```
30
                                         40
                  ------ATGAGGATÁTTTGCTGTCŤTTATATTCAĊGATC---TAĊ----
49 Mmul
           -----ATGAGGATATTTGCTGTTTTTATATTCATGACC---TAC----
77_Cjac
      GGAAATCTGACGGGGACATCAGTTGCTTTGCTTCTTGTGCATCTTGGCCTGAGGAGCAGTGCCAA
85_Tsyr
29_0gar
             -----ATGAAGATATCTAATGTCTTTACATTCACAGCC---TAC----
             -----ATGAGGATATTTGCTGTCTTTATATTCATGACC---TAC----
89_Hsap
             -----ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAG----
55_Hsap
             -----ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAG----
06_Ptro
18_Cjac
           -----ATGATCTTCCTCCTCTAATGTTGAGCCTGGAATTGCAG----
            -----GTGTTTTTCCTCCTGCTGATGTTGAGCCTGGGATTGCAG----
03_Mmur
            ----ATGCAGAACATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAG----
42_Pabe
               -----ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAG----
09_Nleu
          -----ATGAGGATATTTGCTGTCTTTATATTCACGACC---TAC----
50_Ggor
98_Mmur
      ---ATGAGGATATTTCACGTCTTTACATTCACAACCTACTGGCATTTACTGAAC------
       -----ATGAGGATATTTGCTGTCCTTATATTCACGACC---TAC----
43_Pabe
               -----ATGAGGATATTTGCTGTCTTTATATTCATGACC---TAC----
90_Nleu
              -----ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAACTGCAG----
45_Mmul
36_Mmur
04_Ptro
               -----ATGAGGATATTTGCTGTCTTTATATTCATGACC---TAC----
           -----ATGCTTTTCCTACTGCTAAAGCTGAGCCTGGGATTGCAG----
30_Ogar
78_Tsyr
          -----ATGAGGATACTTCCTGTCTTCACATTCACAGCC---TAC----
54_Ggor
           -----ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAG----
       ____
```

```
100
                                                     110
        ----TGGCAT---TTGCTGAATGCA---TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
49_Mmul
77_Cjac
85_Tsyr
        ----TGGCAT---TTGCTGAATGCA---TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
        GTCCTGTCAAGTGCAGAACATGTCCCTCCTACTGTTAATCTTGAGCCTGGAATTGCAGTTTCGTC
       ----TGGCAT---TTACTGAACGCA---TTTACTGTCACAGTTCCCAAAGACCAGTATGTGATAG
29_0gar
        ----TGGCAT---TTGCTGAACGCA---TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
89_Hsap
        ----CTTCAC---CAGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAG
55_Hsap
       ----CTTCAC---CAGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAG
06_Ptro
       ----CTTCAA----CAGACAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAATTGTATATAGTAG
18_Cjac
        ---CTTCAT---CGGACAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAGTTGTACATAGTAG
03_Mmur
        ----CTTCAC---CAAATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAG
42_Pabe
09_Nleu
       ----CTTCAC---CAGATAGCAGCTCTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAG
       ---TGGCAT---TTGCTGAATGCA---TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
50_Ggor
98_Mmur
       -GCATTTACA---GTCACAGTTCCC---AAGGACCTGTATGTGGTGGAGTATGGCAGCAATGTGA
43_Pabe
       ----TGGCAT---TTGCTGAATGCA---TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
       ---TGGCAT---TTGCTGAATGCA---TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
90_Nleu
45_Mmul
       ----CTTCAC---CAGACAGCAGCTTTATTCACGGTGACAGTCCCTAAGGAACTGTACATAATAG
36_Mmur
04_Ptro
        --- TGGCAT --- TTGCTGAACGCA --- TTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG
       ----CTTCAT---CAGACAGCAGCTTTATTCACAGTGACCGTCCCTAAGGAGCTGTACATAGTAG
30_Ogar
        ---TGGCAT---TTGCTGAACGCC---TTTACTGTCACCGTTCCCAAGGACCTGTATGTGGTAG
78_Tsyr
54_Ggor
       ----CTTCAC---CAGATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAACTGTACATAATAG
```

```
170
                          150
                                   160
                                                        180
85_Tsyr
       29_Ogar AGTATGGCAGCAATGTGACAATTGAGTGCAGATTC-----CCAGTAGAAAAACAATTAGACCTG
89_Hsap AGTATGGTAGCAATATGACAATTGAATGCAAATTC-----CCAGTAGAAAAACAATTAGACCTG
55_Hsap AGCATGGCAGCAATGTGACCCTGGAATGCAACTTT-----GACACTGGAAGTCATGTGAACCTT
06_Ptro AGCATGCAGCAATGTGACCCTGGAATGCAACTTT----GACACTGGAAGTCATGTGAACCTT
18_Cjac AGCATGGCAGCAATGTGACCCTGGAATGCAACTTT-----GATACTGGAAGTCATGTGAACGTT
03_Mmur ACCACGGCAGCAATGTGACCCTGGAGTGTGATTT-----GACACTGGAGGTCACGTGAAACCT
42_Pabe AGCATGGCAGCAATGTGACCCTGGAATGCAACTTT-----GACACTGGAAGTCATGTGAACCTT
O9_Nleu AGCATGGCAGCAATGTGACCCTGGAATGCAACTTT-----GACACTGGAAGTCATGTGAACCTT
98_Mmur CCATCGAATGCAGATTCCCAGTGGAAAAACAATTA-----GACCTGATGTCATTAGTTGTCTAC
43_Pabe AGTATGGCAGCAATATGACAATTGAATGCAAATTC-----CCAGTAGAAAAACAATTAGACCTG
90_Nleu AGTATGGCAGCAATATGACAATTGAATGCAAATTC-----CCAGTAGAAAAACAATTAGACCTG
45_Mmul AGCATGGCAGCAATGCGACCCTGGAATGCAACTTT-----GACACTGGAAGTCATGTGAACCTT
36 Mmur ------
O4_Ptro AGTATGGCAGCAATATGACAATTGAATGCAAATTC-----CCAGTAGAAAAACAATTAGACCTG
30_Ogar ACTATGGCAGCAATGTGACCCTGGAGTGTGATTTT-----GACACTGGAGGCCAAGTGAAACTT
78_Tsyr AGCATGCCAGCAATGTGACAATTGAATGCAGATTC-----CCCGTAGACAACACTTAGACCTG
       AGCATGGCAGCAATGTGACCCTGGAATGCAACTTT-----GACACTGGAAGTCATGTGAACCTT
```

```
49_Mmul ACTTCACTAATTGTCTATTGGGAAATGGAGGAT-----AAGAACATTATTCAATTTGTGCATGG
89_Hsap GCTGCACTAATTGTCTATTGGGAAATGGAGGAT-----AAGAACATTATTCAATTTGTGCATGG
55_Hsap GGAGCAATAACAGCCAGTTTGCAAAAGGTG-----GAAAATGAT------
O6_Ptro GGAGCAATAACAGCCAGTTTGCAAAAGGTG-----GAAAATGAT------
18_Cjac GGAGCAATAACAGCCAGTTTGCAGAAGGTG-----GAAAATGAT------
O3_Mmur GAAGCAATAAAAGCCACCTTGCAAAAGGTA-----GAAAATGAT------
50_Ggor GCTGCACTAATTGTCTATTGGGAAATGGAGGAT-----AAGAACATTATTCAATTTGTGCATGG
98_Mmur TGGGAAATGGACAATAAGAATATTATTCAA-----TTTGTTCGTGGCGAGGAAGACCTGAAGGT
43_Pabe GCTGCACTAATTGTCTATTGGGAAATGGAGGAT-----AAGAACATTATTCAATTTGTGCATGG
O4_Ptro GCCGCACTAATTGTCTATTGGGAAATGGAGGAT-----AAGAACATTATTCAATTTGTGCATGG
30_Ogar GAAGAAATAAAAGCCATTTTGCAAAAGGTA-----GAAAACGAT-------
78_Tsyr TTTTCGCTAGTTGTCTACTGGGAAATGGACAAT-----AAGAAAATTATTCAGTTTGTGCGAGG
54_Ggor GGAGCAATAACAGCCAGTTTGCAAAAGGTG-----GAAAATGAT------
```

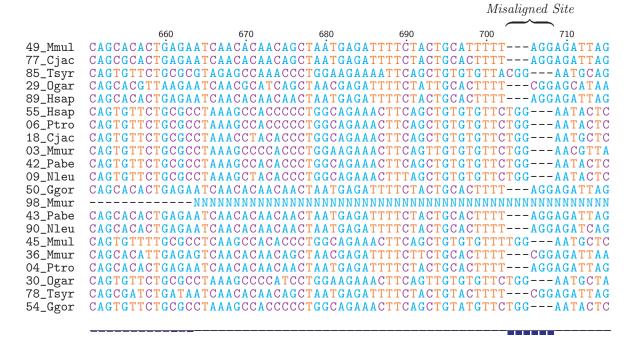
```
280 290
                          300 310
49 Mmul AGAGGAAGAČCTGAAGGTTČAGCATAGTAACTACAGACAĞAGGGCCCAGČTGTTGAAGGACCAGC
    77_Cjac
29_Ogar AGAGGAAGACCTGAAAGTTCAGGACAGTAGCTACCATCAGAGGGCCCGGCTGTTAAAGGACCAAC
55_Hsap -----ACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGC
06_Ptro -----ACATCCCCACACTGTGAAAGAGCCACTTTGCTGGAGGAGCAGC
18_Cjac -----ACATCCTCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGC
O3_Mmur -----ACAGCCTTGCCTGCTGAAAGAGCCGCTTTGCTGGAGGAGCAGC
42_Pabe -----ACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGC
O9_Nleu -----ACATCTCCACACCGTGAAAGGGCCACTTTGCTGGAGGAGCAGC
98_Mmur TCAGGACAGTAGCTACCGTGGCAGGGCCCGGCTACTGAAGGACCAGTTCTTCCTGGGAAGTGCGG
45_Mmul -----ACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGC
36_Mmur ---
30_Ogar -----ACAGCCTTGCCTGCTAAAAGAGCCACTTTGCTGGAGGAGCAGC
78_Tsyr AGAGGAAGACCTGAAGGTTCAGCACCGCAGCTTCAGCCAGAGGGCCCGGCTGCTGAAGGACCAGC
54_Ggor
    -----ACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGC
```

```
410
                                   420
                                             430
                                                        440
       TGCATGATCAGCTATGGTGGTGCC---GACTACAAGCGGATTACCGTGAAAGTCAAT----
        TGCATGATCAGCTATGGTGGTGCT---GACTACAAGCGGATTACTGTGAAAGTCAATGCTTATGA
77_Cjac
       85_Tsyr
29_0gar
       TGCACAATCATCTACGGTGGTGCA---GACTACAAGCGGATTACTTTGAAAGTCAATGCTCATGA
89_Hsap TGCATGATCAGCTATGGTGGTGCC---GACTACAAGCGAATTACTGTGAAAGTCAAT-----
55_Hsap TGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
06_Ptro TGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
18_Cjac TGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
03_Mmur TGCGTGATCATCTGTGGCGTCTCCTGGGACTACAAGTACCTGACTCTGAAAGTCAGA-----
42_Pabe TGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
O9_Nleu TGCATAATCATCTATGGGGTTGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
50_Ggor TGCATGATCAGCTATGGTGGTGCC---GACTACAAGCGAATTACTGTGAAAGTCAAT-----
98_Mmur GGTGCGGACTACAAGCGGATTACT---TTGAAAGTCAATGNNNNNNNNNNNNNNNN------
       TGCATGATCAGCTATGGTGGTGCT---GACTACAAGCGAATTACTGTGAAAGTCAAT-----
43 Pabe
90_Nleu
       TGCATGATCAGCTATGGTGGTGCC---GACTACAAGCGGATTACTGTGAAAGTCAAT-----
45_Mmul TGCATAATCATCTATGGGGTTGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
36 Mmur ------
O4_Ptro TGCATGATCAGCTATGGTGGTGCC---GACTACAAGCGAATTACTGTGAAAGTCAAT-----
30_Ogar TGCCTGATCATCTGTGGGGTTGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAGA-----
78_Tsyr
       TGTATGATCAGCTACGGTGGCGCC---GATTACAAGCGGATCACGTTGAAAGTCAAT-----
54_Ggor
       TGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAGTCAAA-----
```

```
----GCTCCATACAACAAATCAACCAAAGAATTTTGGTTGTCGATCCAGTCACCTCTGAACATG
49 Mmul
77_Cjac CCTAGCCCCATACCACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAATACG
85_Tsyr
       ----NCGTCATACAAGAAAATAATCACTCGCTTC---CTAAAGGTCCCGGGGACAGAAGAAGTGG
29_Ogar CCTAGCTCCATACCGCAAAATCAACCAAAGAATT---TCCGTGGACCAAGCCACCTTGGAACATG
      ----GCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATG
89_Hsap
55_Hsap ----GCTTCCTACAGGAAAATAAACACTCACATC---CTAAAGGTTCCAGAAACAGATGAGGTAG
O6_Ptro ----GCTTCCTACAGGAAAATAAACACTCACATC---CTAAAGGTTCCAGAAACAGATGAGGTAG
18_Cjac ----GCTTCCTACAGGAAGATAAACACTCACATC---CTAAAGGTTCCAGAAACAGATGAGGTAG
03_Mmur
       ----GCTTCCTACAAAAAATAAACACTCGCATC---CTAAACATCCCAGGGACAGACGAGGTGA
42_Pabe
       ----GCTTCCTACAGGAAAATAAACACTCACATC---CTAAAGGTTCCAGAAACAGATGAGGTAG
      ----GCTTCCTACAGGAAAATAAACACTCACATC---CTAAAGGTTCCAGAAACAGATGAGGTAG
09_Nleu
50_Ggor ----GCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATG
43_Pabe ----GCCCCATACAACAAGATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATG
90_Nleu ----GCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATG
45_Mmul
      ----GCTTCCTACAGGAAAATAAACACTCACATC---CTAAAGGTTCCAGAAACAGATGAGGTAG
36_Mmur -----CCGTATCACAAAATCAACCAAAGAATT---TCCATGGACCCAGCCACCTCTGAACACG
O4_Ptro ---GCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATG
30_Ogar ----GCTTCCTACAAGAAAATAAACACTCACGTC---CTAAAGGTCCCAGGGACAGATGAGGTAG
      ----GCCCCATACCGCAACATCAACCAAAGCATT---TCCATGGATCCGGTCACCTCCGAATATA
78_Tsyr
54_Ggor ----GCTTCCTACAGGAAAATAAACACTCACATC---CTAAAGGTTCCAGAAACAGACGAGGTAG
```

```
550
                                                    560
                                                               570
        AACTAACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATTTGGACAAGCAGTGACCATCAA
         AGCTAACATGTCAGGCTGAGGGCTATCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAA
77_Cjac
        AGCTCACCTGCCAGGCTGAAGGCTATCCCGGGGCAGAAGTGTATTGGTCCAACGTCAGTGTTCTT
85_Tsyr
29_0gar
        AACTAACGTGTCAAGCTGAGGGTTACCCCAAGGCTGAAGTCATCTGGACAAGCAGTGACCATCGA
89_Hsap AACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAA
55_Hsap AGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCT
06_Ptro AGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCT
18_Cjac AGCTCACCTGCCAGGCTACAGGTTATCCTCTAGCAGAAGTGTCCTGGCCAGACATCAGCGTTCCT
03_Mmur AGCTCACCTGCCAGGCTAGAGGTTATCCCCTGGCAGAAGTGTCCTGGCCAAACATCAGTGTTCCC
42_Pabe AGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAATGTCAGCATTCCT
O9_Nleu AGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCT
50_Ggor AACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAA
43_Pabe AACTAACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAA 90_Nleu AACTAACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAA
45_Mmul AGCTCACATGCCAGGCTACAGGTTATCCTTTGGCAGAAGTATCCTGGCCAAACATCAGCGTTCCT
36_Mmur AACTAACATGTCAGGCTGAGGGTTACCCCAAGGCTGAAGTCACCTGGACAAGCAGTGACCATCGA
O4_Ptro AACTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAA
30_Ogar AGCTCATCTGCCAGGCTGAAGGTTACCCCCTGGCAGAAGCATCCTGGCCAAACATCAGCATTCCT
78_Tsyr AACTGACATGTCAGGCTGAGGGTTACCCCAAGGCTGAAGTCATCTGGACAAGCAGTGACCATCAA
54_Ggor
        AGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCT
```

```
GTCCTGAGTGGTAAG---ACCACCACCACCACTTCCAAGAGAGAGAGAGAGCTTTTAAATGTGAC
49_Mmul
77_Cjac GTCCTGAGTGGTAAG---ACCACCACCACCACTATTCTGAGAGAGAAGAAGCTTTTCAATGTGAC
       -----GCCAACACCAGCCACACCAGGATTCCTGAAGGCCTCCAG---GTCAC
85_Tsyr
      GTCCTGAATGGCAAG---ACCACTATCACCAATTCTAAGAGGGAGAAGCTTTTGAATGTGAC
29_0gar
      GTCCTGAGTGGTAAG---ACCACCACCACCAATTCCAAGAGAGAGAGAGAGCTTTTCAATGTGAC
89_Hsap
55_Hsap
      -----GCCAACACCAGCCACTCCAGGACCCTGAAGGCCTCTACCAGGTCAC
          -----GCCAACACCAGCCACTCCAGGACCCTGAAGGCCTCTACCAGGTCAC
06_Ptro
           ------GCCAACACTAGCCACTCCAGGACTCCTGAAGGCCTCTACCAGGTCAC
18_Cjac
03_Mmur
         -----GCCAACACCAGCCACATCAGGACCCCTGAAGGCCTCTACCAGGTCAC
42_Pabe
      -----GCCAACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCAC
      -----GCCAACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCAC
09_Nleu
50_Ggor GTCCTGAGTGGTAAG---ACCACCACCACCACTATTCCAAGAGAGAGAGAGCTTTTCAATGTGAC
43_Pabe GTACTGAGTGGTAAG---ACCACCACCACCAATTCCAAGAGAGAGAGAGCTTTTCAATGTGAC
90_Nleu GTCCTGAGTGGTAAG---ACCACCACCACCAATTCCAAGAGAGAGAGAGCTTTTCAATGTGAC
45_Mmul
      -----GCCAACACCAGCCACTCCAGGACCCTGAAGGCCTCTACCAGGTCAC
36_Mmur GTCCTGAGTGGCAGG---ACCACGATCACCAATTCCAAGAGGGAGCAGCTTTTCAATGTGAC
O4_Ptro GTCCTGAGTGGTAAG---ACCACCACCACCAATTCCAAGAGAGAGAGAGCTTTTCAATGTGAC
      -----GCCAACACACCAGCCAGCATCAAGATCCCTGAAGGCCTCTACCAGGTCAC
30_Ogar
78_Tsyr
      GTCCTGAGTGGTCAG---ACCACAATCACCAATTCTGAGAGAGAGAGAGCTTTTCAATGTGAC
54_Ggor
      -----GCCAACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCAC
```



```
740
                                    750
                                             760
49_Mmul ATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCT---CTGGCGCTTCCTCCA
77_Cjac ATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACAACCT---CTGGTACTTCCTCCA
      ACGTGAAGGAACTTACTTCAGCCATCATT---GACCCTCAAAGTCAGGCGGACCCCGGGGCCTCC
85_Tsyr
29_Ogar ATCCCGAGGAAAACAGTACAGCTGAGTTAGTCATTCCAGAATCACCT---CTGGTATTTACCCCA
89_Hsap ATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCT---CTGGCACATCCTCCA
55_Hsap ACGTGAGGGAACTTACTTTGGCCAGCATT---GACCTTCAAAGTCAGATGGAACCC---AGGACC
06_Ptro ACGTGAGGGAACTTACTTTGGCCAGCATT---GACCTTCAAAGTCAGATGGAACCC---AGGACC
18_Cjac CTGTGAGGGAACTTACTTTGGCCAGCATT---GACCCTCAAAGTCAAATGGAACCC---AGGGCC
O3_Mmur ATGTAAAGGAACTTACTGCAGCCAACATCAGTGACCCTCAAAGTTGGATAGATCCC---GAGGTC
42_Pabe ACGTGAGGGAACTTACTTTGGCCAGCATT---GACCTTCAAAGTCAGATGGAATCC---AGGACC
O9_Nleu ACGTGAAGGAATTTACTTCGGCCAGCATT---GACCTTCAAAGTCAGATGGAACCC---AGGACC
50_Ggor
      ATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCT---CTGGCACATCCTCCA
      98_Mmur
43_Pabe ATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCT---CTGGCACATCCTCCA
90_Nleu ATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCT---CTGGCACATCCTCCA
      AAGTGAGGGAACTTACTTTGGCCAGCATT---GACCTTCAAAGTCAGATAGAACCC---AGGACC
45_Mmul
36_Mmur
      ATCTCGAGGAAAACAATACAGCTGAGTTGGTCATCCCAGNNNNNNN---NNNNNNNNNNNNNNNNNN
04_Ptro
      30_0gar
78_Tsyr
      ACGTGAGGGAACTTACTTTGGCCAGCATT---GACCTTCAAAGTCAGATGGAACAC---AGGACC
54_Ggor
```

	790	800		810	820	830	840
49_Mmul	AATGAAAGGAC	TCACTTGGT	AATTCTGGG	AGCCATC	TTTTTACTC	CTTGGTGTA	GCACTGACATT
77_Cjac	AATGAAAGGAC	TCACTTGGT	AATTCTGGG	AGCCATC	TTGTTATTC	CTTGGTGTA	GCACTGACATT
85_Tsyr	ACGACTCC	GCTGCTCCAC	CGCGCTGGT	CCCTTCC	TGCGCCATC	GCCTTTGTC'	TTCACAGCCAC
29_0gar	AATGAGAGGAC	CCACCTGATO	GATTGTAGG	AGCCTTC	CTGTTTTCC	TTTGTTATA	ATGTTGATGGG
89_Hsap	AATGAAAGGAC	TCACTTGGT	AATTCTGGG	AGCCATC	TTATTATGC	CTTGGTGTA	GCACTGACATT
55_Hsap	CATCCAACTTG	GCTGCTTCAC	CATTTTCAT	CCCCTTC	IGCATCATT	GCTTTCATT	TTCATAGCCAC
06_Ptro	CATCCAACTTG	GCTGCTTCAC	CATTTTCAT	CCCCTCC	IGCATCATT	GCTTTCATT	TTCATAGCCAC
18_Cjac	TCTCCAACTTG	GCTGCTTCAC	CATTCTCAT	CCCCTCC	IGCATCATT	GCTTTCATT	TTTACAGCCAC
03_Mmur	ACGCCAACTTC	GCTGCTTCAC	CATTTTCAT	CCCTTCC	TGCACCATO	GCTTTAATT	TTCATAGCCAC
42_Pabe	CGTCCAACTTG	GCTGCTTCAT	FATTTTCAT	CCCCTCC	IGCATCATT	GCTTTCATT	TTCATAGCCAC
09_Nleu	CGTCCAACTTG	GCTGCTTCAC	CATTTTCAT	CCCCTCC	IGCATCATT	GCTTTCATT	TTCATAGCCAC
50_Ggor	AATGAAAGGAC	TCACTTGGT	AATTCTGGG	AGCCATC	TTATTATTC	CTTGGTGTA	GCACTGACATT
98_Mmur	NNNNNNNNNN	NNNNNNN	NNNNNNNN	NNNNNN	NNNNNNNN	NNNNNNNNN	NNNNNNNNNN
43_Pabe	AATGAAAGGAC	TCACCTGGTA	AATTCTGGG	AGCCATC	TTATTATTC	CTTGGTGTA	GCACTGACATT
90_Nleu	AATGAAAGGAC	TCACTTGGT	AATTCTGGG	AGCCATC	TTAGTATTC	CTTGGTGTA	GCACTGACATT
45_Mmul	CATCCAACTTG	GCTGCTTCAC	CATTTTCAT	CCCCTCC	TGCATCATC	GCTTTCATT	TTCATAGCCAC
36_Mmur	NNNNNNNNNN	NNNNNNN	NNNNNNNN	NNNNNNI	NNNNNNNN	NNNNNNNN	NNNNNNNNNN
04_Ptro	AATGAAAGGAC	TCACTTGGT	AATTCTGGG	AGCCATC	TTATTATGC	CTTGGTGTA	GCACTGACATT
30_0gar	CCTACAACTTC	GCTGCTTCAC	CATTCTCAT	CCCTTCC	TGCACTATT	GCTTTAATT	TTCATAACCAC
78_Tsyr	AATCAGAGGAC	TCACTTGGT	GATTCTGGG	AGCCTTC	CTGTTGACC	CTTGGTGTG	GTCCTGGTGAG
54_Ggor	CATCGAACTTG	GCTGCTTCAC	CATTTTCAT	CCCCTCC	TGCATCATT	GCTTTCATT	TTCATAGCCAC
•							

```
880
       CATCTTCTAT----TTA---AGA---AAAGGGAGAATGATGATATGAAAAAAGTGGCA
49_Mmul
       CATCTTCTAT----TTA---AGA---AAAGGGAGATGATGGATTTGAAAATATGTGGCA
77_Cjac
       85_Tsyr
       CATCTTCTGT----TTA---AGAAGAAAAGGGGGAATGAAAGATGTGGAAAAATGTTGCACATCTTCCGT----TTA---AGA---AAAGGGAGAATGATGGATGTGAAAAAAATGTTGCA
29_Ogar
89_Hsap
       AGTGATAGCC-----CTAAGAAAACAACTCTGTCAAAAGCTGTATTCTTCAAAA---GACA
55_Hsap
       AGTGATAGCC-----CTAAGAAAACAACTCTGTCAAAAAGCTGTATTCTTCAAAAA---GACA
06_Ptro
       AATGATAGCC-----CTAAGAAAACAACACTGTCAAAAGCTGTATTCTACAAAAGGTAAAC
18_Cjac
       AATGATAATC-----CTCAGAAAATGGCTCTGCCAAAAGCTCTATTCTAGAAAA---GACA
03_Mmur
       AGTGATAGCC-----CTAAGAAAACAACTCTGTCAAAAGCTGTATTCTTCAAAA---GACAAGTGATAGCC-----CTAAGAAAACAACTCTGTCAAAAGCTGTATTCTTCAAAA---GACA
42_Pabe
09_Nleu
       CATCTTCTGT-----TTA---AGA---AAAGGGAGAATGATGGATGTGAAAAAATGTGGCA
50_Ggor
98_Mmur
       NNNNNNNNNNNNNNNNNNNNNNN---NNNNNNNNTGAGAATAATGGATGTGGAAAGATGTGGCA
43_Pabe
       CATCTTCTGT-----TTA---AGA---AAAGGGAGAATGATGGATGTGAAAAAATGTGGCA
       CATCTTCTGT----TTA---AGA---AAAGGGAGAATGATGATGTGAAAAAATGTGGCA
90_Nleu
45_Mmul
       AGTGATAGCC-----CTAAGAAAACAACTCTGTCAAAAGCTGTATTCTTCAAAAA---GACA
       \verb|NNNNNNNN------NNN------| NNNNNNTGAGAATAATGGATGTGGAAAGATGTGGCA| \\
36_Mmur
       04_Ptro
       AATGATAGTC----CTAAGAAAACGGCTCTGCCATAAGCTGTATTCTGGGAAA---GACA
30_Ogar
       CACCTCCTGT-----CTG--CGAAAA-----
78_Tsyr
       AGTGATAGCC-----CTAAGAAAACAACTCTGTCAAAAGCTGTATTCTTCAAAA---GACA
54_Ggor
```

