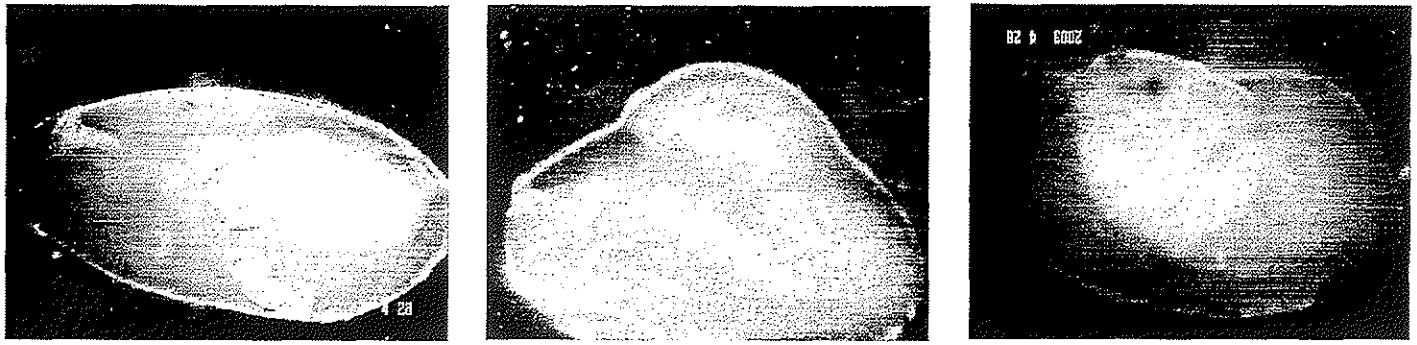
Efficacy of KID3 Antibody with Human Colon Tumor Line
Colo205 in the Kidney Capsule Model

Untreated



KID3 Treated



FIGURE 1

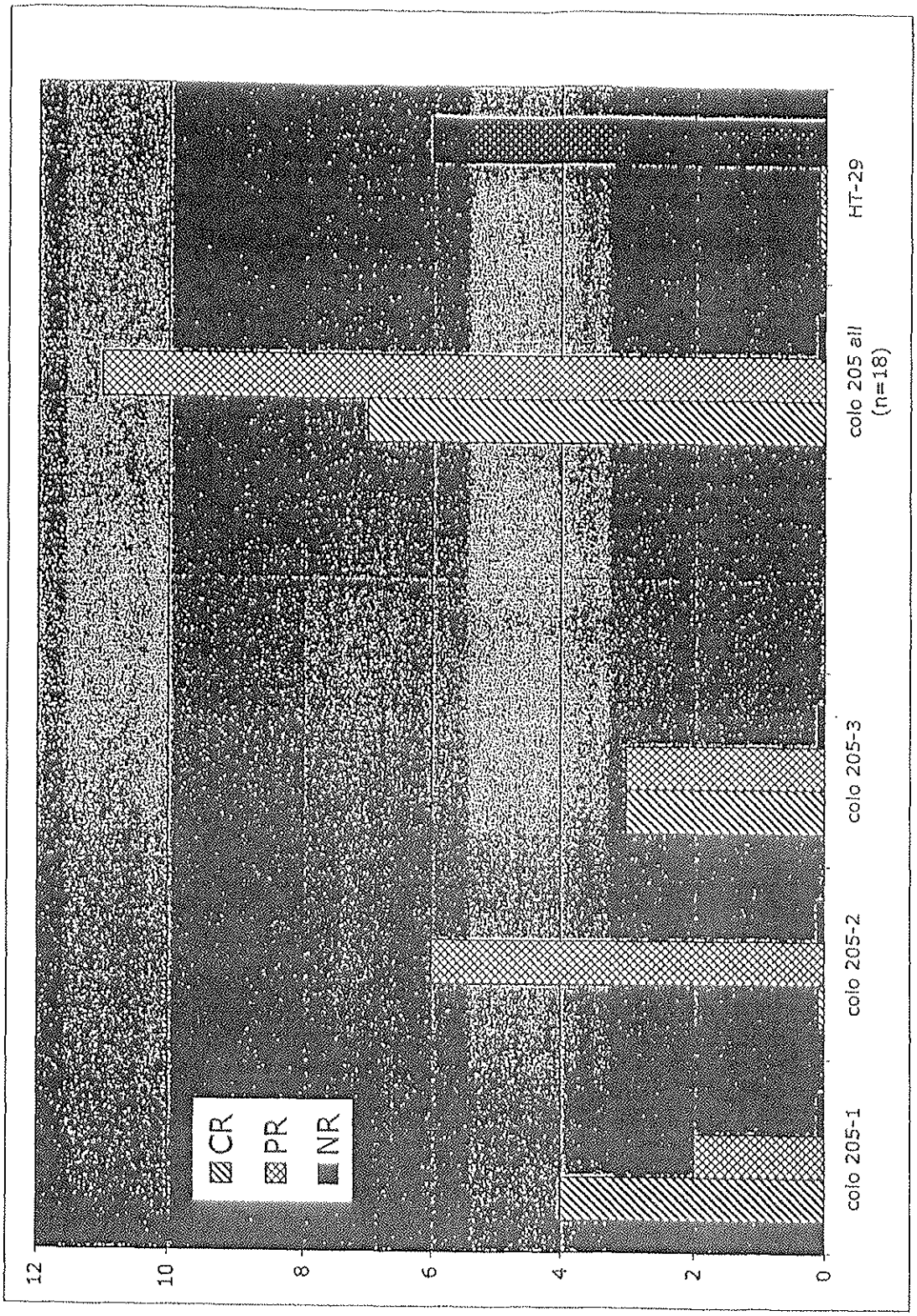

12
10
8
6
4
2
0
CR
PR
NR
colo 205-1
colo 205-2
colo 205-3
colo 205 all (n=18)
HT-29

FIGURE 2

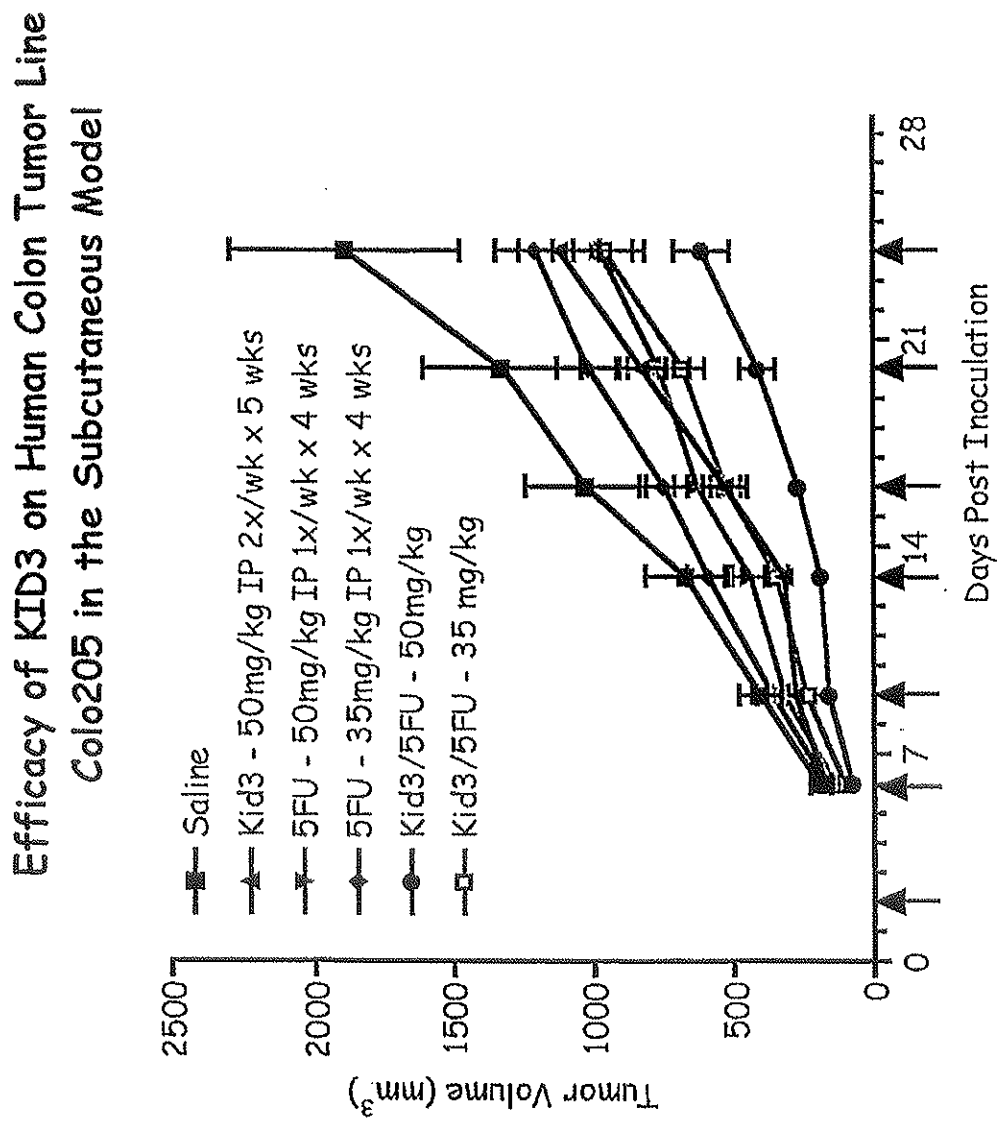

Efficacy of KID3 on Human Colon Tumor Line
Colo205 in the Subcutaneous Model
Saline
Kid3 - 50mg/kg IP 2x/wk x 5 wks
5FU - 50mg/kg IP 1x/wk x 4 wks
5FU - 35mg/kg IP 1x/wk x 4 wks
Kid3/5FU - 50mg/kg
Kid3/5FU - 35 mg/kg
Tumor Volume (mm3)
2500
2000
1500
1000
500
0
0
7
14
21
28
Days Post Inoculation

FIGURE 3

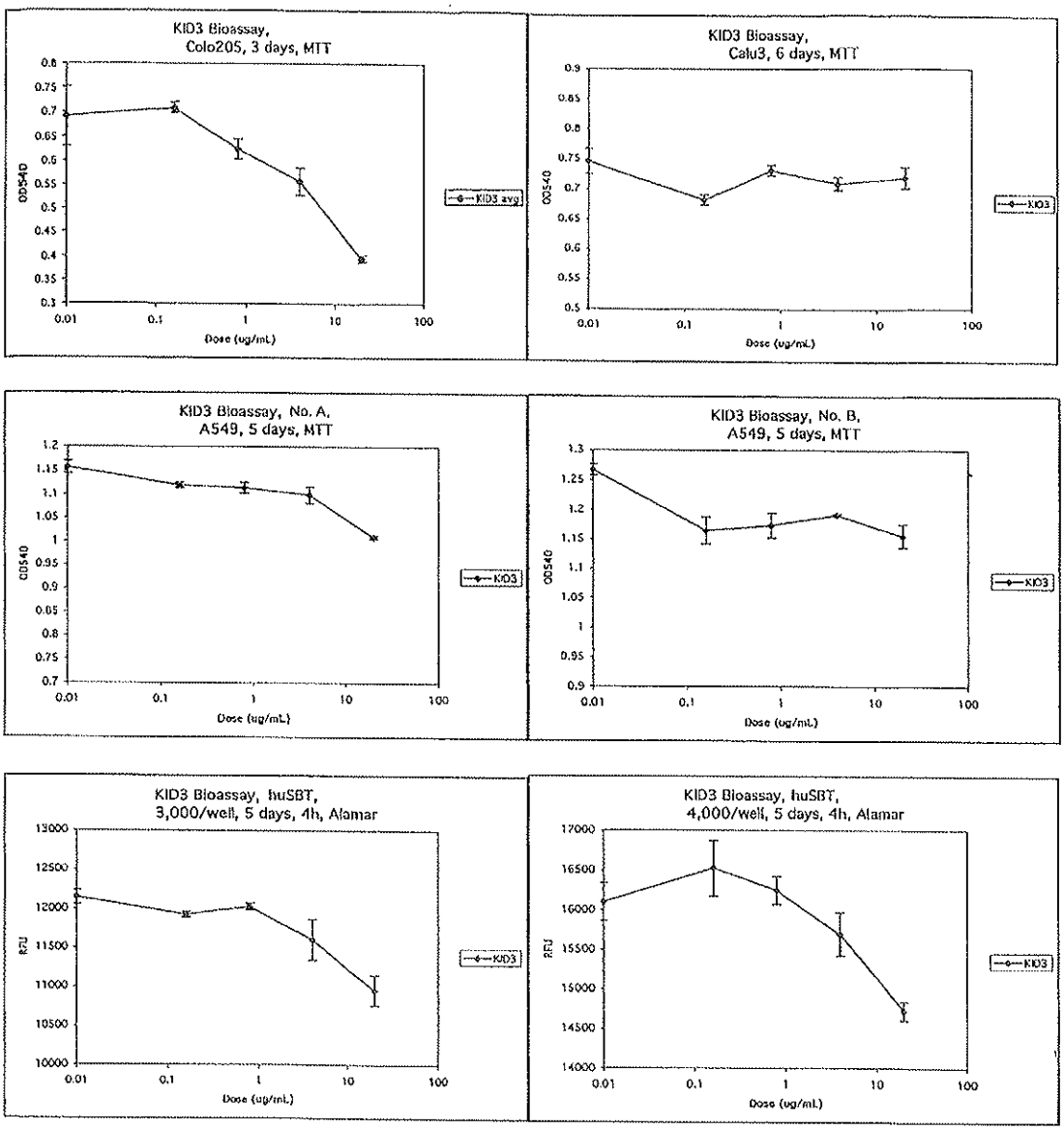
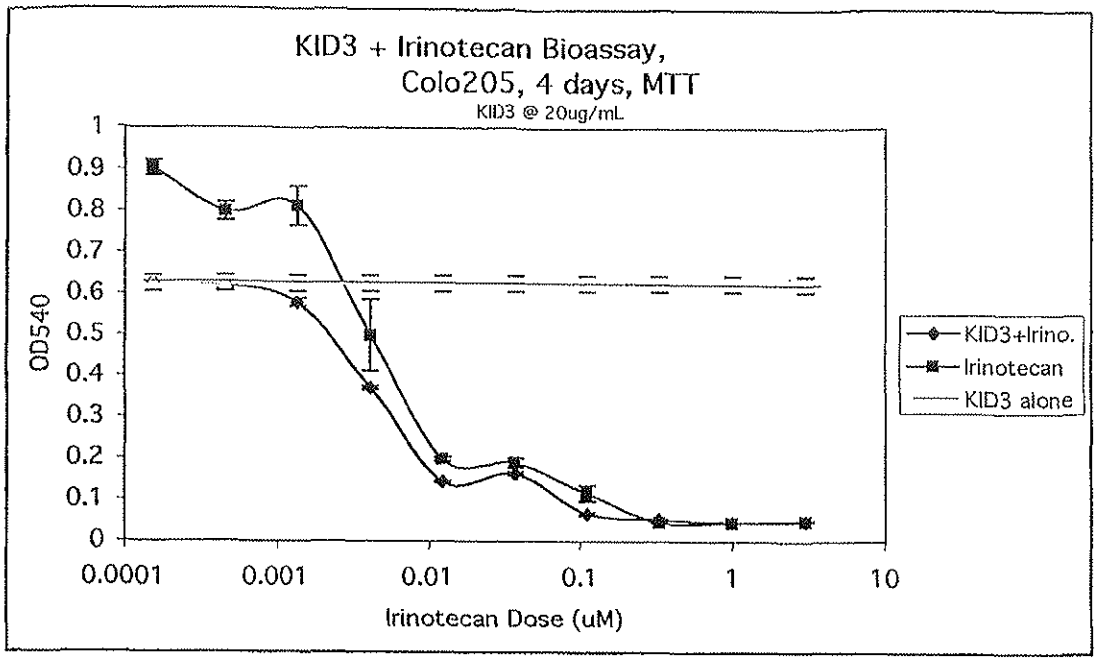

KID3 Bioassay,
Colo205, 3 days, MTT
OD540
Dose (ug/mL)
KID3 avg
KID3 Bioassay,
Calu3, 6 days, MTT
OD540
Dose (ug/mL)
KID3
KID3 Bioassay, No. A,
A549, 5 days, MTT
OD540
Dose (ug/mL)
KID3
KID3 Bioassay, No. B,
A549, 5 days, MTT
OD540
Dose (ug/mL)
KID3
KID3 Bioassay, huSBT,
3,000/well, 5 days, 4h, Alamar
RFU
Dose (ug/mL)
KID3
KID3 Bioassay, huSBT,
4,000/well, 5 days, 4h, Alamar
RFU
Dose (ug/mL)
KID3

FIGURE 4


KID3 + Irinotecan Bioassay,
Colo205, 4 days, MTT
KID3 @ 20ug/mL
OD540
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.0001
0.001
0.01
0.1
1
10
Irinotecan Dose (uM)
KID3+Irino.
Irinotecan
KID3 alone

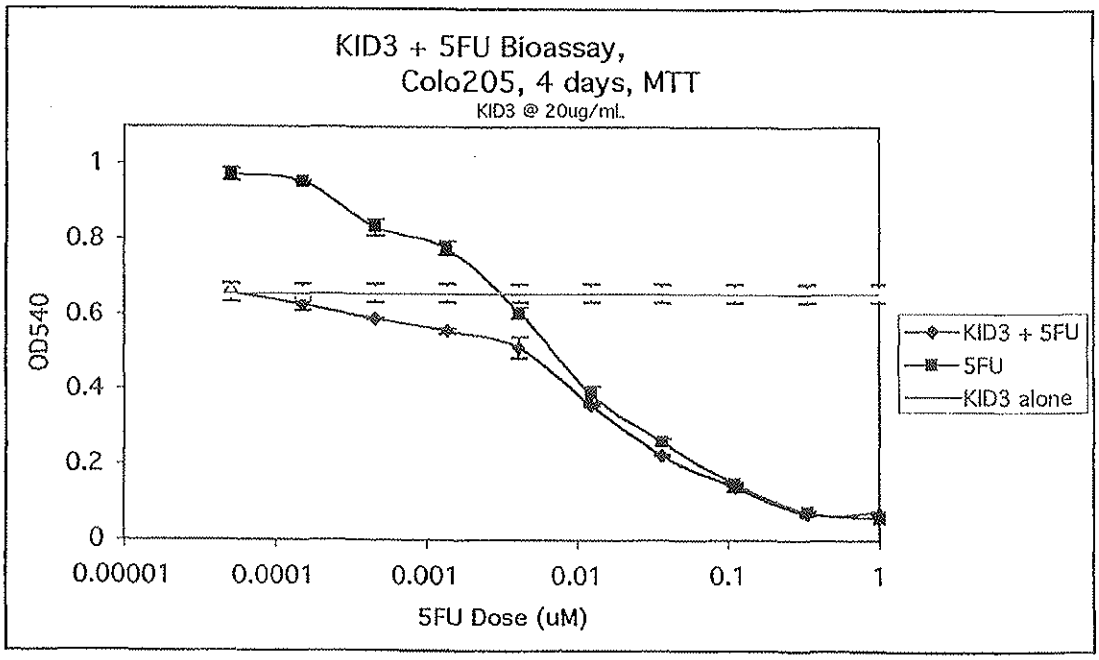

KID3 + 5FU Bioassay,
Colo205, 4 days, MTT
KID3 @ 20ug/mL
OD540
1
0.8
0.6
0.4
0.2
0
0.00001
0.0001
0.001
0.01
0.1
1
5FU Dose (uM)
KID3 + 5FU
5FU
KID3 alone

FIGURE 5

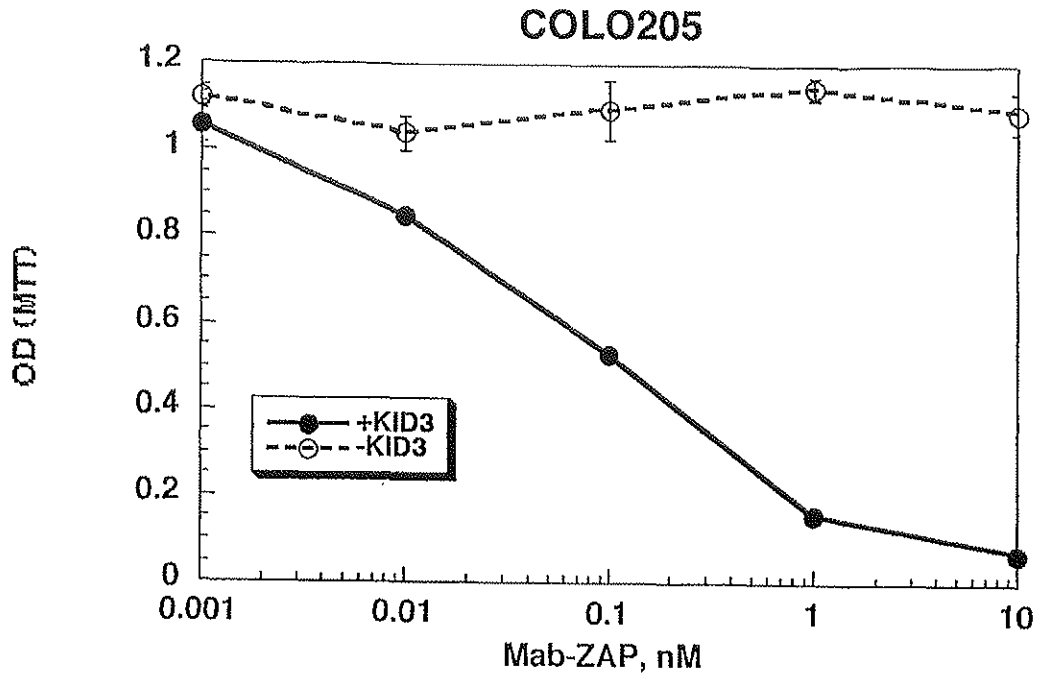

COLO205
OD (MTT)
1.2
1
0.8
0.6
0.4
0.2
0
+KID3
-KID3
0.001
0.01
0.1
1
10
Mab-ZAP, nM

FIGURE 6

```
      M  E  K   D  T  L   L  L  W   V  L  L   L  W  V
  1   ATGGAGAAA GACACACTC CTGCTATGG GTCCTGCTT CTCTGGGTT
      TACCTCTTT CTGTGTGAG GACGATACC CAGGACGAA GAGACCCAA
      P  G  S   T  G  D   I  V  L   T  Q  S   P  A  S
 46   CCAGGTTCC ACAGGTGAC ATTGTGCTG ACCCAATCT CCAGCTTCT
      GGTCCAAGG TGTCCACTG TAACACGAC TGGGTTAGA GGTCGAAGA
      L  A  V   S  L  G   Q  R  A   T  I  S   C  R  A
 91   TTGGCTGTG TCTCTAGGG CAGAGGGCC ACCATCTCC TGCAGAGCC
      AACCGACAC AGAGATCCC GTCTCCCGG TGGTAGAGG ACGTCTCGG
      S  E  S   V  D  N   Y  G  I   S  Y  M   N  W  F
136   AGCGAAAGT GTTGATAAT TATGGCATT AGTTATATG AACTGGTTC
      TCGCTTTCA CAACTATTA ATACCGTAA TCAATATAC TTGACCAAG
      Q  Q  K   P  G  Q   P  P  K   V  L  I   Y  A  A
181   CAACAGAAA CCAGGACAG CCACCCAAA GTCCTCATC TATGCTGCA
      GTTGTCTTT GGTCCTGTC GGTGGGTTT CAGGAGTAG ATACGACGT
      S  N  Q   G  S  G   V  P  A   R  F  S   G  S  G
226   TCCAACCAA GGATCCGGG GTCCCTGCC AGGTTTAGT GGCAGTGGG
      AGGTTGGTT CCTAGGCCC CAGGGACGG TCCAAATCA CCGTCACCC
      S  G  T   D  F  S   L  N  I   H  P  M   E  E  D
271   TCTGGGACA GACTTCAGC CTCAACATC CATCCTATG GAGGAGGAT
      AGACCCTGT CTGAAGTCG GAGTTGTAG GTAGGATAC CTCCTCCTA
      D  T  A   M  Y  F   C  Q  Q   S  K  E   V  P  W
316   GATACTGCA ATGTATTTC TGTCAGCAA AGTAAGGAG GTTCCGTGG
      CTATGACGT TACATAAAG ACAGTCGTT TCATTCCTC CAAGGCACC
      T  F  G   G  G  T   K  L  E   I  K  R   T  V  A
361   ACGTTCGGT GGAGGCACC AAGCTCGAG ATCAAACGG ACTGTGGCT
      TGCAAGCCA CCTCCGTGG TTCGAGCTC TAGTTTGCC TGACACCGA
      A  P  S   V  F  I   F  P  P   S  D  E   Q  L  K
406   GCACCATCT GTCTTCATC TTCCCGCCA TCTGATGAG CAGTTGAAA
      CGTGGTAGA CAGAAGTAG AAGGGCGGT AGACTACTC GTCAACTTT
      S  G  T   A  S  V   V  C  L   L  N  N   F  Y  P
451   TCTGGAACT GCCTCTGTT GTGTGCCTG CTGAATAAC TTCTATCCC
      AGACCTTGA CGGAGACAA CACACGGAC GACTTATTG AAGATAGGG
      R  E  A   K  V  Q   W  K  V   D  N  A   L  Q  S
496   AGAGAGGCC AAAGTACAG TGGAAGGTG GATAACGCC CTCCAATCG
      TCTCTCCGG TTTCATGTC ACCTTCCAC CTATTGCGG GAGGTTAGC
      G  N  S   Q  E  S   V  T  E   Q  D  S   K  D  S
541   GGTAACTCC CAGGAGAGT GTCACAGAG CAGGACAGC AAGGACAGC
      CCATTGAGG GTCCTCTCA CAGTGTCTC GTCCTGTCG TTCCTGTCG
      T  Y  S   L  S  S   T  L  T   L  S  K   A  D  Y
586   ACCTACAGC CTCAGCAGC ACCCTGACG CTGAGCAAA GCAGACTAC
      TGGATGTCG GAGTCGTCG TGGGACTGC GACTCGTTT CGTCTGATG
      E  K  H   K  V  Y   A  C  E   V  T  H   Q  G  L
631   GAGAAACAC AAAGTCTAC GCCTGCGAA GTCACCCAT CAGGGCCTG
      CTCTTTGTG TTTCAGATG CGGACGCTT CAGTGGGTA GTCCCGGAC
      S  S  P   V  T  K   S  F  N   R  G  E   C  *
676   AGCTCGCCC GTCACAAAG AGCTTCAAC AGGGGAGAG TGTTAG
      TCGAGCGGG CAGTGTTTC TCGAAGTTG TCCCCTCTC ACAATC
```

FIGURE 7

```
      M  G  V    L  I  L    L  W  L    F  T  A    F  P  G
  1   ATGGGAGTG  CTGATTCTT  TTGTGGCTG  TTCACAGCC  TTTCCTGGT
      TACCCTCAC  GACTAAGAA  AACACCGAC  AAGTGTCGG  AAAGGACCA
      I  L  S    D  V  Q    L  Q  E    S  G  P    G  L  V
 46   ATCCTGTCT  GATGTGCAG  CTTCAGGAG  TCGGGACCT  GGCCTGGTG
      TAGGACAGA  CTACACGTC  GAAGTCCTC  AGCCCTGGA  CCGGACCAC
      K  P  S    Q  S  L    S  L  T    C  T  V    T  G  Y
 91   AAACCTTCT  CAGTCTCTG  TCCCTCACC  TGCACTGTC  ACTGGCTAC
      TTTGGAAGA  GTCAGAGAC  AGGGAGTGG  ACGTGACAG  TGACCGATG
      S  I  T    S  D  Y    A  W  N    W  I  R    Q  F  P
136   TCAATCACC  AGTGATTAT  GCCTGGAAC  TGGATCCGG  CAGTTTCCA
      AGTTAGTGG  TCACTAATA  CGGACCTTG  ACCTAGGCC  GTCAAAGGT
      G  N  K    L  E  W    M  G  Y    I  S  Y    S  G  S
181   GGAAACAAA  CTGGAGTGG  ATGGGCTAC  ATAAGCTAC  AGTGGTAGC
      CCTTTGTTT  GACCTCACC  TACCCGATG  TATTCGATG  TCACCATCG
      T  S  Y    N  P  S    L  K  S    R  V  S    I  T  R
226   ACTAGCTAC  AACCCATCT  CTCAAAAGT  CGAGTCTCT  ATCACTCGA
      TGATCGATG  TTGGGTAGA  GAGTTTTCA  GCTCAGAGA  TAGTGAGCT
      D  T  S    K  N  Q    F  F  L    Q  L  N    S  V  T
271   GACACATCC  AAGAACCAG  TTCTTCCTG  CAGTTGAAT  TCTGTGACT
      CTGTGTAGG  TTCTTGGTC  AAGAAGGAC  GTCAACTTA  AGACACTGA
      T  E  D    T  A  T    Y  Y  C    A  R  F    Y  Y  R
316   ACTGAGGAC  ACAGCCACA  TATTACTGT  GCAAGATTC  TACTATAGG
      TGACTCCTG  TGTCGGTGT  ATAATGACA  CGTTCTAAG  ATGATATCC
      Y  A  D    Y  F  D    Y  W  G    Q  G  T    T  L  T
361   TACGCCGAC  TACTTTGAC  TACTGGGGC  CAAGGCACC  ACTCTCACA
      ATGCGGCTG  ATGAAACTG  ATGACCCCG  GTTCCGTGG  TGAGAGTGT
      V  S  S    A  S  T    K  G  P    S  V  F    P  L  A
406   GTCTCCTCA  GCTAGCACC  AAGGGCCCA  TCGGTCTTC  CCCCTGGCA
      CAGAGGAGT  CGATCGTGG  TTCCCGGGT  AGCCAGAAG  GGGGACCGT
      P  S  S    K  S  T    S  G  G    T  A  A    L  G  C
451   CCCTCCTCC  AAGAGCACC  TCTGGGGGC  ACAGCGGCT  CTGGGCTGC
      GGGAGGAGG  TTCTCGTGG  AGACCCCCG  TGTCGCCGA  GACCCGACG
      L  V  K    D  Y  F    P  E  P    V  T  V    S  W  N
496   CTGGTCAAG  GACTACTTC  CCCGAACCG  GTGACGGTG  TCGTGGAAC
      GACCAGTTC  CTGATGAAG  GGGCTTGGC  CACTGCCAC  AGCACCTTG
      S  G  A    L  T  S    G  V  H    T  F  P    A  V  L
541   TCAGGCGCC  CTGACCAGC  GGCGTGCAC  ACCTTCCCG  GCTGTCCTA
      AGTCCGCGG  GACTGGTCG  CCGCACGTG  TGGAAGGGC  CGACAGGAT
      Q  S  S    G  L  Y    S  L  S    S  V  V    T  V  P
586   CAGTCCTCA  GGACTCTAC  TCCCTCAGC  AGCGTGGTG  ACTGTGCCC
      GTCAGGAGT  CCTGAGATG  AGGGAGTCG  TCGCACCAC  TGACACGGG
      S  S  S    L  G  T    Q  T  Y    I  C  N    V  N  H
631   TCCAGCAGC  TTGGGCACC  CAGACCTAC  ATCTGCAAC  GTGAATCAC
      AGGTCGTCG  AACCCGTGG  GTCTGGATG  TAGACGTTG  CACTTAGTG
      K  P  S    N  T  K    V  D  K    K  V  E    P  K  S
676   AAGCCCAGC  AACACCAAG  GTGGACAAG  AAAGTTGAG  CCCAAATCT
      TTCGGGTCG  TTGTGGTTC  CACCTGTTC  TTTCAACTC  GGGTTTAGA
```

FIGURE 8A

```
        C  D  K    T  H  T    C  P  P    C  P  A    P  E  L
721     TGTGACAAA  ACTCACACA  TGCCCACCG  TGCCCAGCA  CCTGAACTC
        ACACTGTTT  TGAGTGTGT  ACGGGTGGC  ACGGGTCGT  GGACTTGAG
        L  G  G    P  S  V    F  L  F    P  P  K    P  K  D
766     CTGGGGGGA  CCGTCAGTC  TTCCTCTTC  CCCCCAAAA  CCCAAGGAC
        GACCCCCCT  GGCAGTCAG  AAGGAGAAG  GGGGGTTTT  GGGTTCCTG
        T  L  M    I  S  R    T  P  E    V  T  C    V  V  V
811     ACCCTCATG  ATCTCCCGG  ACCCCTGAG  GTCACATGC  GTGGTGGTG
        TGGGAGTAC  TAGAGGGCC  TGGGGACTC  CAGTGTACG  CACCACCAC
        D  V  S    H  E  D    P  E  V    K  F  N    W  Y  V
856     GACGTGAGC  CACGAAGAC  CCTGAGGTC  AAGTTCAAC  TGGTACGTG
        CTGCACTCG  GTGCTTCTG  GGACTCCAG  TTCAAGTTG  ACCATGCAC
        D  G  V    E  V  H    N  A  K    T  K  P    R  E  E
901     GACGGCGTG  GAGGTGCAT  AATGCCAAG  ACAAAGCCG  CGGGAGGAG
        CTGCCGCAC  CTCCACGTA  TTACGGTTC  TGTTTCGGC  GCCCTCCTC
        Q  Y  N    S  T  Y    R  V  V    S  V  L    T  V  L
946     CAGTACAAC  AGCACGTAC  CGTGTGGTC  AGCGTCCTC  ACCGTCCTG
        GTCATGTTG  TCGTGCATG  GCACACCAG  TCGCAGGAG  TGGCAGGAC
        H  Q  D    W  L  N    G  K  E    Y  K  C    K  V  S
991     CACCAGGAC  TGGCTGAAT  GGCAAGGAG  TACAAGTGC  AAGGTCTCC
        GTGGTCCTG  ACCGACTTA  CCGTTCCTC  ATGTTCACG  TTCCAGAGG
        N  K  A    L  P  A    P  I  E    K  T  I    S  K  A
1036    AACAAAGCC  CTCCCAGCC  CCCATCGAG  AAAACCATC  TCCAAAGCC
        TTGTTTCGG  GAGGGTCGG  GGGTAGCTC  TTTTGGTAG  AGGTTTCGG
        K  G  Q    P  R  E    P  Q  V    Y  T  L    P  P  S
1081    AAAGGGCAG  CCCCGAGAA  CCACAGGTG  TACACCCTG  CCCCCATCC
        TTTCCCGTC  GGGGCTCTT  GGTGTCCAC  ATGTGGGAC  GGGGGTAGG
        R  D  E    L  T  K    N  Q  V    S  L  T    C  L  V
1126    CGGGATGAG  CTGACCAAG  AACCAGGTC  AGCCTGACC  TGCCTGGTC
        GCCCTACTC  GACTGGTTC  TTGGTCCAG  TCGGACTGG  ACGGACCAG
        K  G  F    Y  P  S    D  I  A    V  E  W    E  S  N
1171    AAAGGCTTC  TATCCCAGC  GACATCGCC  GTGGAGTGG  GAGAGCAAT
        TTTCCGAAG  ATAGGGTCG  CTGTAGCGG  CACCTCACC  CTCTCGTTA
        G  Q  P    E  N  N    Y  K  T    T  P  P    V  L  D
1216    GGGCAGCCG  GAGAACAAC  TACAAGACC  ACGCCTCCC  GTGCTGGAC
        CCCGTCGGC  CTCTTGTTG  ATGTTCTGG  TGCGGAGGG  CACGACCTG
        S  D  G    S  F  F    L  Y  S    K  L  T    V  D  K
1261    TCCGACGGC  TCCTTCTTC  CTCTACAGC  AAGCTCACC  GTGGACAAG
        AGGCTGCCG  AGGAAGAAG  GAGATGTCG  TTCGAGTGG  CACCTGTTC
        S  R  W    Q  Q  G    N  V  F    S  C  S    V  M  H
1306    AGCAGGTGG  CAGCAGGGG  AACGTCTTC  TCATGCTCC  GTGATGCAT
        TCGTCCACC  GTCGTCCCC  TTGCAGAAG  AGTACGAGG  CACTACGTA
        E  A  L    H  N  H    Y  T  Q    K  S  L    S  L  S
1351    GAGGCTCTG  CACAACCAC  TACACGCAG  AAGAGCCTC  TCCCTGTCT
        CTCCGAGAC  GTGTTGGTG  ATGTGCGTC  TTCTCGGAG  AGGGACAGA
        P  G  K    *
1396    CCGGGTAAA  TGA
        GGCCCATTT  ACT
```

FIGURE 8B