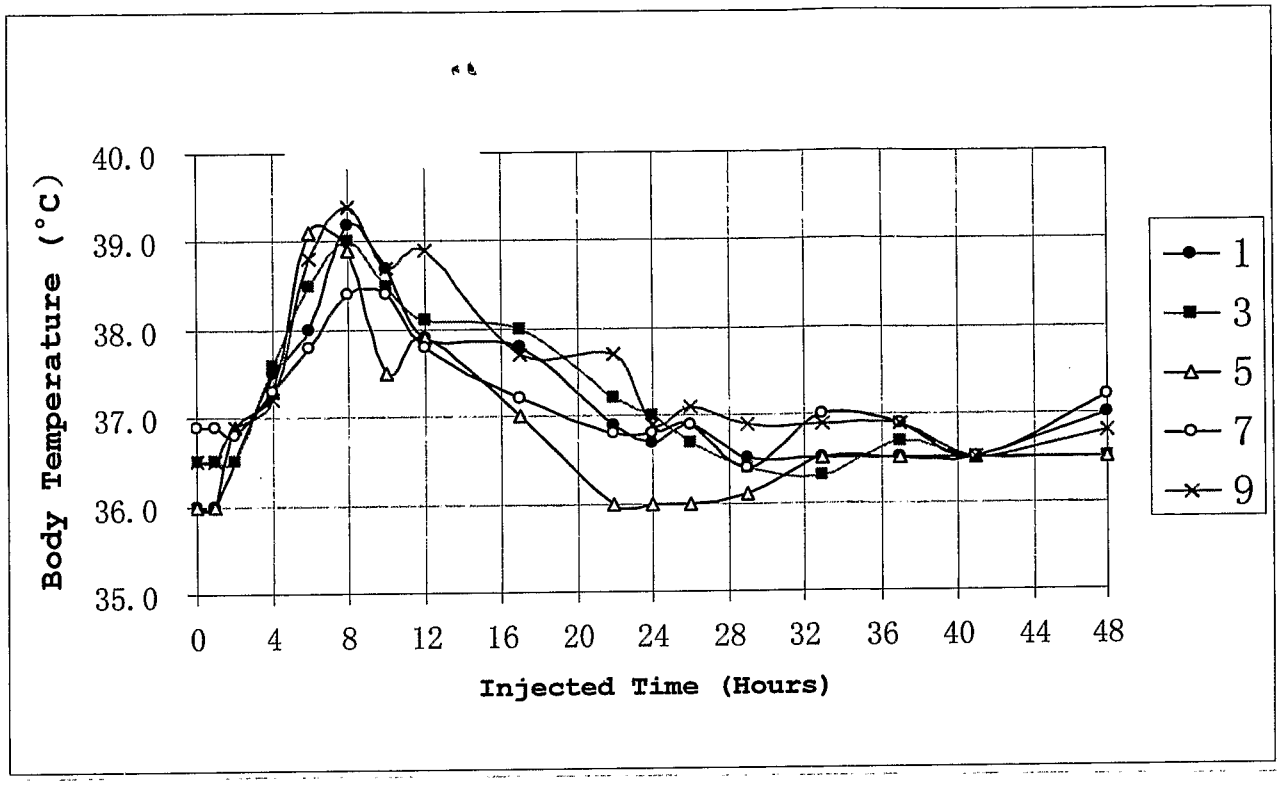

Inhibitory Effect
120
100
80
60
40
20
0
100
48+8
29+6
64+10
No treatment
IFN-con1
IFN-HY
IFN-beta 1b

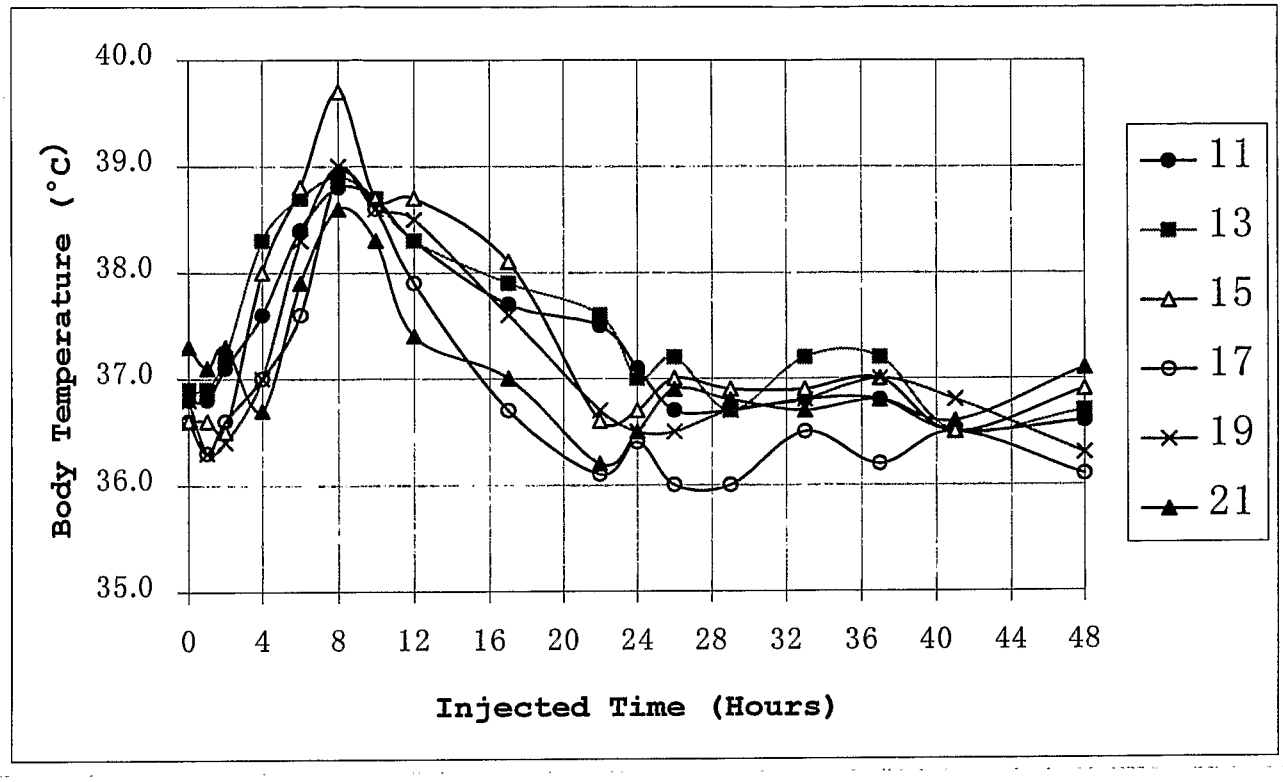
Figure 8

Figure 9B-1


Body Temperature (°C)
40.0
39.0
38.0
37.0
36.0
35.0
0
4
8
12
16
20
24
28
32
36
40
44
48
Injected Time (Hours)
1
3
5
7
9

IPEA/US

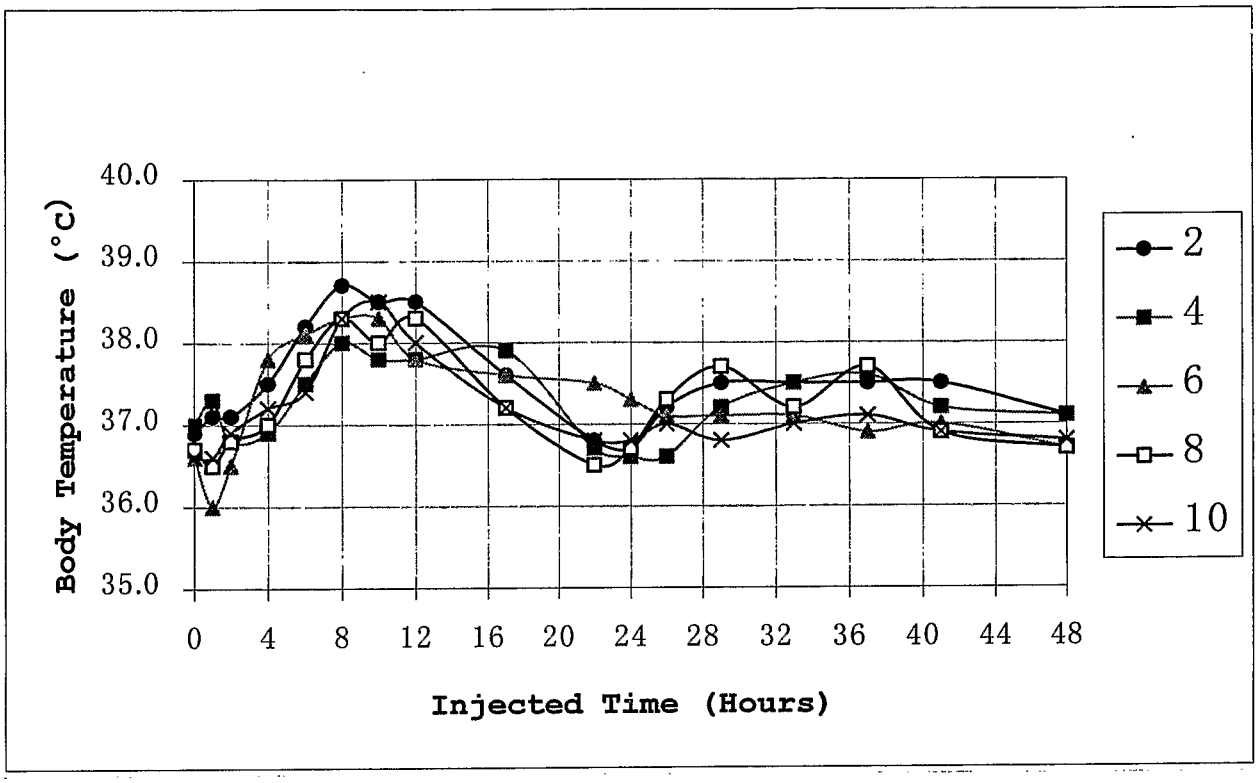
Figure 9B-2



AMENDED SHEET

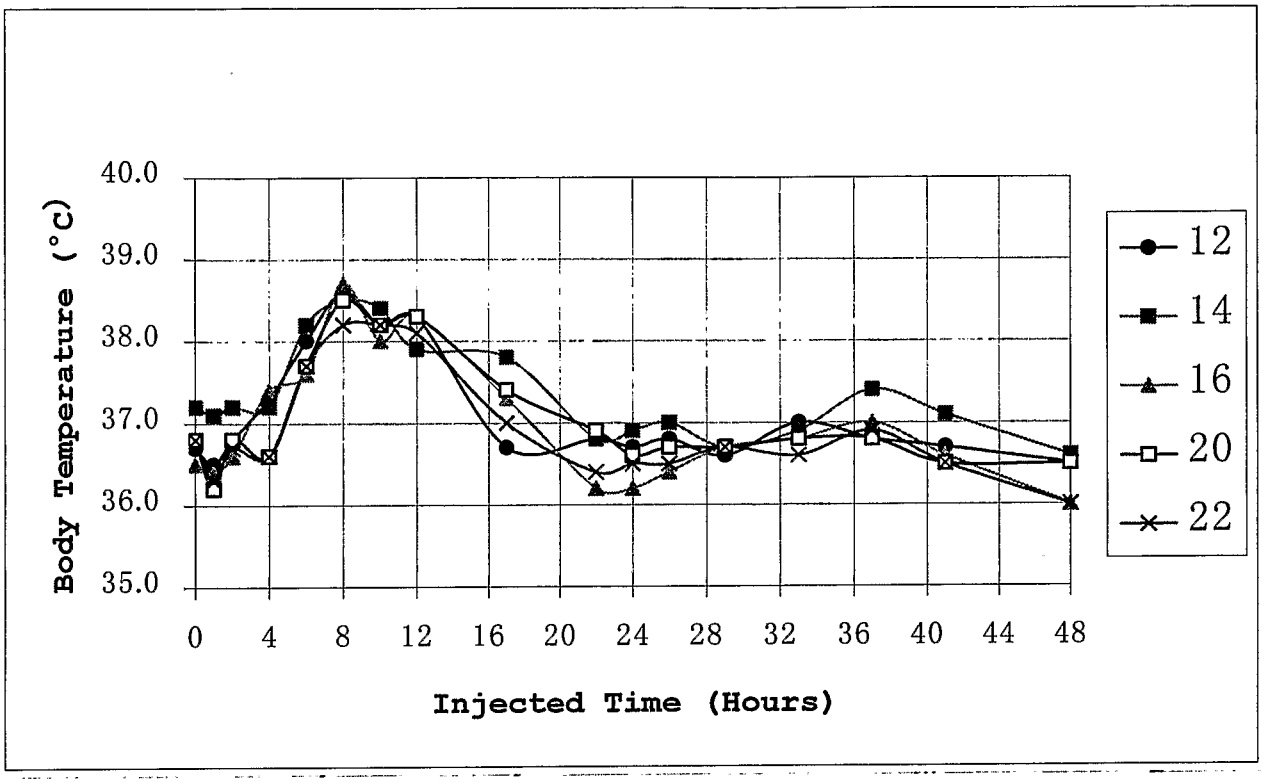
IPEA/US

Figure 9A-1



AMENDED SHEET

Figure 9A-2



AMENDED SHEET

Figure 10

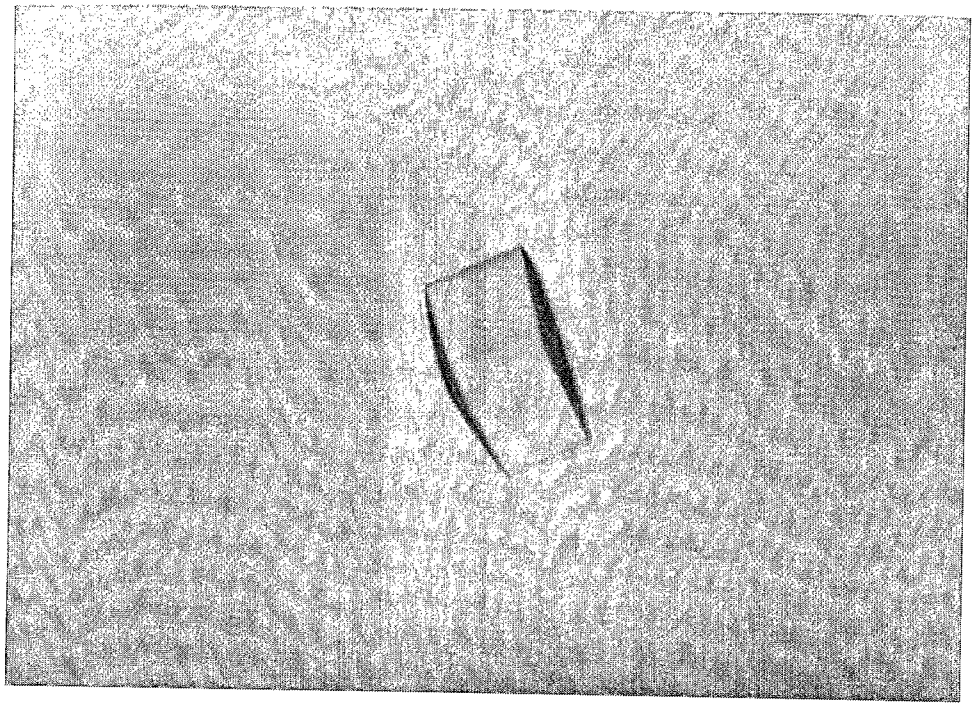


Figure 11

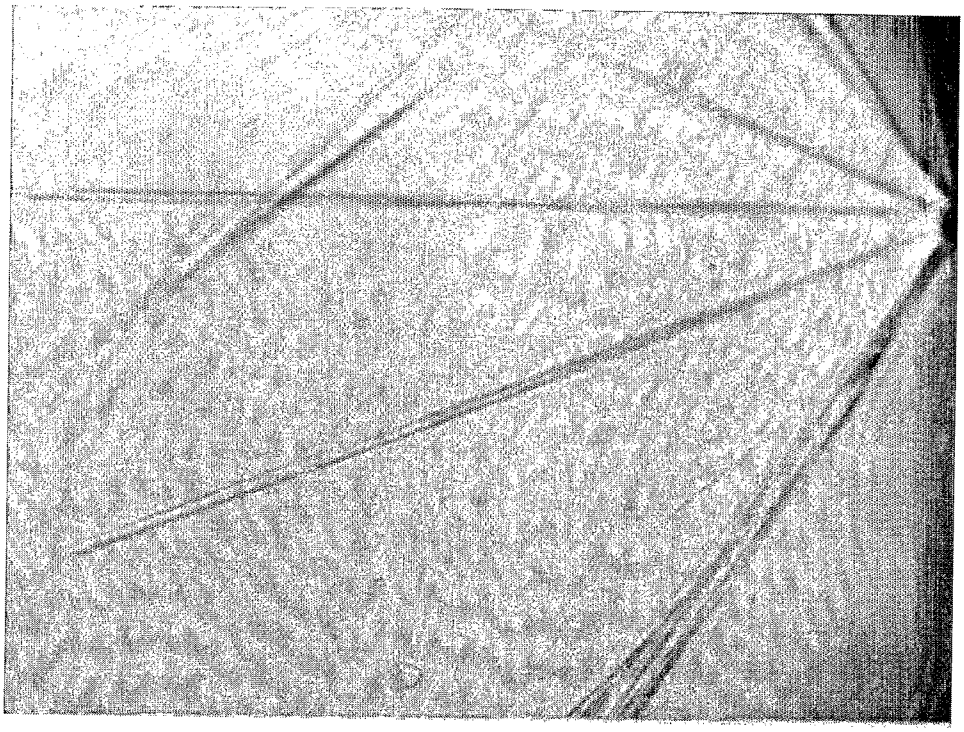
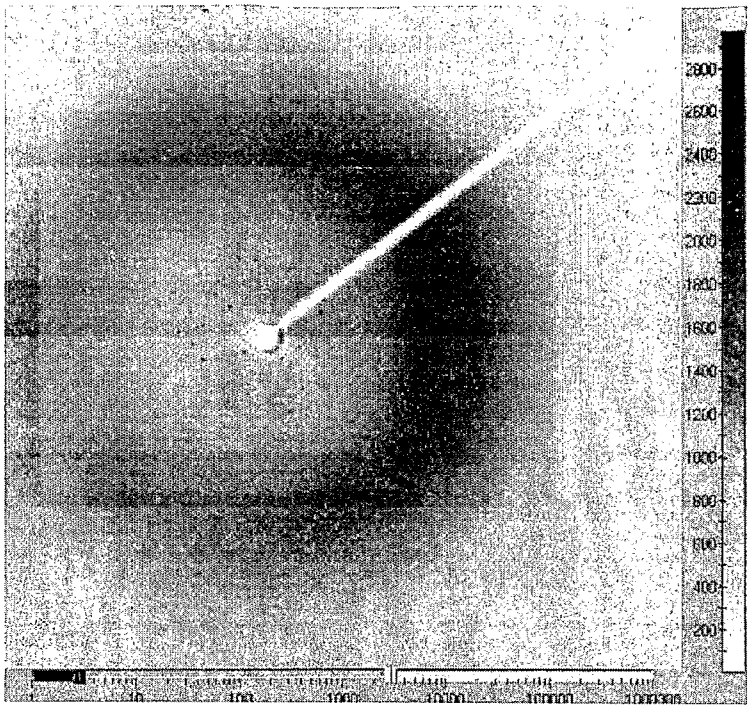


Figure 12


2800
2600
2400
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
10
100
1000
10000
100000
1000000