0 4 DEC 2004

FIGURE 1

SEQ ID NO:1

```
1   MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN
51  LNDQVLFIDQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFFQR SVPGHDNKMQ
151 FESSSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED
```

FIGURE 2

SEQ ID NO:2

```
1                                                    50
ATGGCTGCTG AACCAGTAGA AGACAATTGC ATCAACTTTG TGGCAATGAA
51                                                   100
ATTTATTGAC AATACGCTTT ACTTTATAGC TGAAGATGAT GAAAACCTGG
101                                                  150
AATCAGATTA CTTTGGCAAG CTTGAGAGCA AACTATCGGT CATtCGTAAT
151                                                  200
TTAAATGACC AGGTCCTATT TATCGACCAA GGGAATCGTC CACTATTCGA
201                                                  250
GGACATGACA GACAGTGACT GCCGAGACAA TGCGCCGCGA ACCATtTTCA
251                                                  300
TTATATCTAT GTACAAGGAT TCTCAGCCGC GCGGAATGGC CGTAACTATT
301                                                  350
TCTGTCAAAT GTGAAAAGAT ATCCACGCTG TCGTGTGAGA ACAAgATtAT
351                                                  400
tAGTTTCAAA GAGATGAATC CGCCGGATAA TATCAAGGAC ACGAAGTCTG
401                                                  450
ATATCATATT TTTCCAGCGC AGCGTGCCGG GGCACGATAA CAAGATGCAA
451                                                  500
TTTGAATCAT CCAGCTATGA AGGGTACTTT CTTGCATGCG AGAAGGAACG
501                                                  550
CGATCTCTTT AAACTTATTT TAAAGAAAGA GGACGAGCTA GGCGATCGCA
551                                  582
GCATtATGTT CACTGTCCAA AATGAAGACT AG
```

FIGURE 3

SEQ ID NO:3

```
1   YFGKLESKLS VIRNLNDQVL FIDQGNRPLF EDMTDSDCRD NAPRTIFIIS
51  MYKDSQPRGM AVTISVKCEK ISTLSCENKI ISFKEMNPPD NIKDTKSDII
101 FFQRSVPGHD NKMQFESSSY EGYFLACEKE RDLFKLILKK EDELGDRSIM
```

151 FTVQNED

FIGURE 4

SEQ ID NO:4

1 MGHHHHHHGA LKLCPHEEFL RLCKERAEEI YPIKERNNRT RLALIICNTE
51 FDHLPPRNGA DFDITGMKEL LEGLDYSVDV EENLTARDME SALRAFATRP
101 EHKSSDSTFL VLMSHGILEG ICGTVHDEKK PDVLLYDTIF QIFNNRNCLS
151 LKDKPKVIIV QACRGANRGE LWVRDSPTSL EVASSQSSEN LEEDAVYKTH
201 VEKDFIAFCS STPHNVSWRD STMGSIFITQ LITCFQKYSW CCHLEEVFRK
252 VQQSFETPRA KAQMPTIERL SMTRYFYLFP GN

FIGURE 5

SEQ ID NO: 5

1 ATGGGCCATC ATCATCATCA TCATGGCGCC CTCAAGCTTT GTCCTCATGA 50
51 AGAATTCCTG AGACTATGTA AAGAAAGAGC TGAAGAGATC TATCCAATAA 100
101 AGGAGAGAAA CAACCGCACA CGCCTGGCTC TCATCATATG CAATACAGAG 150
151 TTTGACCATC TGCCTCCGAG GAATGGAGCT GACTTTGACA TCACAGGGAT 200
201 GAAGGAGCTA CTTGAGGGTC TGGACTATAG TGTAGATGTA GAAGAGAATC 250
251 TGACAGCCAG GGATATGGAG TCAGCGCTGA GGGCATTTGC TACCAGACCA 300
301 GAGCACAAGT CCTCTGACAG CACATTCTTG GTACTCATGT CTCATGGCAT 350
351 CCTGGAGGGA ATCTGCGGAA CTGTGCATGA TGAGAAAAAA CCAGATGTGC 400
401 TGCTTTATGA CACCATCTTC CAGATATTCA ACAACCGCAA CTGCCTCAGT 450
451 CTGAAGGACA AACCCAAGGT CATCATTGTC CAGGCCTGCA GAGGTGCAAA 500
501 CCGTGGGGAA CTGTGGGTCA GAGACTCTCC AGCATCCTTG GAAGTGGCCT 550
551 CTTCACAGTC ATCTGAGAAC CTGGAGGAAG ATGCTGTTTA CAAGACCCAC 600
601 GTGGAGAAGG ACTTCATTGC TTTCTGCTCT TCAACGCCAC ACAACGTGTC 650
651 CTGGAGAGAC AGCACAATGG GCTCTATCTT CATCACACAA CTCATCACAT 700
701 GCTTCCAGAA ATATTCTTGG TGCTGCCACC TAGAGGAAGT ATTTCGGAAG 750
751 800

GTACAGCAAT CATTTGAAAC TCCAAGGGCC AAAGCTCAAA TGCCCACCAT
801 849
AGAACGACTG TCCATGACAA GATATTTCTA CCTCTTTCCT GGCAATTGA

FIGURE 6

SEQ ID NO:6

1 MGHHHHHHGI LKLCPREEFL RLCKKNHDEI YPIKKREDRR RLALIICNTK
51 FDHLPARNGA HYDIVGMKRL LQGLGYTVVD EKNLTARDME SVLRAFAARP
101 EHKSSDSTFL VLMSHGILEG ICGTAHKKKK PDVLLYDTIF QIFNNRNCLS
151 LKDKPKVIIV QACRGEKHGE LWVRDSPASL AVISSQSSEN LEADSVCKIH
201 EEKDFIAFCS STPHNVSWRD RTRGSIFITE LITCFQKYSC CCHLMEIFRK
251 VQKSFEVPQA KAQMPTIERA TLTRDFYLFP GN

FIGURE 7

SEQ ID NO:7

1 50
ATGGGCCATC ATCATCATCA TCATGGCATA CTCAAACTTT GTCCTCGTGA
51 100
AGAATTCCTG AGACTGTGTA AAAAAAATCA TGATGAGATC TATCCAATAA
101 150
AAAAGAGAGA GGACCGCAGA CGCCTGGCTC TCATCATATG CAATACAAAG
151 200
TTTGATCACC TGCCTGCAAG GAATGGGGCT CACTATGACA TCGTGGGGAT
201 250
GAAAAGGCTG CTTCAAGGCC TGGGCTACAC TGTGGTTGAC GAAAAGAATC
251 300
TCACAGCCAG GGATATGGAG TCAGTGCTGA GGGCATTTGC TGCCAGACCA
301 350
GAGCACAAGT CCTCTGACAG CACGTTCTTG GTACTCATGT CTCATGGCAT
351 400
CCTAGAGGGA ATCTGCGGAA CTGCGCATAA AAAGAAAAAA CCGGATGTGC
401 450
TGCTTTATGA CACCATCTTC CAGATATTCA ACAACCGCAA CTGCCTCAGT
451 500
CTAAAGGACA AACCCAAGGT CATCATTGTC CAGGCCTGCA GAGGTGAAAA
501 550
ACATGGGGAA CTCTGGGTCA GAGACTCTCC AGCATCCTTG GCAGTCATCT
551 600
CTTCACAGTC ATCTGAGAAC CTGGAGGCAG ATTCTGTTTG CAAGATCCAC
601 650
GAGGAGAAGG ACTTCATTGC TTTCTGTTCT TCAACACCAC ATAACGTGTC
651 700
CTGGAGAGAC CGCACAAGGG GCTCCATCTT CATTACGGAA CTCATCACAT

```
701                                                          750
GCTTCCAGAA ATATTCTTGC TGCTGCCACC TAATGGAAAT ATTTCGGAAG
751                                                          800
GTACAGAAAT CATTTGAAGT TCCACAGGCT AAAGCCCAGA TGCCCACCAT
801                                                          849
AGAACGAGCA ACCTTGACAA GAGATTTCTA CCTCTTTCCT GGCAATTGA
```

FIGURE 8.



FIGURE 9.

SEQ ID NO:8

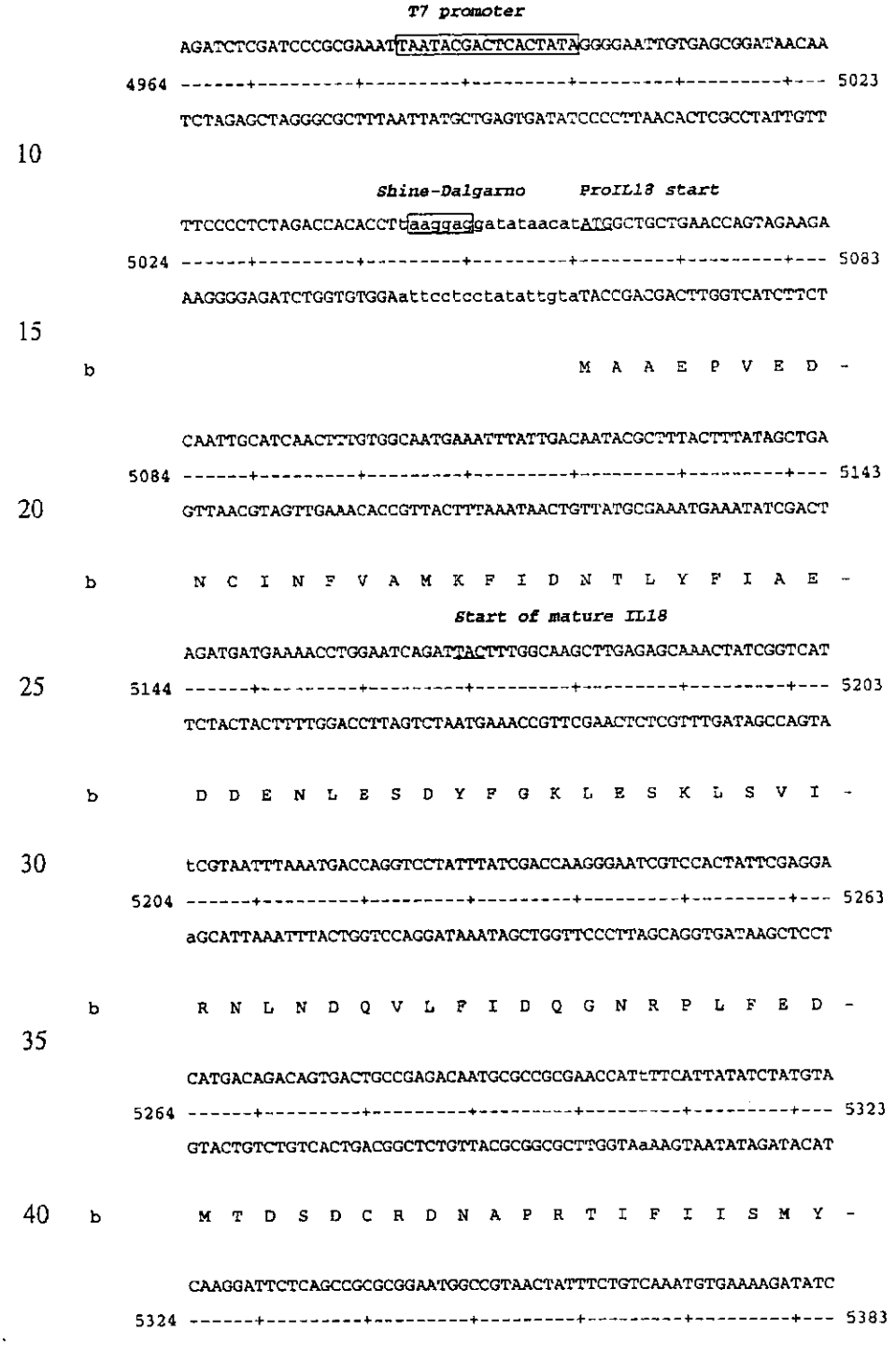
```
1                                                            50
AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG
51                                                           100
CGGATAACAA TTCCCCTCTA GACCACACCT taaggaggat ataacatATG
101                                                          150
GCTGCTGAAC CAGTAGAAGA CAATTGCATC AACTTTGTGG CAATGAAATT
151                                                          200
TATTGACAAT ACGCTTTACT TTATAGCTGA AGATGATGAA AACCTGGAAT
201                                                          250
CAGATTACTT TGGCAAGCTT GAGAGCAAAC TATCGGTCAT tCGTAATTTA
251                                                          300
AATGACCAGG TCCTATTTAT CGACCAAGGG AATCGTCCAC TATTCGAGGA
301                                                          350
CATGACAGAC AGTGACTGCC GAGACAATGC GCCGCGAACC ATtTTCATTA
351                                                          400
TATCTATGTA CAAGGATTCT CAGCCGCGCG GAATGGCCGT AACTATTTCT
401                                                          450
GTCAAATGTG AAAAGATATC CACGCTGTCG TGTGAGAACA AgATtATtAG
451                                                          500
TTTCAAAGAG ATGAATCCGC CGGATAATAT CAAGGACACG AAGTCTGATA
501                                                          550
TCATATTTTT CCAGCGCAGC GTGCCGGGGC ACGATAACAA GATGCAATTT
551                                                          600
GAATCATCCA GCTATGAAGG GTACTTTCTT GCATGCGAGA AGGAACGCGA
601                                                          650
TCTCTTTAAA CTTATTTTAA AGAAAGAGGA CGAGCTAGGC GATCGCAGCA
```

651 700
TtATGTTCAC TGTCCAAAAT GAAGACTAGT ggaggatata aTACCAgGaa
701 750
taaataaaat ccatgGgcca tcatcatcat catcatggcG CCCTCAAGCT
751 800
TTGTCCTCAT GAAGAATTCC TGAGACTATG TAAAGAAAGA GCTGAAGAGA
801 850
TCTATCCAAT AAAGGAGAGA AACAACCGCA CACGCCTGGC TCTCATCATA
851 900
TGCAATACAG AGTTTGACCA TCTGCCTCCG AGGAATGGAG CTGACTTTGA
901 950
CATCACAGGG ATGAAGGAGC TACTTGAGGG TCTGGACTAT AGTGTAGATG
951 1000
TAGAAGAGAA TCTGACAGCC AGGGATATGG AGTCAGCGCT GAGGGCATTT
1001 1050
GCTACCAGAC CAGAGCACAA GTCCTCTGAC AGCACATTCT TGGTACTCAT
1051 1100
GTCTCATGGC ATCCTGGAGG GAATCTGCGG AACTGTGCAT GATGAGAAAA
1101 1150
AACCAGATGT GCTGCTTTAT GACACCATCT TCCAGATATT CAACAACCGC
1151 1200
AACTGCCTCA GTCTGAAGGA CAAACCCAAG GTCATCATTG TCCAGGCCTG
1201 1250
CAGAGGTGCA AACCGTGGGG AACTGTGGGT CAGAGACTCT CCAGCATCCT
1251 1300
TGGAAGTGGC CTCTTCACAG TCATCTGAGA ACCTGGAGGA AGATGCTGTT
1301 1350
TACAAGACCC ACGTGGAGAA GGACTTCATT GCTTTCTGCT CTTCAACGCC
1351 1400
ACACAACGTG TCCTGGAGAG ACAGCACAAT GGGCTCTATC TTCATCACAC
1401 1450
AACTCATCAC ATGCTTCCAG AAATATTCTT GGTGCTGCCA CCTAGAGGAA
1451 1500
GTATTTCGGA AGGTACAGCA ATCATTTGAA ACTCCAAGGG CCAAAGCTCA
1501 1550
AATGCCCACC ATAGAACGAC TGTCCATGAC AAGATATTTC TACCTCTTTC
1551 1600
CTGGCAATTG AAAATGGATC CGAATTCGAG CTCCGTCGAC AAGCTTGCGG
1601 1650
CCGCACTCGA GCACCACCAC CACCACCACT GAGATCCGGC TGCTAACAAA
1651 1700
GCCCGAAAGG AAGCTGAGTT GGCTGCTGCC ACCGCTGAGC AATAACTAGC

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1701 1743
ATAACCCCTT GGGGCCTCTA AACGGGTCTT GAGGGGTTTT TTG

FIGURE 10.



```
          GTTCCTAAGAGTCGGCGCGCCTTACCGGCATTGATAAAGACAGTTTACACTTTTCTATAG

    b      K  D  S  Q  P  R  G  M  A  V  T  I  S  V  K  C  E  K  I  S  -

5         CACGCTGTCGTGTGAGAACAAgATtATtAGTTTCAAAGAGATGAATCCGCCGGATAATAT
       5384 ------+---------+---------+---------+---------+---------+--- 5443
          GTGCGACAGCACACTCTTGTTcTAaTAaTCAAAGTTTCTCTACTTAGGCGGCCTATTATA

    b      T  L  S  C  Z  N  K  I  I  S  F  K  E  M  N  P  P  D  N  I  -
10
          CAAGGACACGAAGTCTGATATCATATTTTTCCAGCGCAGCGTGCCGGGGCACGATAACAA
       5444 ------+---------+---------+---------+---------+---------+--- 5503
          GTTCCTGTGCTTCAGACTATAGTATAAAAAGGTCGCGTCGCACGGCCCCGTGCTATTGTT

15  b      K  D  T  K  S  D  I  I  F  F  Q  R  S  V  P  G  H  D  N  K  -

          GATGCAATTTGAATCATCCAGCTATGAAGGGTACTTTCTTGCATGCGAGAAGGAACGCGA
       5504 ------+---------+---------+---------+---------+---------+--- 5563
          CTACGTTAAACTTAGTAGGTCGATACTTCCCATGAAAGAACGTACGCTCTTCCTTGCGCT
20
    b      M  Q  F  E  S  S  S  Y  E  G  Y  F  L  A  C  E  K  E  R  D  -

          TCTCTTTAAACTTATTTTAAAGAAAGAGGACGAGCTAGGCGATCGCAGCATtATGTTCAC
       5564 ------+---------+---------+---------+---------+---------+--- 5623
25        AGAGAAATTTGAATAAAATTTCTTTCTCCTGCTCGATCCGCTAGCGTCGTAaTACAAGTG

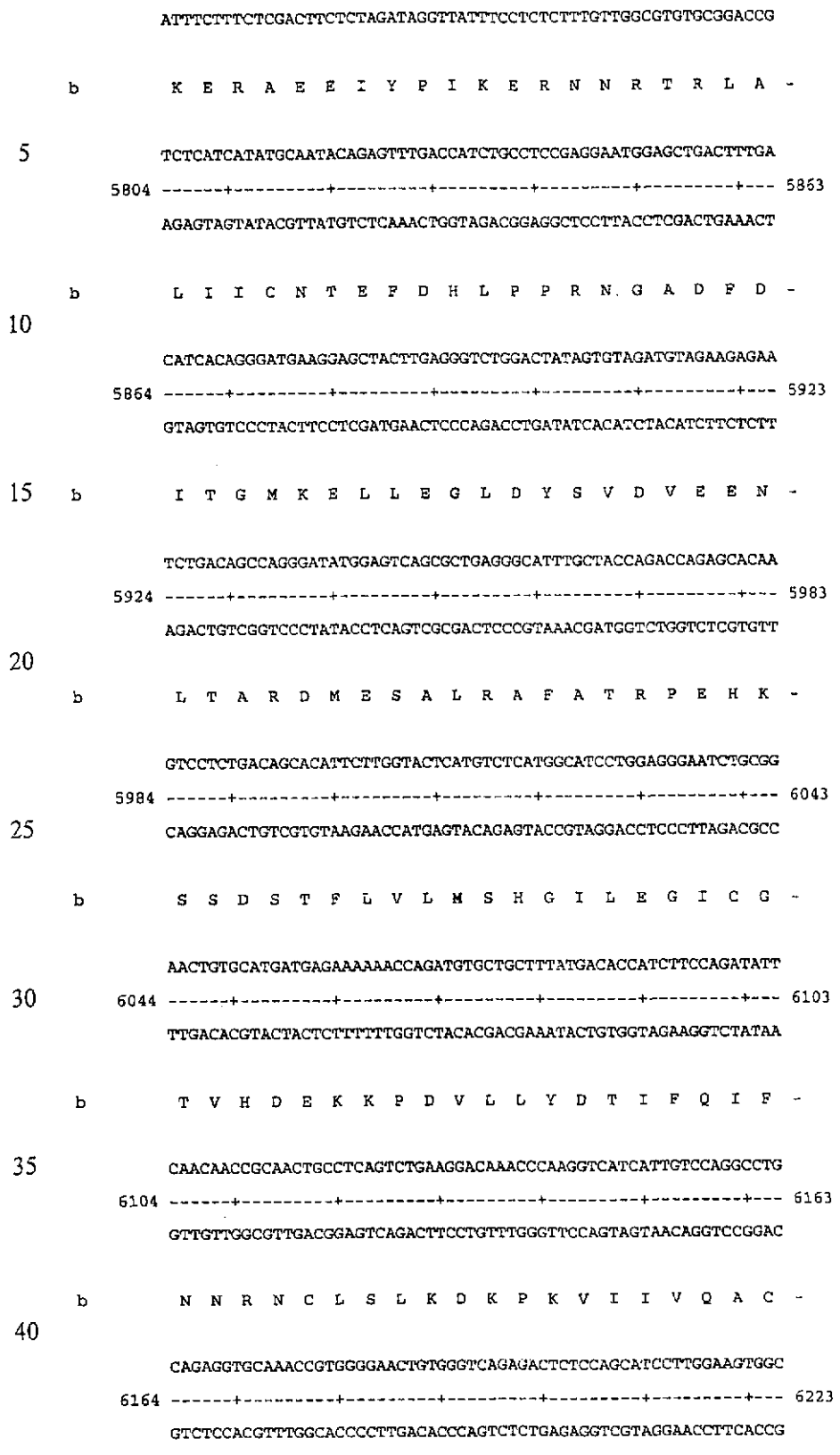
    b      L  F  K  L  I  L  K  K  E  D  E  L  G  D  R  S  I  M  F  T  -

                                  Defective Shine-Dalgarno    Start of Caspase-4
30        TGTCCAAAATGAAGACTAGTggaggatataaTACCAgGaataaataaaatccatgGgcca
       5624 ------+---------+---------+---------+---------+---------+--- 5683
          ACAGGTTTTACTTCTGATCAcctcctatattATGGTcCttatttatttttaggtacCcggt

    b      V  Q  N  E  D                                          M  G  H  -
35
          tcatcatcatcatcatggcGCCCTCAAGCTTTGTCCTCATGAAGAATTCCTGAGACTATG
       5684 ------+---------+---------+---------+---------+---------+--- 5743
          agtagtagtagtagtaccgCGGGAGTTCGAAACAGGAGTACTTCTTAAGGACTCTGATAC

40  b      H  H  H  H  H  G  A  L  K  L  C  P  H  E  E  F  L  R  L  C  -

          TAAAGAAAGAGCTGAAGAGATCTATCCAATAAAGGAGAGAAACAACCGCACACGCCTGGC
       5744 ------+---------+---------+---------+---------+---------+--- 5803
```


ATTTCTTTCTCGACTTCTCTAGATAGGTTATTTCCTCTCTTTGTTGGCGTGTGCGGACCG
b K E R A E E I Y P I K E R N N R T R L A -
TCTCATCATATGCAATACAGAGTTTGACCATCTGCCTCCGAGGAATGGAGCTGACTTTGA
5804 ------+---------+---------+---------+---------+---------+--- 5863
AGAGTAGTATACGTTATGTCTCAAACTGGTAGACGGAGGCTCCTTACCTCGACTGAAACT
b L I I C N T E F D H L P P R N G A D F D -
CATCACAGGGATGAAGGAGCTACTTGAGGGTCTGGACTATAGTGTAGATGTAGAAGAGAA
5864 ------+---------+---------+---------+---------+---------+--- 5923
GTAGTGTCCCTACTTCCTCGATGAACTCCCAGACCTGATATCACATCTACATCTTCTCTT
b I T G M K E L L E G L D Y S V D V E E N -
TCTGACAGCCAGGGATATGGAGTCAGCGCTGAGGGCATTTGCTACCAGACCAGAGCACAA
5924 ------+---------+---------+---------+---------+---------+--- 5983
AGACTGTCGGTCCCTATACCTCAGTCGCGACTCCCGTAAACGATGGTCTGGTCTCGTGTT
b L T A R D M E S A L R A F A T R P E H K -
GTCCTCTGACAGCACATTCTTGGTACTCATGTCTCATGGCATCCTGGAGGGAATCTGCGG
5984 ------+---------+---------+---------+---------+---------+--- 6043
CAGGAGACTGTCGTGTAAGAACCATGAGTACAGAGTACCGTAGGACCTCCCTTAGACGCC
b S S D S T F L V L M S H G I L E G I C G -
AACTGTGCATGATGAGAAAAAACCAGATGTGCTGCTTTATGACACCATCTTCCAGATATT
6044 ------+---------+---------+---------+---------+---------+--- 6103
TTGACACGTACTACTCTTTTTTGGTCTACACGACGAAATACTGTGGTAGAAGGTCTATAA
b T V H D E K K P D V L L Y D T I F Q I F -
CAACAACCGCAACTGCCTCAGTCTGAAGGACAAACCCAAGGTCATCATTGTCCAGGCCTG
6104 ------+---------+---------+---------+---------+---------+--- 6163
GTTGTTGGCGTTGACGGAGTCAGACTTCCTGTTTGGGTTCCAGTAGTAACAGGTCCGGAC
b N N R N C L S L K D K P K V I I V Q A C -
CAGAGGTGCAAACCGTGGGGAACTGTGGGTCAGAGACTCTCCAGCATCCTTGGAAGTGGC
6164 ------+---------+---------+---------+---------+---------+--- 6223
GTCTCCACGTTTGGCACCCCTTGACACCCAGTCTCTGAGAGGTCGTAGGAACCTTCACCG

```
    b       R  G  A  N  R  G  E  L  W  V  R  D  S  P  A  S  L  E  V  A  -

            CTCTTCACAGTCATCTGAGAACCTGGAGGAAGATGCTGTTTACAAGACCCACGTGGAGAA
    6224 ------+---------+---------+---------+---------+---------+--- 6283
            GAGAAGTGTCAGTAGACTCTTGGACCTCCTTCTACGACAAATGTTCTGGGTGCACCTCTT

    b       S  S  Q  S  S  E  N  L  E  E  D  A  V  Y  K  T  H  V  E  K  -

            GGACTTCATTGCTTTCTGCTCTTCAACGCCACACAACGTGTCCTGGAGAGACAGCACAAT
    6284 ------+---------+---------+---------+---------+---------+--- 6343
            CCTGAAGTAACGAAAGACGAGAAGTTGCGGTGTGTTGCACAGGACCTCTCTGTCGTGTTA

    b       D  F  I  A  F  C  S  S  T  P  H  N  V  S  W  R  D  S  T  M  -

            GGGCTCTATCTTCATCACACAACTCATCACATGCTTCCAGAAATATTCTTGGTGCTGCCA
    6344 ------+---------+---------+---------+---------+---------+--- 6403
            CCCGAGATAGAAGTAGTGTGTTGAGTAGTGTACGAAGGTCTTTATAAGAACCACGACGGT

    b       G  S  I  F  I  T  Q  L  I  T  C  F  Q  K  Y  S  W  C  C  H  -

            CCTAGAGGAAGTATTTCGGAAGGTACAGCAATCATTTGAAACTCCAAGGGCCAAAGCTCA
    6404 ------+---------+---------+---------+---------+---------+--- 6463
            GGATCTCCTTCATAAAGCCTTCCATGTCGTTAGTAAACTTTGAGGTTCCCGGTTTCGAGT

    b       L  E  E  V  F  R  K  V  Q  Q  S  F  E  T  P  R  A  K  A  Q  -

            AATGCCCACCATAGAACGACTGTCCATGACAAGATATTTCTACCTCTTTCCTGGCAATTG
    6464 ------+---------+---------+---------+---------+---------+--- 6523
            TTACGGGTGGTATCTTGCTGACAGGTACTGTTCTATAAAGATGGAGAAAGGACCGTTAAC

    b       M  P  T  I  E  R  L  S  M  T  R  Y  F  Y  L  F  P  G  N  *  -

            AAAATGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCAC
    6524 ------+---------+---------+---------+---------+---------+--- 6583
            TTTTACCTAGGCTTAAGCTCGAGGCAGCTGTTCGAACGCCGGCGTGAGCTCGTGGTGGTG

    b       K  W  I  R  I  R  A  P  S  T  S  L  R  P  H  S  S  T  T  T  -

            CACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCC
    6584 ------+---------+---------+---------+---------+---------+--- 6643
            GTGGTGGTGACTCTAGGCCGACGATTGTTTCGGGCTTTCCTTCGACTCAACCGACGACGG
```

```
b        T  T  T  E  I  R  L  L  T  K  P  E  R  K  L  S  W  L  L  P  -
                                  T7 Terminator
         ACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTT
      6644 ------+---------+---------+---------+---------+---------+--- 6703
         TGGCGACTCGTTATTGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAA

b        P  L  S  N  N  *  H  N  P  L  G  P  L  N  G  S  *  G  V  F  -

         TTG
      6704 --- 6706
         AAC
```

FIGURE 11.

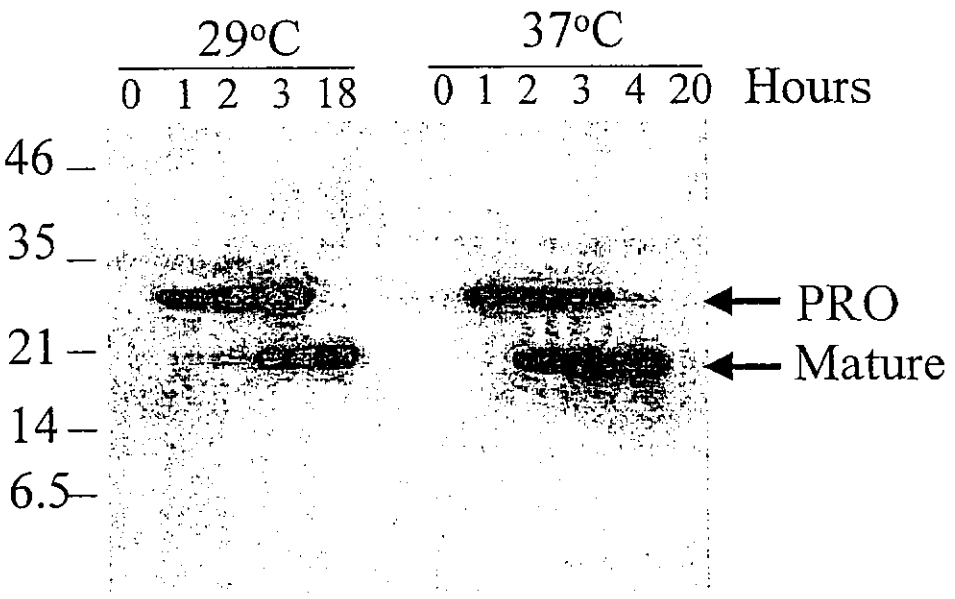


FIGURE 12.



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FIGURE 13.
SEQ ID NO:9

1 50
ATGGCTGCTG AACCAGTAGA AGACAATTGC ATCAACTTTG TGGCAATGAA
51 100
ATTTATTGAC AATACGCTTT ACTTTATAGC TGAAGATGAT GAAAACCTGG
101 150
AATCAGATTA CTTTGGCAAG CTTGAGAGCA AACTATCGGT CATTCGTAAT
151 200
TTAAATGACC AGGTCCTATT TATCGACCAA GGGAATCGTC CACTATTCGA
201 250
GGACATGACA GACAGTGACT GCCGAGACAA TGCGCCGCGA ACCATTTTCA
251 300
TTATATCTAT GTACAAGGAT TCTCAGCCGC GCGGAATGGC CGTAACTATT
301 350
TCTGTCAAAT GTGAAAAGAT ATCCACGCTG TCGTGTGAGA ACAAGATTAT
351 400
TAGTTTCAAA GAGATGAATC CGCCGGATAA TATCAAGGAC ACGAAGTCTG
401 450
ATATCATATT TTTCCAGCGC AGCGTGCCGG GGCACGATAA CAAGATGCAA
451 500
TTTGAATCAT CCAGCTATGA AGGGTACTTT CTTGCATGCG AGAAGGAACG
501 550
CGATCTCTTT AAACTTATTT TAAAGAAAGA GGACGAGCTA GGCGATCGCA
551 600
IGCATTATGTT CACTGTCCAA AATGAAGACT AGTGGAGGAT ATAATACCAG
601 650
GAATAAATAA AATCCATGGG CCATCATCAT CATCATCATG GCATACTCAA
651 700
ACTTTGTCCT CGTGAAGAAT TCCTGAGACT GTGTAAAAAA AATCATGATG
701 750
AGATCTATCC AATAAAAAAG AGAGAGGACC GCAGACGCCT GGCTCTCATC
751 800
ATATGCAATA CAAAGTTTGA TCACCTGCCT GCAAGGAATG GGGCTCACTA
801 850
TGACATCGTG GGGATGAAAA GGCTGCTTCA AGGCCTGGGC TACACTGTGG
851 900
TTGACGAAAA GAATCTCACA GCCAGGGATA TGGAGTCAGT GCTGAGGGCA
901 950
TTTGCTGCCA GACCAGAGCA CAAGTCCTCT GACAGCACGT TCTTGGTACT
951 1000
CATGTCTCAT GGCATCCTAG AGGGAATCTG CGGAACTGCG CATAAAAAGA
1001 1050

```
AAAAACCGGA TGTGCTGCTT TATGACACCA TCTTCCAGAT ATTCAACAAC
1051                                                1100
CGCAACTGCC TCAGTCTAAA GGACAAACCC AAGGTCATCA TTGTCCAGGC
1101                                                1150
CTGCAGAGGT GAAAAACATG GGGAACTCTG GGTCAGAGAC TCTCCAGCAT
1151                                                1200
CCTTGGCAGT CATCTCTTCA CAGTCATCTG AGAACCTGGA GGCAGATTCT
1201                                                1250
GTTTGCAAGA TCCACGAGGA GAAGGACTTC ATTGCTTTCT GTTCTTCAAC
1251                                                1300
ACCACATAAC GTGTCCTGGA GAGACCGCAC AAGGGGCTCC ATCTTCATTA
1301                                                1350
CGGAACTCAT CACATGCTTC CAGAAATATT CTTGCTGCTG CCACCTAATG
1351                                                1400
GAAATATTTC GGAAGGTACA GAAATCATTT GAAGTTCCAC AGGCTAAAGC
1401                                                1450
CCAGATGCCC ACCATAGAAC GAGCAACCTT GACAAGAGAT TTCTACCTCT
1451        1464
TTCCTGGCAA TTGA
```

FIGURE 14.

```
          GCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGATCTCGATCCCGCGA
      4921 ---------+---------+---------+---------+---------+---------+ 4980
          CGCGGCCACTACGGCCGGTGCTACGCAGGCCGCATCTCCTAGCTCTAGAGCTAGGGCGCT

      c     A  G  D  A  G  H  D  A  S  G  V  E  D  R  D  L  D  P  A  K -
                T7 Promoter
          AATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGACCACA
      4981 ---------+---------+---------+---------+---------+---------+ 5040
          TTAATTATGCTGAGTGATATCCCCTTAACACTCGCCTATTGTTAAGGGGAGATCTGGTGT

      c     L  I  R  L  T  I  G  E  L  *  A  D  N  N  S  P  L  D  H  T -
              Shine-Dalgarno   ProIL18 start
          CCTtaaggaggatataacatATGGCTGCTGAACCAGTAGAAGACAATTGCATCAACTTTG
      5041 ---------+---------+---------+---------+---------+---------+ 5100
          GGAattcctcctatattgtaTACCGACGACTTGGTCATCTTCTGTTAACGTAGTTGAAAC

      c     L  R  R  I  *  H  M  A  A  E  P  V  E  D  N  C  I  N  F  V -

          TGGCAATGAAATTTATTGACAATACGCTTTACTTTATAGCTGAAGATGATGAAAACCTGG
      5101 ---------+---------+---------+---------+---------+---------+ 5160
          ACCGTTACTTTAAATAACTGTTATGCGAAATGAAATATCGACTTCTACTACTTTTGGACC

      c     A  M  K  F  I  D  N  T  L  Y  F  I  A  E  D  D  E  N  L  E -
```

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Start of mature IL18

```
          AATCAGATTACTTTGGCAAGCTTGAGAGCAAACTATCGGTCATtCGTAATTTAAATGACC
      5161 ---------+---------+---------+---------+---------+---------+ 5220
          TTAGTCTAATGAAACCGTTCGAACTCTCGTTTGATAGCCAGTAaGCATTAAATTTACTGG

c           S  D  Y  F  G  K  L  E  S  K  L  S  V  I  R  N  L  N  D  Q -

          AGGTCCTATTTATCGACCAAGGGAATCGTCCACTATTCGAGGACATGACAGACAGTGACT
      5221 ---------+---------+---------+---------+---------+---------+ 5280
          TCCAGGATAAATAGCTGGTTCCCTTAGCAGGTGATAAGCTCCTGTACTGTCTGTCACTGA

c           V  L  F  I  D  Q  G  N  R  P  L  F  E  D  M  T  D  S  D  C -

          GCCGAGACAATGCGCCGCGAACCATtTTCATTATATCTATGTACAAGGATTCTCAGCCGC
      5281 ---------+---------+---------+---------+---------+---------+ 5340
          CGGCTCTGTTACGCGGCGCTTGGTAaAAGTAATATAGATACATGTTCCTAAGAGTCGGCG

c           R  D  N  A  P  R  T  I  F  I  I  S  M  Y  K  D  S  Q  P  R -

          GCGGAATGGCCGTAACTATTTCTGTCAAATGTGAAAAGATATCCACGCTGTCGTGTGAGA
      5341 ---------+---------+---------+---------+---------+---------+ 5400
          CGCCTTACCGGCATTGATAAAGACAGTTTACACTTTTCTATAGGTGCGACAGCACACTCT

c           G  M  A  V  T  I  S  V  K  C  E  K  I  S  T  L  S  C  E  N -

          ACAAgATtATtAGTTTCAAAGAGATGAATCCGCCGGATAATATCAAGGACACGAAGTCTG
      5401 ---------+---------+---------+---------+---------+---------+ 5460
          TGTTcTAaTAaTCAAAGTTTCTCTACTTAGGCGGCCTATTATAGTTCCTGTGCTTCAGAC

c           K  I  I  S  F  K  E  M  N  P  P  D  N  I  K  D  T  K  S  D -

          ATATCATATTTTTCCAGCGCAGCGTGCCGGGGCACGATAACAAGATGCAATTTGAATCAT
      5461 ---------+---------+---------+---------+---------+---------+ 5520
          TATAGTATAAAAAGGTCGCGTCGCACGGCCCCGTGCTATTGTTCTACGTTAAACTTAGTA

c           I  I  F  F  Q  R  S  V  P  G  H  D  N  K  M  Q  F  E  S  S -

          CCAGCTATGAAGGGTACTTTCTTGCATGCGAGAAGGAACGCGATCTCTTTAAACTTATTT
      5521 ---------+---------+---------+---------+---------+---------+ 5580
          GGTCGATACTTCCCATGAAAGAACGTACGCTCTTCCTTGCGCTAGAGAAATTTGAATAAA

c           S  Y  E  G  Y  F  L  A  C  E  K  E  R  D  L  F  K  L  I  L -

          TAAAGAAAGAGGACGAGCTAGGCGATCGCAGCATtATGTTCACTGTCCAAAATGAAGACT
      5581 ---------+---------+---------+---------+---------+---------+ 5640
          ATTTCTTTCTCCTGCTCGATCCGCTAGCGTCGTAaTACAAGTGACAGGTTTTACTTCTGA

c           K  K  E  D  E  L  G  D  R  S  I  M  F  T  V  Q  N  E  D  * -
```

Defective Shine-Dalgarno Start Caspase 5

```
          AGTggaggatataaTACCAgGaataaataaaatccatgGgccatcatcatcatcatcatg
```

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```
          5641 ---------+---------+---------+---------+---------+---------+ 5700
               TCAcctcctatattATGGTcCttatttatttaggtacCcggtagtagtagtagtagtac

     c           W  R  I  *  Y  Q  E  *  I  K  S  M  G  H  H  H  H  H  H  G -

               gcATACTCAAACTTTGTCCTCGTGAAGAATTCCTGAGACTGTGTAAAAAAAATCATGATG
          5701 ---------+---------+---------+---------+---------+---------+ 5760
               cgTATGAGTTTGAAACAGGAGCACTTCTTAAGGACTCTGACACATTTTTTTTAGTACTAC

     c           I  L  K  L  C  P  R  E  E  F  L  R  L  C  K  K  N  H  D  E -

               AGATCTATCCAATAAAAAAGAGAGAGGACCGCAGACGCCTGGCTCTCATCATATGCAATA
          5761 ---------+---------+---------+---------+---------+---------+ 5820
               TCTAGATAGGTTATTTTTTCTCTCTCCTGGCGTCTGCGGACCGAGAGTAGTATACGTTAT

     c           I  Y  P  I  K  K  R  E  D  R  R  R  L  A  L  I  I  C  N  T -

               CAAAGTTTGATCACCTGCCTGCAAGGAATGGGGCTCACTATGACATCGTGGGGATGAAAA
          5821 ---------+---------+---------+---------+---------+---------+ 5880
               GTTTCAAACTAGTGGACGGACGTTCCTTACCCCGAGTGATACTGTAGCACCCCTACTTTT

     c           K  F  D  H  L  P  A  R  N  G  A  H  Y  D  I  V  G  M  K  R -

               GGCTGCTTCAAGGCCTGGGCTACACTGTGGTTGACGAAAAGAATCTCACAGCCAGGGATA
          5881 ---------+---------+---------+---------+---------+---------+ 5940
               CCGACGAAGTTCCGGACCCGATGTGACACCAACTGCTTTTCTTAGAGTGTCGGTCCCTAT

     c           L  L  Q  G  L  G  Y  T  V  V  D  E  K  N  L  T  A  R  D  M -

               TGGAGTCAGTGCTGAGGGCATTTGCTGCCAGACCAGAGCACAAGTCCTCTGACAGCACGT
          5941 ---------+---------+---------+---------+---------+---------+ 6000
               ACCTCAGTCACGACTCCCGTAAACGACGGTCTGGTCTCGTGTTCAGGAGACTGTCGTGCA

     c           E  S  V  L  R  A  F  A  A  R  P  E  H  K  S  S  D  S  T  F -

               TCTTGGTACTCATGTCTCATGGCATCCTAGAGGGAATCTGCGGAACTGCGCATAAAAAGA
          6001 ---------+---------+---------+---------+---------+---------+ 6060
               AGAACCATGAGTACAGAGTACCGTAGGATCTCCCTTAGACGCCTTGACGCGTATTTTTCT

     c           L  V  L  M  S  H  G  I  L  E  G  I  C  G  T  A  H  K  K  K -

               AAAAACCGGATGTGCTGCTTTATGACACCATCTTCCAGATATTCAACAACCGCAACTGCC
          6061 ---------+---------+---------+---------+---------+---------+ 6120
               TTTTTGGCCTACACGACGAAATACTGTGGTAGAAGGTCTATAAGTTGTTGGCGTTGACGG

     c           K  P  D  V  L  L  Y  D  T  I  F  Q  I  F  N  N  R  N  C  L -

               TCAGTCTAAAGGACAAACCCAAGGTCATCATTGTCCAGGCCTGCAGAGGTGAAAAACATG
          6121 ---------+---------+---------+---------+---------+---------+ 6180
               AGTCAGATTTCCTGTTTGGGTTCCAGTAGTAACAGGTCCGGACGTCTCCACTTTTTGTAC
```

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```
    c        S  L  K  D  K  P  K  V  I  I  V  Q  A  C  R  G  E  K  H  G -

             GGGAACTCTGGGTCAGAGACTCTCCAGCATCCTTGGCAGTCATCTCTTCACAGTCATCTG
       6181 ---------+---------+---------+---------+---------+---------+ 6240
             CCCTTGAGACCCAGTCTCTGAGAGGTCGTAGGAACCGTCAGTAGAGAAGTGTCAGTAGAC

    c        E  L  W  V  R  D  S  P  A  S  L  A  V  I  S  S  Q  S  S  E -

             AGAACCTGGAGGCAGATTCTGTTTGCAAGATCCACGAGGAGAAGGACTTCATTGCTTTCT
       6241 ---------+---------+---------+---------+---------+---------+ 6300
             TCTTGGACCTCCGTCTAAGACAAACGTTCTAGGTGCTCCTCTTCCTGAAGTAACGAAAGA

    c        N  L  E  A  D  S  V  C  K  I  H  E  E  K  D  F  I  A  F  C -

             GTTCTTCAACACCACATAACGTGTCCTGGAGAGACCGCACAAGGGGCTCCATCTTCATTA
       6301 ---------+---------+---------+---------+---------+---------+ 6360
             CAAGAAGTTGTGGTGTATTGCACAGGACCTCTCTGGCGTGTTCCCCGAGGTAGAAGTAAT

    c        S  S  T  P  H  N  V  S  W  R  D  R  T  R  G  S  I  F  I  T -

             CGGAACTCATCACATGCTTCCAGAAATATTCTTGCTGCTGCCACCTAATGGAAATATTTC
       6361 ---------+---------+---------+---------+---------+---------+ 6420
             GCCTTGAGTAGTGTACGAAGGTCTTTATAAGAACGACGACGGTGGATTACCTTTATAAAG

    c        E  L  I  T  C  F  Q  K  Y  S  C  C  C  H  L  M  E  I  F  R -

             GGAAGGTACAGAAATCATTTGAAGTTCCACAGGCTAAAGCCCAGATGCCCACCATAGAAC
       6421 ---------+---------+---------+---------+---------+---------+ 6480
             CCTTCCATGTCTTTAGTAAACTTCAAGGTGTCCGATTTCGGGTCTACGGGTGGTATCTTG

    c        K  V  Q  K  S  F  E  V  P  Q  A  K  A  Q  M  P  T  I  E  R -

             GAGCAACCTTGACAAGAGATTTCTACCTCTTTCCTGGCAATTGACTCGAGCACCACCACC
       6481 ---------+---------+---------+---------+---------+---------+ 6540
             CTCGTTGGAACTGTTCTCTAAAGATGGAGAAAGGACCGTTAACTGAGCTCGTGGTGGTGG

    c        A  T  L  T  R  D  F  Y  L  F  P  G  N  *  L  E  H  H  H  H -

             ACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCA
       6541 ---------+---------+---------+---------+---------+---------+ 6600
             TGGTGGTGACTCTAGGCCGACGATTGTTTCGGGCTTTCCTTCGACTCAACCGACGACGGT

    c        H  H  *  D  P  A  A  N  K  A  R  K  E  A  E  L  A  A  A  T -

                                                T7 Terminator
             CCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTT
       6601 ---------+---------+---------+---------+---------+---------+ 6660
             GGCGACTCGTTATTGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAA

    c        A  E  Q  *  L  A  *  P  L  G  A  S  K  R  V  L  R  G  F  L -
```

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```
          TGCTGAAAGGAGGAACTATATCCGGT
      6661 ---------+---------+------- 6687
          ACGACTTTCCTCCTTGATATAGGCCA
c           L  K  G  G  T  I  S  G   -
```

FIGURE 15.

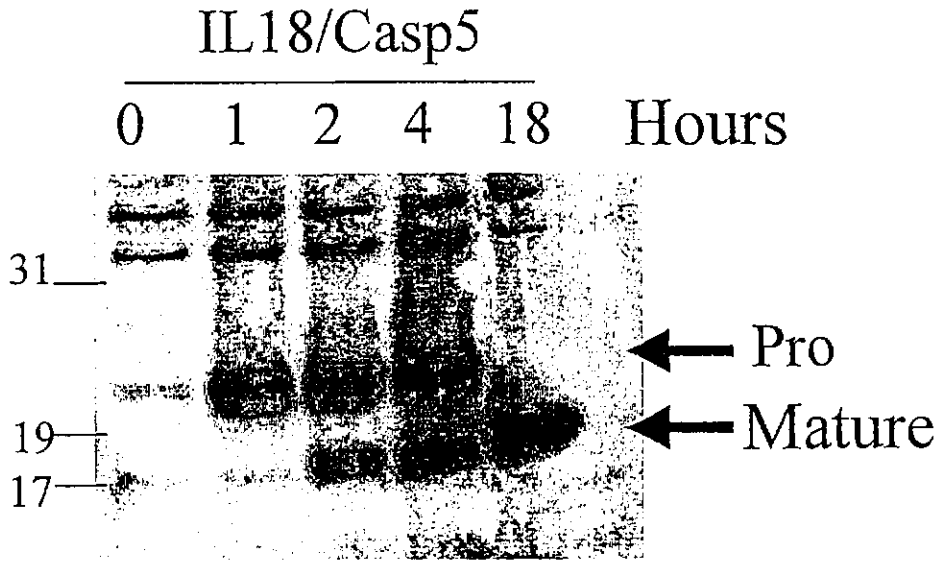


FIGURE 16.

SEQ ID NO:10

```
1   MQIFVKTLTG KTITLEVESS DTIDNVKSKI QDKEGIPPDQ QRLIFAGKQL
51  EDGRTLSDYN IQKESTLHLV LRLRGGYFGK LESKLSVIRN LNDQVLFIDQ
101 GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI SVKCEKISTL
151 SCENKIISFK EMNPPDNIKD TKSDIIFFQR SVPGHDNKMQ FESSSYEGYF
201 LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED
```

FIGURE 17.

SEQ ID NO:11

```
1                                                        50
ATGCAGATCT TCGTCAAGAC GTTAACCGGT AAAACCATAA CTCTAGAAGT
51                                                       100
TGAATCTTCC GATACCATCG ACAACGTTAA GTCGAAAATT CAAGACAAGG
101                                                      150
```

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AAGGCATTCC ACCTGATCAA CAAAGATTGA TCTTTGCCGG TAAGCAGCTC
151 200
GAAGACGGTA GAACGCTGTC TGATTACAAC ATTCAGAAGG AGTCGACCTT
201 250
ACATCTTGTC TTAAGACTAA GAGGAGGGTA CTTTGGCAAG CTTGAGAGCA
251 300
AACTATCGGT CATTCGTAAT TTAAATGACC AGGTCCTATT TATCGACCAA
301 350
GGGAATCGTC CACTATTCGA GGACATGACA GACAGTGACT GCCGAGACAA
351 400
TGCGCCGCGA ACCATTTTCA TTATATCTAT GTACAAGGAT TCTCAGCCGC
401 450
GCGGAATGGC CGTAACTATT TCTGTCAAAT GTGAAAAGAT ATCCACGCTG
451 500
TCGTGTGAGA ACAAGATTAT TAGTTTCAAA GAGATGAATC CGCCGGATAA
501 550
TATCAAGGAC ACGAAGTCTG ATATCATATT TTTCCAGCGC AGCGTGCCGG
551 600
GGCACGATAA CAAGATGCAA TTTGAATCAT CCAGCTATGA AGGGTACTTT
601 650
CTTGCATGCG AGAAGGAACG CGATCTCTTT AAACTTATTT TAAAGAAAGA
651 700
GGACGAGCTA GGCGATCGCA GCATTATGTT CACTGTCCAA AATGAAGACT
701
AG

FIGURE 18.

SEQ ID NO:12

1 50
AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG
51 100
CGGATAACAA TTCCCCTCTA GACCACACCT TAAGGAGGAT ATAACATATG
101 150
CAGATCTTCG TCAAGACGTT AACCGGTAAA ACCATAACTC TAGAAGTTGA
151 200
ATCTTCCGAT ACCATCGACA ACGTTAAGTC GAAAATTCAA GACAAGGAAG
201 250
GCATTCCACC TGATCAACAA AGATTGATCT TTGCCGGTAA GCAGCTCGAG
251 300
GACGGTAGAA CGCTGTCTGA TTACAACATT CAGAAGGAGT CGACCTTACA
301 350

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TCTTGTCTTA AGACTAAGAG GAGGGTACTT TGGCAAGCTT GAGAGCAAAC
351 400
TATCGGTCAT TCGTAATTTA AATGACCAGG TCCTATTTAT CGACCAAGGG
401 450
AATCGTCCAC TATTCGAGGA CATGACAGAC AGTGACTGCC GAGACAATGC
451 500
GCCGCGAACC ATTTTCATTA TATCTATGTA CAAGGATTCT CAGCCGCGCG
501 550
GAATGGCCGT AACTATTTCT GTCAAATGTG AAAAGATATC CACGCTGTCG
551 600
TGTGAGAACA AGATTATTAG TTTCAAAGAG ATGAATCCGC CGGATAATAT
601 650
CAAGGACACG AAGTCTGATA TCATATTTTT CCAGCGCAGC GTGCCGGGGC
651 700
ACGATAACAA GATGCAATTT GAATCATCCA GCTATGAAGG GTACTTTCTT
701 750
GCATGCGAGA AGGAACGCGA TCTCTTTAAA CTTATTTTAA AGAAAGAGGA
751 800
CGAGCTAGGC GATCGCAGCA TTATGTTCAC TGTCCAAAAT GAAGACTAGT
801 850
GGAGGATATA ATACCAGGAA TAAATAAAAT CCATGGGCCA TCATCATCAT
851 900
CATCATGGCA TGGATGAAAG CAAGATAAAC AGTTTATTAC AATTTTTATT
901 950
TGGTTCCCGA CAGGATTTTT TGAGAAATTT TAAAACTTGG AGTAACAACA
951 1000
ATAACAATCT ATCGATTTAT TTATTAATTT TTGGCATAGT AGTATTTTTT
1001 1050
TATAAAAAAC CAGACCATCT AAACTACATT GTTGAGAGCG TTAGTGAAAT
1051 1100
GACAACAAAC TTCAGAAATA ATAATAGCCT TAGCCGTTGG TTGCCCAGAA
1101 1150
GTAAGTTTAC CCACTTAGAC GAAGAGATCT TGAAAAGAGG TGGTTTCATT
1151 1200
GCTGGTTTAG TTAATGATGG TAACACTTGT TTTATGAACT CTGTTTTGCA
1201 1250
ATCATTGGCA TCATCCAGAG AATTAATGGA GTTCTTGGAC AATAATGTCA
1251 1300
TAAGGACCTA TGAGGAGATA GAACAAAATG AACACAATGA AGAAGGAAAC
1301 1350
GGGCAAGAAT CTGCTCAAGA TGAAGCCACT CATAAGAAAA ACACTCGTAA
1351 1400
GGGTGGCAAA GTTTATGGTA AGCATAAGAA GAAATTGAAT AGGAAGTCAA

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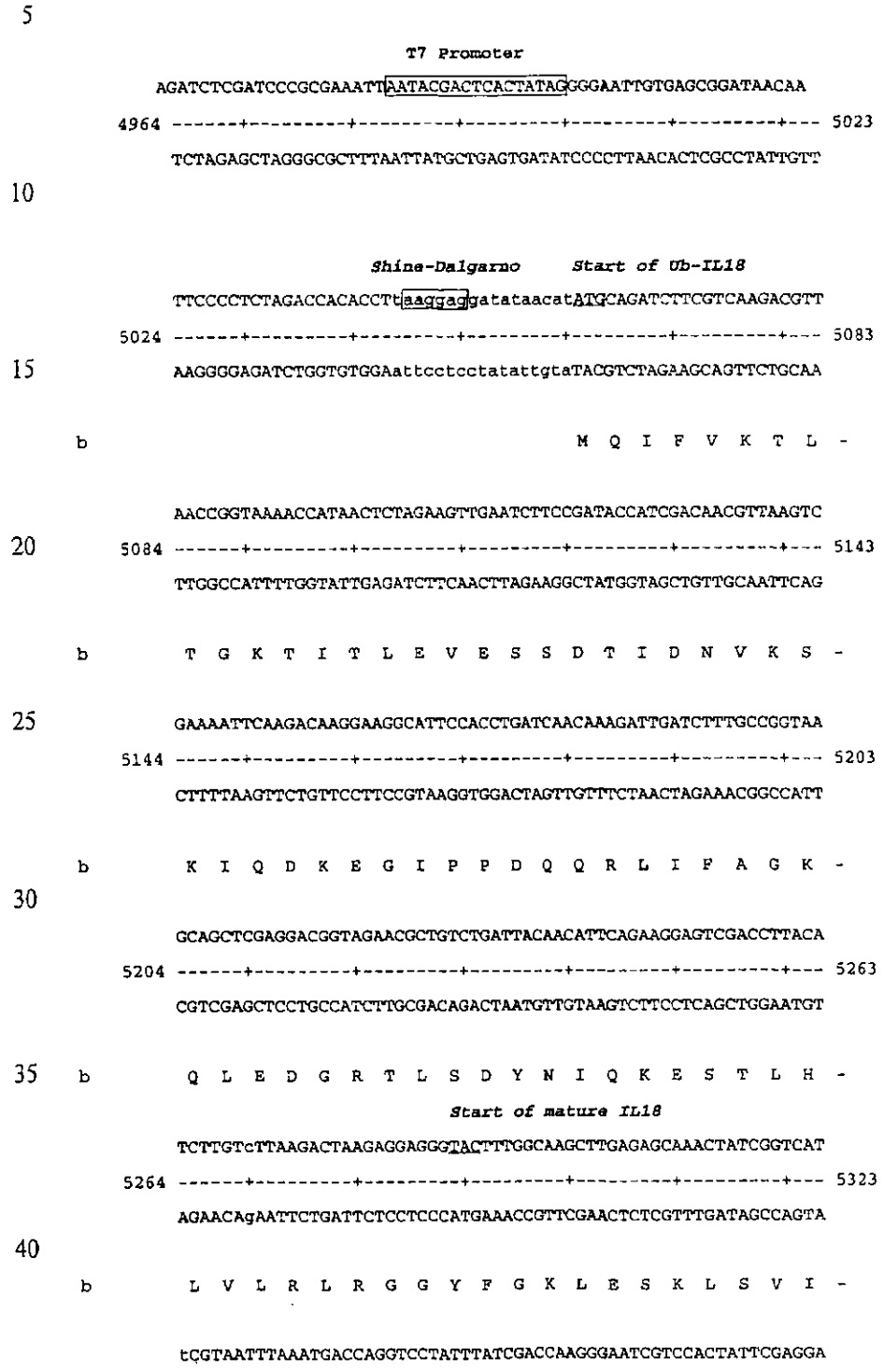
1401 1450
GTTCGAAAGA AGACGAAGAA AAGAGCCAGG AGCCAGATAT CACTTTCAGT
1451 1500
GTCGCCTTAA GGGATCTACT TTCTGCCTTA AATGCGAAGT ATTATCGGGA
1501 1550
TAAACCCTAT TTCAAAACCA ATAGTTTATT GAAAGCAATG TCCAAATCTC
1551 1600
CAAGAAAAAA TATTCTTCTT GGCTACGACC AAGAGGACGC GCAAGAATTC
1601 1650
TTCCAGAACA TACTAGCCGA GTTGGAAAGT AACGTTAAAT CATTGAATAC
1651 1700
TGAAAAACTA GATACCACTC CAGTTGCGAA ATCAGAATTA CCCGATGATG
1701 1750
CTTTAGTAGG TCAACTTAAC CTTGGTGAAG TTGGCACTGT TTACATTCCA
1751 1800
ACTGAACAGA TTGATCCTAA CTCTATACTA CATGACAAGT CCATTCAAAA
1801 1850
TTTCACACCT TTCAAACTAA TGACTCCTTT AGATGGTATC ACGGCAGAAA
1851 1900
GAATTGGTTG TTTACAGTGT GGTGAGAACG GTGGCATAAG ATATTCCGTA
1901 1950
TTTTCGGGAT TAAGCTTAAA TTTACCGAAC GAGAATATTG GTTCCACTTT
1951 2000
AAAATTATCT CAGTTATTGA GCGACTGGAG TAAACCTGAA ATCATCGAAG
2001 2050
TCGTAGAATG TAACCGTTGT GCCCTCACAG CAGCGCACTC TCATTTATTT
2051 2100
GGTCAGTTGA AAGAATTTGA AAAAAAACCT GAGGGTTCGA TCCCAGAAAA
2101 2150
GCCAATTAAC GCTGTAAAAG ATAGGGTCCA TCAAATCGAA GAAGTTCTTG
2151 2200
CCAAACCAGT TATTGACGAT GAAGATTATA AGAAGTTGCA TACAGCAAAT
2201 2250
ATGGTACGTA AATGCTCTAA ATCTAAGCAG ATTTTAATAT CAAGACCTCC
2251 2300
ACCATTATTA TCCATTCATA TCAACAGATC CGTATTTGAT CCAAGAACGT
2301 2350
ACATGATTAG AAAAAATAAC TCGAAAGTAT TGTTTAAGTC AACGTTGAAT
2351 2400
CTTGCCCCTT GGTGTTGTGA TATTAATGAA ATCAATTTGG ATGCTCGTTT
2401 2450
GCCAATGTCA AAAAAGGAAA AAGCTGCGCA ACAAGATTCA AGTGAAGATG
2451 2500

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AAAACATTGG CGGTGAATAC TATACGAAAT TACATGAACG CTTCGAGCAG
2501 2550
GAATTTGAAG ACAGCGAGGA AGAAAAAGAA TACGATGACG CAGAGGGGAA
2551 2600
CTATGCGTCT CATTACAATC ATACCAAGGA TATCAGTAAC TATGATCCCC
2601 2650
TAAACGGTGA AGTCGATGGC GTGACATCCG ATGATGAAGA TGAGTACATT
2651 2700
GAAGAAACCG ATGCTTTAGG GAATACAATC AAAAAAAGGA TCATAGAACA
2701 2750
TTCTGATGTT GAAAACGAGA ATGTAAAAGA TAATGAAGAA CTGCAAGAAA
2751 2800
TCGACAATGT GAGCCTTGAC GAACCAAAGA TCAATGTTGA AGATCAACTA
2801 2850
GAAACATCAT CTGATGAGGA AGATGTTATA CCAGCTCCAC CTATCAATTA
2851 2900
TGCTAGGTCA TTTTCCACAG TTCCAGCCAC TCCATTGACA TATTCATTGC
2901 2950
GCTCTGTCAT TGTTCACTAC GGTACCCATA ATTATGGTCA TTACATTGCA
2951 3000
TTTAGAAAAT ACAGGGGTTG TTGGTGGAGA ATATCTGATG AGACTGTGTA
3001 3050
CGTTGTGGAC GAAGCTGAAG TCCTTTCAAC ACCCGGTGTA TTTATGTTAT
3051 3100
TTTACGAATA TGACTTTGAT GAAGAAACTG GGAAGATGAA GGATGATTTG
3101 3150
GAAGCTATTC AGAGTAATAA TGAAGAAGAT GATGAAAAAG AGCAGGAGCA
3151 3200
AAAAGGAGTC CAGGAGCCAA AGGAAAGCCA AGAGCAAGGA GAAGGTGAAG
3201 3250
AGCAAGAGGA AGGTCAAGAG CAGATGAAGT TCGAGAGAAC AGAAGACCAT
3251 3300
AGAGATATTT CTGGTAAAGA TGTAAACTAA GCTCGAGCAC CACCACCACC
3301 3350
ACCACTGAGA TCCGGCTGCT AACAAAGCCC GAAAGGAAGC TGAGTTGGCT
3351 3400
GCTGCCACCG CTGAGCAATA ACTAGCATAA CCCCTTGGGG CCTCTAAACG
3401 3419
GGTCTTGAGG GGTTTTTTG

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FIGURE 19.



```
          5324 ------+---------+---------+---------+---------+---------+--- 5383
               aGCATTAAATTTACTGGTCCAGGATAAATAGCTGGTTCCCTTAGCAGGTGATAAGCTCCT

     b          R  N  L  N  D  Q  V  L  F  I  D  Q  G  N  R  P  L  F  E  D  -

               CATGACAGACAGTGACTGCCGAGACAATGCGCCGCGAACCATtTTCATTATATCTATGTA
          5384 ------+---------+---------+---------+---------+---------+--- 5443
               GTACTGTCTGTCACTGACGGCTCTGTTACGCGGCGCTTGGTAaAAGTAATATAGATACAT

     b          M  T  D  S  D  C  R  D  N  A  P  R  T  I  F  I  I  S  M  Y  -

               CAAGGATTCTCAGCCGCGCGGAATGGCCGTAACTATTTCTGTCAAATGTGAAAAGATATC
          5444 ------+---------+---------+---------+---------+---------+--- 5503
               GTTCCTAAGAGTCGGCGCGCCTTACCGGCATTGATAAAGACAGTTTACACTTTTCTATAG

     b          K  D  S  Q  P  R  G  M  A  V  T  I  S  V  K  C  E  K  I  S  -

               CACGCTGTCGTGTGAGAACAAgATtATtAGTTTCAAAGAGATGAATCCGCCGGATAATAT
          5504 ------+---------+---------+---------+---------+---------+--- 5563
               GTGCGACAGCACACTCTTGTTcTAaTAaTCAAAGTTTCTCTACTTAGGCGGCCTATTATA

     b          T  L  S  C  E  N  K  I  I  S  F  K  E  M  N  P  P  D  N  I  -

               CAAGGACACGAAGTCTGATATCATATTTTTCCAGCGCAGCGTGCCGGGGCACGATAACAA
          5564 ------+---------+---------+---------+---------+---------+--- 5623
               GTTCCTGTGCTTCAGACTATAGTATAAAAAGGTCGCGTCGCACGGCCCCGTGCTATTGTT

     b          K  D  T  K  S  D  I  I  F  F  Q  R  S  V  P  G  H  D  N  K  -

               GATGCAATTTGAATCATCCAGCTATGAAGGGTACTTTCTTGCATGCGAGAAGGAACGCGA
          5624 ------+---------+---------+---------+---------+---------+--- 5683
               CTACGTTAAACTTAGTAGGTCGATACTTCCCATGAAAGAACGTACGCTCTTCCTTGCGCT

     b          M  Q  F  E  S  S  S  Y  E  G  Y  F  L  A  C  E  K  E  R  D  -

               TCTCTTTAAACTTATTTTAAAGAAAGAGGACGAGCTAGGCGATCGCAGCATtATGTTCAC
          5684 ------+---------+---------+---------+---------+---------+--- 5743
               AGAGAAATTTGAATAAAATTTCTTTCTCCTGCTCGATCCGCTAGCGTCGTAaTACAAGTG

     b          L  F  K  L  I  L  K  K  E  D  E  L  G  D  R  S  I  M  F  T  -
```

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Defective Shine-Dalgarno *Start of Opb-1*

```
      TGTCCAAAATGAAGACTAGTggaggatataaTACCAgGaataaataaaatccatgggcca
5744  ------+---------+---------+---------+---------+---------+--- 5803
      ACAGGTTTTACTTCTGATCAcctcctatattATGGTcCttatttatttttaggtacccggt

b      V  Q  N  E  D  *                                  M  G  H  -

      tcatcatcatcatcatggcATGGATGAAAGCAAGATAAACAGTTTATTACAATTTTTATT
5804  ------+---------+---------+---------+---------+---------+--- 5863
      agtagtagtagtagtaccgTACCTACTTTCGTTCTATTTGTCAAATAATGTTAAAAATAA

b      H  H  H  H  H  G  M  D  E  S  K  I  N  S  L  L  Q  F  L  F  -

      TGGTTCCCGACAGGATTTTTTGAGAAATTTTAAAACTTGGAGTAACAACAATAACAATCT
5864  ------+---------+---------+---------+---------+---------+--- 5923
      ACCAAGGGCTGTCCTAAAAAACTCTTTAAAATTTTGAACCTCATTGTTGTTATTGTTAGA

b      G  S  R  Q  D  F  L  R  N  F  K  T  W  S  N  N  N  N  N  L  -

      ATCGATTTATTTATTAATTTTTGGCATAGTAGTATTTTTTTTATAAAAAACCAGACCATCT
5924  ------+---------+---------+---------+---------+---------+--- 5983
      TAGCTAAATAAATAATTAAAAACCGTATCATCATAAAAAAAATATTTTTTGGTCTGGTAGA

b      S  I  Y  L  L  I  F  G  I  V  V  F  F  Y  K  K  P  D  H  L  -

      AAACTACATTGTTGAGAGCGTTAGTGAAATGACAACAAACTTCAGAAATAATAATAGCCT
5984  ------+---------+---------+---------+---------+---------+--- 6043
      TTTGATGTAACAACTCTCGCAATCACTTTACTGTTGTTTGAAGTCTTTATTATTATCGGA

b      N  Y  I  V  E  S  V  S  E  M  T  T  N  F  R  N  N  N  S  L  -

      TAGCCGTTGGTTGCCCAGAAGTAAGTTTACCCACTTAGACGAAGAGATCTTGAAAAGAGG
6044  ------+---------+---------+---------+---------+---------+--- 6103
      ATCGGCAACCAACGGGTCTTCATTCAAATGGGTGAATCTGCTTCTCTAGAACTTTTCTCC

b      S  R  W  L  P  R  S  K  F  T  H  L  D  E  E  I  L  K  R  G  -

      TGGTTTCATTGCTGGTTTAGTTAATGATGGTAACACTTGTTTTATGAACTCTGTTTTGCA
6104  ------+---------+---------+---------+---------+---------+--- 6163
      ACCAAAGTAACGACCAAATCAATTACTACCATTGTGAACAAAATACTTGAGACAAAACGT

b      G  F  I  A  G  L  V  N  D  G  N  T  C  F  M  N  S  V  L  Q  -
```

```
          ATCATTGGCATCATCCAGAGAATTAATGGAGTTCTTGGACAATAATGTCATAAGGACCTA
      6164 ------+---------+---------+---------+---------+---------+--- 6223
          TAGTAACCGTAGTAGGTCTCTTAATTACCTCAAGAACCTGTTATTACAGTATTCCTGGAT

  b        S  L  A  S  S  R  E  L  M  E  F  L  D  N  N  V  I  R  T  Y  -

          TGAGGAGATAGAACAAAATGAACACAATGAAGAAGGAAACGGGCAAGAATCTGCTCAAGA
      6224 ------+---------+---------+---------+---------+---------+--- 6283
          ACTCCTCTATCTTGTTTTACTTGTGTTACTTCTTCCTTTGCCCGTTCTTAGACGAGTTCT

  b        E  E  I  E  Q  N  E  H  N  E  E  G  N  G  Q  E  S  A  Q  D  -

          TGAAGCCACTCATAAGAAAAACACTCGTAAGGGTGGCAAAGTTTATGGTAAGCATAAGAA
      6284 ------+---------+---------+---------+---------+---------+--- 6343
          ACTTCGGTGAGTATTCTTTTTGTGAGCATTCCCACCGTTTCAAATACCATTCGTATTCTT

  b        E  A  T  H  K  K  N  T  R  K  G  G  K  V  Y  G  K  H  K  K  -

          GAAATTGAATAGGAAGTCAAGTTCGAAAGAAGACGAAGAAAAGAGCCAGGAGCCAGATAT
      6344 ------+---------+---------+---------+---------+---------+--- 6403
          CTTTAACTTATCCTTCAGTTCAAGCTTTCTTCTGCTTCTTTTCTCGGTCCTCGGTCTATA

  b        K  L  N  R  K  S  S  S  K  E  D  E  E  K  S  Q  E  P  D  I  -

          CACTTTCAGTGTCGCCTTAAGGGATCTACTTTCTGCCTTAAATGCGAAGTATTATCGGGA
      6404 ------+---------+---------+---------+---------+---------+--- 6463
          GTGAAAGTCACAGCGGAATTCCCTAGATGAAAGACGGAATTTACGCTTCATAATAGCCCT

  b        T  F  S  V  A  L  R  D  L  L  S  A  L  N  A  K  Y  Y  R  D  -

          TAAACCCTATTTCAAAACCAATAGTTTATTGAAAGCAATGTCCAAATCTCCAAGAAAAAA
      6464 ------+---------+---------+---------+---------+---------+--- 6523
          ATTTGGGATAAAGTTTTGGTTATCAAATAACTTTCGTTACAGGTTTAGAGGTTCTTTTTT

  b        K  P  Y  Y  F  K  T  N  S  L  L  K  A  M  S  K  S  P  R  K  N  -

          TATTCTTCTTGGCTACGACCAAGAGGACGCGCAAGAATTCTTCCAGAACATACTAGCCGA
      6524 ------+---------+---------+---------+---------+---------+--- 6583
          ATAAGAAGAACCGATGCTGGTTCTCCTGCGCGTTCTTAAGAAGGTCTTGTATGATCGGCT

  b        I  L  L  G  Y  D  Q  E  D  A  Q  E  F  F  Q  N  I  L  A  E  -

          GTTGGAAAGTAACGTTAAATCATTGAATACTGAAAAACTAGATACCACTCCAGTTGCGAA
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      6584 ------+---------+---------+---------+---------+---------+--- 6643
           CAACCTTTCATTGCAATTTAGTAACTTATGACTTTTTGATCTATGGTGAGGTCAACGCTT

      b     L  E  S  N  V  K  S  L  N  T  E  K  L  D  T  T  P  V  A  K  -

           ATCAGAATTACCCGATGATGCTTTAGTAGGTCAACTTAACCTTGGTGAAGTTGGCACTGT
      6644 ------+---------+---------+---------+---------+---------+--- 6703
           TAGTCTTAATGGGCTACTACGAAATCATCCAGTTGAATTGGAACCACTTCAACCGTGACA

      b     S  E  L  P  D  D  A  L  V  G  Q  L  N  L  G  E  V  G  T  V  -

           TTACATTCCAACTGAACAGATTGATCCTAACTCTATACTACATGACAAGTCCATTCAAAA
      6704 ------+---------+---------+---------+---------+---------+--- 6763
           AATGTAAGGTTGACTTGTCTAACTAGGATTGAGATATGATGTACTGTTCAGGTAAGTTTT

      b     Y  I  P  T  E  Q  I  D  P  N  S  I  L  H  D  K  S  I  Q  N  -

           TTTCACACCTTTCAAACTAATGACTCCTTTAGATGGTATCACGGCAGAAAGAATTGGTTG
      6764 ------+---------+---------+---------+---------+---------+--- 6823
           AAAGTGTGGAAAGTTTGATTACTGAGGAAATCTACCATAGTGCCGTCTTTCTTAACCAAC

      b     F  T  P  F  K  L  M  T  P  L  D  G  I  T  A  E  R  I  G  C  -

           TTTACAGTGTGGTGAGAACGGTGGCATAAGATATTCCGTATTTTCGGGATTAAGCTTAAA
      6824 ------+---------+---------+---------+---------+---------+--- 6883
           AAATGTCACACCACTCTTGCCACCGTATTCTATAAGGCATAAAAGCCCTAATTCGAATTT

      b     L  Q  C  G  E  N  G  G  I  R  Y  S  V  F  S  G  L  S  L  N  -

           TTTACCGAACGAGAATATTGGTTCCACTTTAAAATTATCTCAGTTATTgAGCGACTGGAG
      6884 ------+---------+---------+---------+---------+---------+--- 6943
           AAATGGCTTGCTCTTATAACCAAGGTGAAATTTTAATAGAGTCAATAAcTCGCTGACCTC

      b     L  P  N  E  N  I  G  S  T  L  K  L  S  Q  L  L  S  D  W  S  -

           TAAACCTGAAATCATCGAAGTCGTAGAATGTAACCGTTGTGCCCTCACAGCAGCGCACTC
      6944 ------+---------+---------+---------+---------+---------+--- 7003
           ATTTGGACTTTAGTAGCTTCAGCATCTTACATTGGCAACACGGGAGTGTCGTCGCGTGAG

      b     K  P  E  I  I  E  V  V  E  C  N  R  C  A  L  T  A  A  H  S  -

           TCATTTATTTGGTCAGTTGAAAGAATTTGAAAAAAAACCTGAGGGTTCGATCCCAGAAAA
      7004 ------+---------+---------+---------+---------+---------+--- 7063
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          AGTAAATAAACCAGTCAACTTTCTTAAACTTTTTTTTGGACTCCCAAGCTAGGGTCTTTT

    b      H  L  F  G  Q  L  K  E  F  E  K  K  P  E  G  S  I  P  E  K  -

          GCCAATTAACGCTGTAAAAGATAGGGTCCATCAAATCGAAGAAGTTCTTGCCAAACCAGT
       7064 ------+---------+---------+---------+---------+---------+--- 7123
          CGGTTAATTGCGACATTTTCTATCCCAGGTAGTTTAGCTTCTTCAAGAACGGTTTGGTCA

    b      P  I  N  A  V  K  D  R  V  H  Q  I  E  E  V  L  A  K  P  V  -

          TATTGACGATGAAGATTATAAGAAGTTGCATACAGCAAATATGGTACGTAAATGCTCTAA
       7124 ------+---------+---------+---------+---------+---------+--- 7183
          ATAACTGCTACTTCTAATATTCTTCAACGTATGTCGTTTATACCATGCATTTACGAGATT

    b      I  D  D  E  D  Y  K  K  L  H  T  A  N  M  V  R  K  C  S  K  -

          ATCTAAGCAGATTTTAATATCAAGACCTCCACCATTATTATCCATTCATATCAACAGATC
       7184 ------+---------+---------+---------+---------+---------+--- 7243
          TAGATTCGTCTAAAATTATAGTTCTGGAGGTGGTAATAATAGGTAAGTATAGTTGTCTAG

    b      S  K  Q  I  L  I  S  R  P  P  P  L  L  S  I  H  I  N  R  S  -

          CGTATTTGATCCAAGAACGTACATGATTAGAAAAAATAACTCGAAAGTATTGTTTAAGTC
       7244 ------+---------+---------+---------+---------+---------+--- 7303
          GCATAAACTAGGTTCTTGCATGTACTAATCTTTTTTATTGAGCTTTCATAACAAATTCAG

    b      V  F  D  P  R  T  Y  M  I  R  K  N  N  S  K  V  L  F  K  S  -

          AACGTTGAATCTTGCCCCTTGGTGTTGTGATATTAATGAAATCAATTTGGATGCTCGTTT
       7304 ------+---------+---------+---------+---------+---------+--- 7363
          TTGCAACTTAGAACGGGGAACCACAACACTATAATTACTTTAGTTAAACCTACGAGCAAA

    b      T  L  N  L  A  P  W  C  C  D  I  N  E  I  N  L  D  A  R  L  -

          GCCAATGTCAAAAAAGGAAAAAGCTGCGCAACAAGATTCAAGTGAAGATGAAAACATTGG
       7364 ------+---------+---------+---------+---------+---------+--- 7423
          CGGTTACAGTTTTTTCCTTTTTCGACGCGTTGTTCTAAGTTCACTTCTACTTTTGTAACC

    b      P  M  S  K  K  E  K  A  A  Q  Q  D  S  S  E  D  E  N  I  G  -

          CGGTGAATACTATACGAAATTACATGAACGCTTCGAGCAGGAATTTGAAGACAGCGAGGA
       7424 ------+---------+---------+---------+---------+---------+--- 7483
          GCCACTTATGATATGCTTTAATGTACTTGCGAAGCTCGTCCTTAAACTTCTGTCGCTCCT
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    b       G  E  Y  Y  T  K  L  H  E  R  F  E  Q  E  F  E  D  S  E  E  -

            AGAAAAAGAATACGATGACGCAGAGGGGAACTATGCGTCTCATTACAATCATACCAAGGA
 7484 ------+---------+---------+---------+---------+---------+---------+--- 7543
            TCTTTTTCTTATGCTACTGCGTCTCCCCTTGATACGCAGAGTAATGTTAGTATGGTTCCT

    b       E  K  E  Y  D  D  A  E  G  N  Y  A  S  H  Y  N  H  T  K  D  -

            TATCAGTAACTATGATCCCCTAAACGGTGAAGTCGATGGCGTGACATCCGATGATGAAGA
 7544 ------+---------+---------+---------+---------+---------+---------+--- 7603
            ATAGTCATTGATACTAGGGGATTTGCCACTTCAGCTACCGCACTGTAGGCTACTACTTCT

    b       I  S  N  Y  D  P  L  N  G  E  V  D  G  V  T  S  D  D  E  D  -

            TGAGTACATTGAAGAAACCGATGCTTTAGGGAATACAATCAAAAAAAGGATCATAGAACA
 7604 ------+---------+---------+---------+---------+---------+---------+--- 7663
            ACTCATGTAACTTCTTTGGCTACGAAATCCCTTATGTTAGTTTTTTTCCTAGTATCTTGT

    b       E  Y  I  E  E  T  D  A  L  G  N  T  I  K  K  R  I  I  E  H  -

            TTCTGATGTTGAAAACGAGAATGTAAAAGATAATGAAGAACTGCAAGAAATCGACAATGT
 7664 ------+---------+---------+---------+---------+---------+---------+--- 7723
            AAGACTACAACTTTTGCTCTTACATTTTCTATTACTTCTTGACGTTCTTTAGCTGTTACA

    b       S  D  V  E  N  E  N  V  K  D  N  E  E  L  Q  E  I  D  N  V  -

            GAGCCTTGACGAACCAAAGATCAATGTTGAAGATCAACTAGAAACATCATCTGATGAGGA
 7724 ------+---------+---------+---------+---------+---------+---------+--- 7783
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    b       S  L  D  E  P  K  I  N  V  E  D  Q  L  E  T  S  S  D  E  E  -

            AGATGTTATACCAGCTCCACCTATCAATTATGCTAGGTCATTTTCCACAGTTCCAGCCAC
 7784 ------+---------+---------+---------+---------+---------+---------+--- 7843
            TCTACAATATGGTCGAGGTGGATAGTTAATACGATCCAGTAAAAGGTGTCAAGGTCGGTG

    b       D  V  I  P  A  P  P  I  N  Y  A  R  S  F  S  T  V  P  A  T  -

            TCCATTGACATATTCATTGCGCTCTGTCATTGTTCACTACGGTACCCATAATTATGGTCA
 7844 ------+---------+---------+---------+---------+---------+---------+--- 7903
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b       Y  I  A  F  R  K  Y  R  G  C  W  W  R  I  S  D  E  T  V  Y  -

        CGTTGTGGACGAAGCTGAAGTCCTTTCAACACCCGGTGTATTTATGTTATTTTACGAATA
     7964 ------+---------+---------+---------+---------+---------+--- 8023
        GCAACACCTGCTTCGACTTCAGGAAAGTTGTGGGCCACATAAATACAATAAAATGCTTAT

b       V  V  D  E  A  E  V  L  S  T  P  G  V  F  M  L  F  Y  E  Y  -

        TGACTTTGATGAAGAAACTGGGAAGATGAAGGATGATTTGGAAGCTATTCAGAGTAATAA
     8024 ------+---------+---------+---------+---------+---------+--- 8083
        ACTGAAACTACTTCTTTGACCCTTCTACTTCCTACTAAACCTTCGATAAGTCTCATTATT

b       D  F  D  E  E  T  G  K  M  K  D  D  L  E  A  I  Q  S  N  N  -

        TGAAGAAGATGATGAAAAAGAgCAGGAGCAAAAAGGAGTCCAGGAGCCAAAGGAAAGCCA
     8084 ------+---------+---------+---------+---------+---------+--- 8143
        ACTTCTTCTACTACTTTTTCTcGTCCTCGTTTTTCCTCAGGTCCTCGGTTTCCTTTCGGT

b       E  E  D  D  E  K  E  Q  E  Q  K  G  V  Q  E  P  K  E  S  Q  -

        AGAGCAAGGAGAAGGTGAAGAGCAAGAGGAAGGTCAAGAGCAGATGAAGTTCGAGAGAAC
     8144 ------+---------+---------+---------+---------+---------+--- 8203
        TCTCGTTCCTCTTCCACTTCTCGTTCTCCTTCCAGTTCTCGTCTACTTCAAGCTCTCTTG

b       E  Q  G  E  G  E  E  Q  E  E  G  Q  E  Q  M  K  F  E  R  T  -

        AGAAGACCATAGAGATATTTCTGGTAAAGATGTAAACTAAGCTCGAGCACCACCACCACC
     8204 ------+---------+---------+---------+---------+---------+--- 8263
        TCTTCTGGTATCTCTATAAAGACCATTTCTACATTTGATTCGAGCTCGTGGTGGTGGTGG

b       E  D  H  R  D  I  S  G  K  D  V  N

        ACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCG
     8264 ------+---------+---------+---------+---------+---------+--- 8323
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b

T7 Terminator Sequence

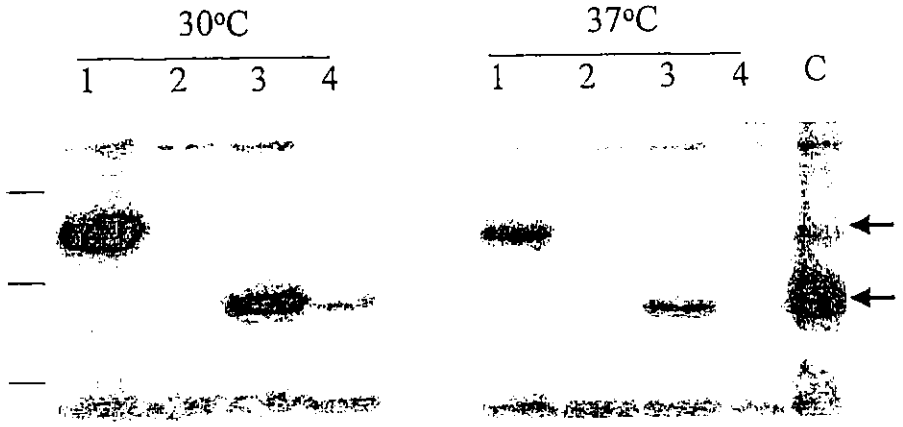
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5

FIGURE 20.

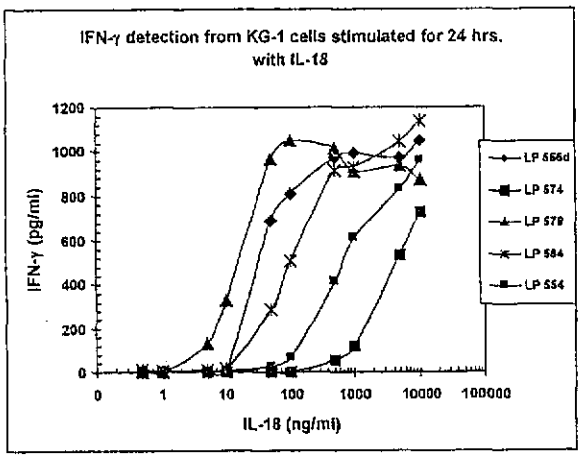


1. Ub-human IL18, 3 hours
2. Ub-human IL18/Ubp-1, O hours
3. Ub-human IL18/Ubp-1, 3 hours
4. Ub-human IL18/Ubp-1, 18 hours

C. Control- ProIL18/Casp 4

Western: Anti IL18

FIGURE 21:

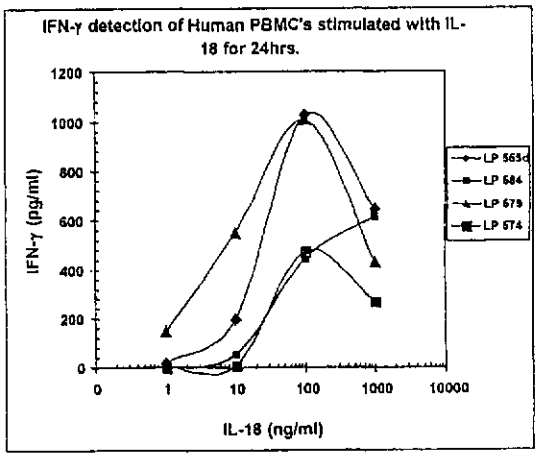


Description of different human/murine IL-18 samples (different lots/constructs)

LP555d (standard) E. COLI ICE-CLEAVED (*IN VITRO*)
LP 554 E. coli murine IL-18 Ice-cleaved (*IN VITRO*)
LP559 E. coli expressed mature IL-18 containing N-terminal methionine
LP574 E. coli expressed mature IL-18 containing N-terminal Methionine
LP579 Pichia expressed, secreted, mature IL18
LP584 E.coli IL-18/ICE bicistronic co-expression (*IN VIVO*)
LP594 E. coli ICE-cleaved (*IN VITRO*)
LP613 E. coli caspase 4 cleaved (*IN VITRO*)
LP614 E. coli ICE co-expressed (*IN VITRO*)
LP623 caspase 4 co-expressed (*IN VIVO*)

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Figure 22



Description of different human/murine IL-18 samples (different lots/constructs)

LP555d (standard) E. COLI ICE-CLEAVED (*IN VITRO*)
LP 554 E. coli murine IL-18 Ice-cleaved (*IN VITRO*)
LP559 E. coli expressed mature IL-18 containing N-terminal methionine
LP574 E. coli expressed mature IL-18 containing N-terminal Methionine
LP579 Pichia expressed, secreted, mature IL18
LP584 E.coli IL-18/ICE bicistronic co-expression (*IN VIVO*)
LP594 E. coli ICE-cleaved (*IN VITRO*)
LP613 E. coli caspase 4 cleaved (*IN VITRO*)
LP614 E. coli ICE co-expressed (*IN VITRO*)
LP623 caspase 4 co-expressed (*IN VIVO*)

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SEQUENCE LISTING

<110> SMITHKLINE BEECHAM CORPORATION

<120> METHOD FOR PREPARING A PHYSIOLOGICALLY ACTIVE IL-18 POLYPEPTIDE

<130> P51137

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Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
        35                  40                  45
Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
    50                  55                  60
Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
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85 90 95
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Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
115 120 125
Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
130 135 140
His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
145 150 155 160
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Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
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Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
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gagcacaagt cctctgacag cacattcttg gtactcatgt ctcatggcat cctggaggga    360
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04 DEC 2004

<213> Homo sapien

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35 40 45
Thr Lys Phe Asp His Leu Pro Ala Arg Asn Gly Ala His Tyr Asp Ile
50 55 60
Val Gly Met Lys Arg Leu Leu Gln Gly Leu Gly Tyr Thr Val Val Asp
65 70 75 80
Glu Lys Asn Leu Thr Ala Arg Asp Met Glu Ser Val Leu Arg Ala Phe
85 90 95
Ala Ala Arg Pro Glu His Lys Ser Ser Asp Ser Thr Phe Leu Val Leu
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Met Ser His Gly Ile Leu Glu Gly Ile Cys Gly Thr Ala His Lys Lys
115 120 125
Lys Lys Pro Asp Val Leu Leu Tyr Asp Thr Ile Phe Gln Ile Phe Asn
130 135 140
Asn Arg Asn Cys Leu Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Val
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180 185 190
Ala Asp Ser Val Cys Lys Ile His Glu Glu Lys Asp Phe Ile Ala Phe
195 200 205
Cys Ser Ser Thr Pro His Asn Val Ser Trp Arg Asp Arg Thr Arg Gly
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Cys Cys His Leu Met Glu Ile Phe Arg Lys Val Gln Lys Ser Phe Glu
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<212> DNA

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<213> Homo sapien

<400> 7

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<212> DNA
<213> Homo sapien

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<400> 10

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Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
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Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Tyr Phe Gly Lys
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Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn Asp Gln Val Leu
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Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp Met Thr Asp Ser
            100                 105                 110
Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr
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Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Cys
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Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys
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Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu Lys Glu Arg Asp
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<400> 11

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04 DEC 2001

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