

## MX-HIV-0086 PROTEASE FRAGMENT (Fwd & Rev)

>86\_PR\_F

GGAgGaGcTatAtCCTCTAACctcCCTCAAATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAGATAGGAGGGCAACTAAAGGAAGCTCTGTTAGAT  
ACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTACCAGGAAGATGGAAACCAAAAATGATAGGGGGAATTTGGAGGTTTTATCAAAGTAAGGCAG  
TATGATCAGGTACCCATAGAAATCTGCGGACATAAACTGTAGGTACAGTATTAATAGGACCTACACCTGTCAACATAATTGGAAGAAATCTATTGACT  
CAAATTTGGCTGTACTTTAAATTTTCCCATTAGTCCATTGAGACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGTTAAACAATGGCCA  
TTGACAGAA

>86\_PR\_R

AGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATAACAACCTCCCTCTCAGAAACAGGAGGAGCTATATCCTCTAACCTCCCTCAA  
ATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAGATAGGAGGGCAACTAAAGGAAGCTCTGTTAGATACAGGAGCAGATGATACAGTATTAGAAGAA  
ATGAATTTACCAGGAAGATGGAAACCAAAAATGATAGGGGGAATTTGGAGGTTTTATCAAAGTAAGGCAGTATGATCAGGTACCCATAGAAATCTGCGGA  
CATAAACTGTAGGTACAGTATTAATAGGACCTACACCTGTCAACATAATTGGAAGAAATCTATTGACTCAAATTTGGCTGTACTTTAAATTTTCCCATT  
AGTCTATTGAGACTGTACCAGTAAAATTAAGCC

### Nucleotide Alignments

```
1
|
86_PR_F *****GGAGGA
86_PR_R AGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATAACAACCTCCCTCTCAGAAACA-----

101
|
86_PR_F GCTATATCCTCTAACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAGATAGGAGGGCAACTA
86_PR_R -----

201
|
86_PR_F AAGGAAGCTCTGTTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTACCAGGAAGATGGAAACCA
86_PR_R -----

301
|
86_PR_F AAAATGATAGGGGGAATTTGGAGGTTTTATCAAAGTAAGGCAGTATGATCAGGTACCCATAGAAATCTGCGGACAT
86_PR_R -----

401
|
86_PR_F AAAACTGTAGGTACAGTATTAATAGGACCTACACCTGTCAACATAATTGGAAGAAATCTATTGACTCAAATTTGGC
86_PR_R -----

501
|
86_PR_F TGTACTTTAAATTTTCCCATTAGTCCATTGAGACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAA
86_PR_R -----*****

601
|
86_PR_F GTTAAACAATGGCCATTGACAGAA
86_PR_R *****
```

>86\_PR

AGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATAACAACCTCCCTCTCAGAAACAGGAgGaGcTatAtCCTCTAACctcCCTCAA  
ATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAGATAGGAGGGCAACTAAAGGAAGCTCTGTTAGATACAGGAGCAGATGATACAGTATTAGAAGAA  
ATGAATTTACCAGGAAGATGGAAACCAAAAATGATAGGGGGAATTTGGAGGTTTTATCAAAGTAAGGCAGTATGATCAGGTACCCATAGAAATCTGCGGA  
CATAAACTGTAGGTACAGTATTAATAGGACCTACACCTGTCAACATAATTGGAAGAAATCTATTGACTCAAATTTGGCTGTACTTTAAATTTTCCCATT  
AGTCTATTGAGACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGTTAAACAATGGCCATTGACAGAA

## MX-HIV-0086 REVERSE TRANSCRIPTASE FRAGMENT A (Fwd & Rev)

>86\_RTa\_F

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aAATCTATTGACTCAaATTGGCTGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGT
TAAACAATGGCCATTGACAGAAGAAAAATAAAGCATTAGTAGAAATTTGTACAGAAGTGGAAAAGGAAGAAAAATTTCAAAGATTGGGCCTGAAAA
CCCATACAATACTCCAGTATTTGCCATAAAAGAAAAGGATAGTACTAAATGGAGAAAATTAGTAGATTTTCAGAGAAGTAAATAAAAGAACTCAAGACTT
CTGGGAAGTTCAATTAGGGATACCACATCCTGCAGGGTTAAAAAAGAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCTT
AGATAAAGGCTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAACAATGAGACACCGGGATCAGATATCAGTACAATGTGCTTCCACAAGGATG
GAAAGGATCACCAGCAATATTTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGGAAACAAAAATCCAGACATAGTTATCTATCAATACATGGATGA
TTTGTATGTAGGATCTGACTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAACTAAGACAACATCTGTTGAGGTGGGGATTTGACACACCAGACAA
AAAGCATCAAAAAGAACCTCCATTCCTTTGGATGGGGTATGAACCTCCATCCTGAAAAATGGaCAGTACAGCCTATAGAAGTCCAGAAAAGGATAGCTG
GACTGTCAATGACATACAGAAGTTAGTGGGAAAATTAATTTGGGCAAGTCaGATTTATGCAGGGATTCaGTAAGCAATTTATGTAAACTCCTTAGGGG
AACCAAGCACTAACAGAAGTGATACCCTaCTaCAGCAGA
```

>86\_RTa\_R

```
AAACTGTaCCAGTaAAATtAAAGCCAGGAATGGATGGCCAAAAGTtAAACAATgGCCAtTGACAGAAGAAAAATAAAGCATTAGTAGAAATTTGTA
CAGAAGTGGAAAAGGAAGGAAAAATTTCAAAGATTGGGCCTGAAAACCCATACAATActCCAGTATTTGCCATAAAAGAAAAGGATAGTACTAAATGGA
GAAAATTAGTAGATTTTCAGAGAAGTAAATAAAAGAACTCAAGACTTCTGGGAAGTTCAATTAGGGATACCACATCCTGCAGGGTTAAAAAAGAAAAAT
CAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCTTAGATAAAGGCTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAACAATG
AGACACCGGGGATCAGATATCAGTACAATGTGCTTCCACAAGGATGAAAAGGATCACCAGCAATATTCAAAGTAGCATGACAAAAATCTTAGAGCCTT
TTAGGAAACAAAAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGG
AACTAAGACAACATCTGTTGAGGTGGGGATTTGACACACCAGACAAAAAGCATCAAAAAGAACCTCCATTCCTTTGGATGGGGTATGAAGTCCATCCTG
AAAAATGGACAGTACAGCCTATAGAAGTGCAGAAAAGGATAGCTGGACTGTCAATGACATACAGAAGTTAGTGGGAAAATTAATTTGGGCAAGTCAGA
TTTATGCAGGGATTCAGTAAAGCAATTTATGTAAACTCCTTAGGGGAACCAAGCACTAACAGAAGTGATACCCTAACAGCAGAAGCAGAGCTAGAAC
TGGCAGAAAACAGGGAG
```

### Nucleotide Alignments

```

      1
      |
86_RTa_F  AAATCTATTGACTCAaATTGGCTGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAA
86_RTa_R  *****-----

     101
     |
86_RTa_F  GCCAGGAATGGATGGCCAAAAGTtAAACAATGGCCATTGACAGAAGAAAAATAAAGCATTAGTAGAAATTTG
86_RTa_R  -----

     201
     |
86_RTa_F  TACAGAAGTGGAAAAGGAAGGAAAAATTTCAAAGATTGGGCCTGAAAACCCATACAATACTCCAGTATTTGCCAT
86_RTa_R  -----

     301
     |
86_RTa_F  AAAGAAAAGGATAGTACTAAATGGAGAAAATTAGTAGATTTTCAGAGAAGTAAATAAAAGAACTCAAGACTTCTG
86_RTa_R  -----

     401
     |
86_RTa_F  GGAAGTTCAATTAGGGATACCACATCCTGCAGGGTTAAAAAAGAAAAATCAGTAACAGTACTGGATGTGGGTGA
86_RTa_R  -----

     501
     |
86_RTa_F  TGCATATTTTTCAGTTCCTTAGATAAAGGCTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAACAATGA
86_RTa_R  -----

     601
     |
86_RTa_F  GACACCGGGGATCAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAGGATCACCAGCAATATTCAAAGTAG
86_RTa_R  -----
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```

701
|
86_RTa_F CATGACAAAAATCTTAGAGCCTTTTAGGAAACAAAATCCAGACATAGTTATCTATCAATACATGGATGATTGTA
86_RTa_R -----
801
|
86_RTa_F TGTAGGATCTGACTTAGAAAATAGGGCAGCATAGAACAAAATAGAGGAAC TAAGACAACATCTGTTGAGGTGGGG
86_RTa_R -----
901
|
86_RTa_F ATTTGACACACCAGACAAAAGCATCAAAAAGAACCTCCATTCCCTTGGATGGGGTATGAACTCCATCCTGAAAA
86_RTa_R -----
1001
|
86_RTa_F ATGGACAGTACAGCCTATAGAACTGCCAGAAAAGGATAGCTGGACTGTCAATGACATACAGAAGTTAGTGGGAAA
86_RTa_R -----
1101
|
86_RTa_F ATTAAATTGGGCAAGTCAGATTTATGCAGGGATTCAAGTAAAGCAATTATGTAAACTCCTTAGGGGAACCAAAGC
86_RTa_R -----
1201
|
86_RTa_F ACTAACAGAAGTGATACCACTAACAGCAGA*****
86_RTa_R -----AGCAGAGCTAGAACTGGCAGAAAACAGGGAG

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Written by James Robinson, Last modified 11/02/03.

>86\_RTa

```

aAATCTATTGACTCAaATTGGCTGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGT
TAAACAATGGCCATTGACAGAAGAAAAATAAAGCATTAGTAGAAATTTGTACAGAACTGGAAAAGGAAGGAAAAATTTCAAAGATTGGGCCTGAAAA
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CTGGGAAGTTCAATTAGGGATACCACATCCTGCAGGGTTAAAAAAGAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCTT
AGATAAAGGCTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAACAATGAGACACCGGGGATCAGATATCAGTACAATGTGCTTCCACAAGGATG
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TTTGTATGTAGGATCTGACTTAGAAAATAGGGCAGCATAGAACAAAATAGAGGAAC TAAGACAACATCTGTTGAGGTGGGGATTTGACACACCAGACAA
AAAGCATCAAAAAGAACCTCCATTCCCTTGGATGGGGTATGAACTCCATCCTGAAAAATGGaCAGTACAGCCTATAGAACTGCCAGAAAAGGATAGCTG
GACTGTCAATGACATACAGAAGTTAGTGGGAAAATTAATTTGGGCAAGTCaGATTTATGCAGGGATTCaagTAAAGCAATTATGTAAACTCCTTAGGGG
AACCAAAGCACTAACAGAAGTGATACCcTAaCAGCAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAG

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# MX-HIV-0086 REVERSE TRANSCRIPTASE FRAGMENT B (Fwd & Rev)

>86\_RTb\_F

TTCAAGTAAAGCAATTATGTAAACTCCTTAGGGGAACCAAAGCACTAACAGAAGTGATACCCTAACAGCAGAAGCAGAGCTAGAAGTGGCAGAAAACA  
GGGAGATTCTAAAAGAACCAGTACATGGAGTGTATTATGACCCCTCAAAGACTTAATAGCAGAAAATACAGAAGCAGGGACATGGCCAATGGACCTATC  
AAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATTCAAGAATAAGGGGTGCCACACTAATGATGTAAAACAATTAACAGAGGCAGTGC  
AAAAATATCCATAGAAGCCATAGTCATATGGGAAAGGTCCCTAAATTTAGATTACCCATACAAAAAGAAACATGGGAAACATGGTGGACAGAGTATT  
GGCAGGCCACCTGGGTTCCTGAGTGGGAATTTGTCAATACCCCTCCTTTAGTAAAATTTATGGTATCAGCTAGAAAAAGAACCCATAGTGGGAGCAGAAA  
CTTTCTATGTAGATGGGCAGCTAATAGGGAAACTAAACTAGGAAAAGCAGGATATGTTACAGACAGAGGAAGACAAAAAGTTGTCCCCCTAACGGACA  
CAACAAATCAGAAGACTGAATTACAAGCAATTTATCTAGCTTTGCAGGATTCAGGATTTAGAAGTAAACATAGTAACAGATTCACAATATGCATTAGGAA  
TCCTTCAGGCACAACCGATAAAAAGTGAATCAGAAATGGTCAATCAATAATAGAGCAGTTAATAAAAAAGGAAAAAGATCTACCTGGCATGGGTACCAG  
CACAAAAGGAATTGGagGAAATGAACAAGTAGATAAATTAGTCAGTCTGGAATCAGGAAAGTACTAtTtTTAGATGGAATAgATAaGGcTCAagAtG  
AACATGAAAAATATC

>86\_RTb\_R

AGGGGaaCCAAAGCAcTaACAGAAGTGATacCACTaACAGCAGaAGCAGAGCTAGaACTGGCAGaaaACAGGGAGATTCTAAAAGAACCAGTACATGGA  
GTGTATTATGACCCCTCAAAGACTTAATAGCAGAAAATACAGAAGCAGGGACATGgCCAATGGACCTATCAAATTTATCAAGAGCCATTTAAAAATCTG  
AAAACAGGAAAGTATTCAGAATAAGGGGTGCCACACTAATGATGTAAAACAATTAACAGAGGCAGTGCAAAAAATATCCATAGAAGCCATAGTCATA  
TGGGAAAGGTCCCTAAATTTAGATTACCCATACAAAAAGAAACATGGGAAACATGGTGGACAGAGTATTGGCAGGCCACCTGGGTTCCTGAGTGGGAA  
TTTGTCAATACCCCTCCTTTAGTAAAATTTATGGTATCAGCTAGAAAAAGAACCCATAGTGGGAGCAGAAACTTTCTATGTAGATGGGCAGCTAATAGG  
GAACTAAACTAGGAAAAGCAGGATATGTTACAGACAGAGGAAGACAAAAAGTTGTCCCCCTAACGGACACAACAAATCAGAAGACTGAATTACAAGCA  
ATTTATCTAGCTTTGCAGGATTCAGGATTTAGAAGTAAACATAGTAACAGATTCACAATATGCATTAGGAATCCTTCAGGCACAACCGGATAAAAAGTGAA  
TCAGAAATGGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGAAAAAGATCTACCTGGCATGGGTACCAGCACACAAGGAATTGGAGGAAATGAACAA  
GTAGATAAATTAGTCAGTCTGGAATCAGGAAAGTACTATTTtTTAGATgGAATAGATaAg

## Nucleotide Alignments

```

      1
      |
86_RTb_F  TTCAAGTAAAGCAATTATGTAAACTCCTTAGGGGAACCAAAGCACTAACAGAAGTGATACCCTAACAGCAGAAG
86_RTb_R  *****_-----

     101
     |
86_RTb_F  CAGAGCTAGAAGTGGCAGAAAACAGGGAGATTCTAAAAGAACCAGTACATGGAGTGTATTATGACCCCTCAAAG
86_RTb_R  -----

     201
     |
86_RTb_F  ACTTAATAGCAGAAAATACAGAAGCAGGGACATGGCCAATGGACCTATCAAATTTATCAAGAGCCATTTAAAAATC
86_RTb_R  -----

     301
     |
86_RTb_F  TGAAAACAGGAAAGTATTCAAGAATAAGGGGTGCCACACTAATGATGTAAAACAATTAACAGAGGCAGTGCAAA
86_RTb_R  -----

     401
     |
86_RTb_F  AAATATCCATAGAAGCCATAGTCATATGGGAAAGGTCCCTAAATTTAGATTACCCATACAAAAAGAAACATGGG
86_RTb_R  -----

     501
     |
86_RTb_F  AAACATGGTGGACAGAGTATTGGCAGGCCACCTGGGTTCCTGAGTGGGAATTTGTCAATACCCCTCCTTTAGTAA
86_RTb_R  -----

     601
     |
86_RTb_F  AATTATGGTATCAGCTAGAAAAAGAACCCATAGTGGGAGCAGAACTTTCTATGTAGATGGGCAGCTAATAGG
86_RTb_R  -----

     701
     |
86_RTb_F  AAACAACTAGGAAAAGCAGGATATGTTACAGACAGAGGAAGACAAAAAGTTGTCCCCCTAACGGACACAACAA
86_RTb_R  -----
```

```

801
|
86_RTb_F ATCAGAAGACTGAATTACAAGCAATTTATCTAGCTTTGCAGGATTCAGGATTAGAAGTAAACATAGTAACAGATT
86_RTb_R -----

901
|
86_RTb_F CACAATATGCATTAGGAATCCTTCAGGCACAACCGGATAAAAAGTGAATCAGAAATGGTCAATCAAATAATAGAGC
86_RTb_R -----

1001
|
86_RTb_F AGTTAATAAAAAAGGAAAAGATCTACCTGGCATGGGTACCAGCACACAAAGGAATGGAGGAAATGAACAAGTAG
86_RTb_R -----

1101
|
86_RTb_F ATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTTTAGATGGAATAGATAAGGCTCAAGATGAACATGAAA
86_RTb_R -----*****

1201
|
86_RTb_F AATATC
86_RTb_R *****

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Written by James Robinson, Last modified 11/02/03.

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>86_RTb
TTCAAGTAAAGCAATTATGTAAACTCCTTAGGGGAACCAAAGCACTAACAGAAGTGATACCACTAACAGCAGAAGCAGAGCTAGAACTGGCAGAAAACA
GGGAGATTCTAAAAGAACAGTACATGGAGTGTATTTATGACCCCTCAAAGACTTAATAGCAGAAATACAGAAGCAGGGACATGGCCAATGGACCTATC
AAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATTCAGAATAAGGGGTGCCACACTAATGATGTAAAACAATTAACAGAGGCAGTGC
AAAAAATATCCATAGAAGCCATAGTCATATGGGGAAAGGTCCCTAAATTTAGATTACCCATACAAAAAGAAACATGGGAAACATGGTGGACAGAGTATT
GGCAGGCCACCTGGGTTCCTGAGTGGGAATTTGTCAATACCCCTCCTTTAGTAAAAATTATGGTATCAGCTAGAAAAAGAACCCTAGTGGGAGCAGAAA
CTTTCATGTAGATGGGGCAGCTAATAGGGAAACTAAACTAGGAAAAGCAGGATATGTTACAGACAGAGGAAGACAAAAAGTTGTCCCTAACGGACA
CAACAAATCAGAAGACTGAATTACAAGCAATTTATCTAGCTTTGCAGGATTCAGGATTAGAAGTAAACATAGTAACAGATTCAATATGCATTAGGAA
TCCTTCAGGCACAACCGGATAAAAAGTGAATCAGAAATGGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGATCTACCTGGCATGGGTACCAG
CACACAAAGGAATTTGGagGAAATGAACAAGTAGATAAAATTAGTCAGTGCTGGAATCAGGAAAGTACTAtTTTTAGATGGAATAgATAaGGcTCaagAtG
AACATGAAAAATATC

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# MX-HIV-0086 INTEGRASE FRAGMENT (Fwd & Rev)

>86\_IN\_F

tATTTT TAGATGGaaTAGATAAGGCTCAAGATGAACATGAAAAATATCACAGTAATTGGAGAGCGATGGCTAGTGATTTTAACCTGCCACCTATAGTAG  
CAAAAGAAATAGTGGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAGCTAGATTGTA  
CACACTTAGAAGGAAAAGTTATTCTAGTAGCAGTTCATGTGGCCAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGGCCAGAAACAGCAT  
ACTTCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGTGGCAATTCATCAGTAATGCAGTTAAGGCCGCTGTGGT  
GGCAGGGATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAAGGAGTAGTGAATCTATAAATAAAGAATTAAAGAAAATTATAGGACAAG  
TAAAAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGTACAGTGCAGGGG  
AAAGAATAGTAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAACCAATTTACAAAATTTCAAATTTTCGGGTTTATTACAGGGACAGCA  
GAGATCCACTTTGAAAAGGACCAGCAAAGCTTCTCTGAAAAGGTGAAGGGCAGTAGTGATACAAGATAATAGTGAATAAAAGTAGTGCCAAGAAGAA  
AAGCAAAGATCATTAGGGATTATGAAAAACAGATGGCAGGTGATGATTTGTGTGGCAGTAGACAGGATGAGGATTAGCAAATGGAAAA

>86\_IN\_R

TGCTgGaATCAGGAAAGTACTATTTT TAGATGGAATAGATAAGGCTCAAGATGAACATGAAAAATATCACAGTAATTGGAGAGCGATGGCTAGTGATTT  
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AATATGGCAGCTAGATTGTACACACTTAGAAGGAAAAGTTATTCTAGTAGCAGTTCATGTGGCCAGTGGATATATAGAAGCAGAAGTTATTCAGCAGA  
GACAGGGCCAGAAAACAGCATACTTCCCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGTGGCAATTCATCAGTAATGC  
AGTTAAGGCCGCTGTGGTGGCCAGGGATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAAGGAGTAGTGAATCTATAAATAAAGAATT  
AAAGAAAATTATAGGACAAGTAAAAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGAT  
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GGTTTATTACAGGGACAGCAGAGATCCACTTTGAAAAGGACCAGCAAAGCTTCTCTGAAAAGGTGAAGGGCAGTAGTGATACAAGATAATAGTGAAT  
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## Nucleotide Alignments

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      1
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86_IN_F *****TATTTT TAGATGGAATAGATAAGGCTCAAGATGAACATGAAAAATATCACAGTAA
86_IN_R TGCTGGAATCAGGAAAGTAC-----

     101
     |
86_IN_F TTGGAGAGCGATGGCTAGTGATTTTAACCTGCCACCTATAGTAGCAAAAGAAATAGTGGCCAGCTGTGATAAATG
86_IN_R -----

     201
     |
86_IN_F TCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAGCTAGATTGTACACACTT
86_IN_R -----

     301
     |
86_IN_F AGAAGGAAAAGTTATTCTAGTAGCAGTTCATGTGGCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGAC
86_IN_R -----

     401
     |
86_IN_F AGGGCCAGAAAACAGCATACTTCCCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGG
86_IN_R -----

     501
     |
86_IN_F TGGCAATTTTCATCAGTAATGCAGTTAAGGCCGCTGTGGTGGCAGGGATCAAGCAGGAATTTGGCATTCCCTA
86_IN_R -----

     601
     |
86_IN_F CAATCCCCAAAGTCAAGGAGTAGTGGAACTATAAATAAAGAATTAAAGAAAATTATAGGACAAGTAAAAGATCA
86_IN_R -----

     701
     |
86_IN_F GGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGG
86_IN_R -----
```

86\_IN\_F 801  
|  
GTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAACCAAATTAC  
86\_IN\_R -----

86\_IN\_F 901  
|  
AAAAATTTCAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGACCAGCAAAGCTTCTCTG  
86\_IN\_R -----

86\_IN\_F 1001  
|  
GAAAGGTGAAGGGGCAGTAGTGATACAAGATAATAGTGAAATAAAAAGTAGTGCCAAGAAGAAAAGCAAAGATCAT  
86\_IN\_R -----

86\_IN\_F 1101  
|  
TAGGGATTATGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGCAAATGGAAAA  
86\_IN\_R -----\*\*\*\*\*

Written by James Robinson, Last modified 11/02/03.

>86\_IN  
TGCTGGAATCAGGAAAGTACTATTTTTAGATGGaaTAGATAAGGCTCAAGATGAACATGAAAAATATCACAGTAATTGGAGAGCGATGGCTAGTGATTT  
TAACCTGCCACCTATAGTAGCAAAAGAAATAGTGGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGG  
AATATGGCAGCTAGATTGTACACACTTAGAAGGAAAAGTTATTCTAGTAGCAGTTCATGTGGCCAGTGGATATATAGAAGCAGAAGTTATCCAGCAGA  
GACAGGGCCAGAAACAGCATACTTCCTCTTAAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGTGGCAATTCATCAGTAATGC  
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AAAGAAAATTATAGGACAAGTAAAAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGAT  
TGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAACCAAATTACAAAAATTTCAAATTTTCG  
GGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGACCAGCAAAGCTTCTCTGGAAAGGTGAAGGGGCAGTAGTGATACAAGATAATAGTGAAT  
AAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGGATTATGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGCA  
AATGGAAAA





2685 2759  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
AAA ATT TCA AAA ATT GGG CCT GAA AAT CCA TAC AAT ACT CCA GTA TTT GCC ATA AAG AAA AAA GAC AGT ACT AAA  
\*\*\* \*\*

2760 2834  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
TGG AGA AAA TTA GTA GAT TTC AGA GAA CTT AAT AAG AGA ACT CAA GAC TTC TGG GAA GTT CAA TTA GGA ATA CCA  
\*\*\* \*\*

2835 2909  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
CAT CCC GCA GGG TTA AAA AAG AAA AAA TCA GTA ACA GTA CTG GAT GTG GGT GAT GCA TAT TTT TCA GTT CCC TTA  
\*\*\* \*\*

2910 2984  
B.FR.83.HXB2  
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86\_RTa  
86\_RTb  
86\_IN  
GAT GAA GAC TTC AGG AAG TAT ACT GCA TTT ACC ATA CCT AGT ATA AAC AAT GAG ACA CCA GGG ATT AGA TAT CAG  
\*\*\* \*\*

2985 3059  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
TAC AAT GTG CTT CCA CAG GGA TGG AAA GGA TCA CCA GCA ATA TTC CAA AGT AGC ATG ACA AAA ATC TTA GAG CCT  
\*\*\* \*\*

3060 3134  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
TTT AGA AAA CAA AAT CCA GAC ATA GTT ATC TAT CAA TAC ATG GAT GAT TTG TAT GTA GGA TCT GAC TTA GAA ATA  
\*\*\* \*\*

3135 3209  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
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3210 3284  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
CAT CAG AAA GAA CCT CCA TTC CTT TGG ATG GGT TAT GAA CTC CAT CCT GAT AAA TGG ACA GTA CAG CCT ATA GTG  
\*\*\* \*\*



3885 3959  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
GCT AAC AGG GAG ACT AAA TTA GGA AAA GCA GGA TAT GTT ACT AAT AGA GGA AGA CAA AAA GTT GTC ACC CTA ACT  
\*\*\* \*\*  
--- -T --- -A --- C- --- --- --- --- --- -A G-C --- --- --- --- --- C- --- -G  
A N R E T K L G K A G Y V T N/D R G R Q K V V T/P L T

3960 4034  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
GAC ACA ACA AAT CAG AAG ACT GAG TTA CAA GCA ATT TAT CTA GCT TTG CAG GAT TCG GGA TTA GAA GTA AAC ATA  
\*\*\* \*\*  
--- --- --- --- --- -A --- --- --- --- --- -A --- --- --- --- ---  
D T T N Q K T E L Q A I Y L A L Q D S G L E V N I

4035 4109  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
GTA ACA GAC TCA CAA TAT GCA TTA GGA ATC ATT CAA GCA CAA CCA GAT CAA AGT GAA TCA GAG TTA GTC AAT CAA  
\*\*\* \*\*  
--- --- -T --- --- --- --- --- --- --- C- -G --- -G --- A- --- --- -A A-G --- --- ---  
V T D S Q Y A L G I I/L Q A Q P D Q/K S E S E L/M V N Q

4110 4184  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
ATA ATA GAG CAG TTA ATA AAA AAG GAA AAG GTC TAT CTG GCA TGG GTA CCA GCA CAC AAA GGA ATT GGA GGA AAT  
\*\*\* \*\*  
--- --- --- --- --- --- --- --- --- --- --- A- -C --- --- --- --- --- --- --- --- --- --- ---  
I I E Q L I K K E K V/I Y L A W V P A H K G I G G N

4185 4229 4230 4259  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
GAA CAA GTA GAT AAA TTA GTC AGT GCT GGA ATC AGG AAA GTA CTA TTT TTA GAT GGA ATA GAT AAG GCC CAA GAT  
\*\*\* \*\*  
--- -T --- ---  
E Q V D K L V S A G I R K V L F L D G I D K A Q D

4260 4334  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
GAA CAT GAG AAA TAT CAC AGT AAT TGG AGA GCA ATG GCT AGT GAT TTT AAC CTG CCA CCT GTA GTA GCA AAA GAA  
\*\*\* \*\*  
--- --- -A ---  
E H E K Y H S N W R A M A S D F N L P P V/I V A K E

4335 4409  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
ATA GTA GCC AGC TGT GAT AAA TGT CAG CTA AAA GGA GAA GCC ATG CAT GGA CAA GTA GAC TGT AGT CCA GGA ATA  
\*\*\* \*\*  
--- -G ---  
I V A S C D K C Q L K G E A M H G Q V D C S P G I

4410 4484  
B.FR.83.HXB2  
86\_PR  
86\_RTa  
86\_RTb  
86\_IN  
TGG CAA CTA GAT TGT ACA CAT TTA GAA GGA AAA GTT ATC CTG GTA GCA GTT CAT GTA GCC AGT GGA TAT ATA GAA  
\*\*\* \*\*  
--- -G --- --- --- --- -C --- --- --- --- -T -A --- --- --- -G --- --- --- --- --- --- --- --- ---  
W Q L D C T H L E G K V I L V A V H V A S G Y I E

4485 4559

```

|-----|
B.FR.83.HXB2 GCA GAA GTT ATT CCA GCA GAA ACA GGG CAG GAA ACA GCA TAT TTT CTT TTA AAA TTA GCA GGA AGA TGG CCA GTA
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --G --CA --C --C
A E V I P A E T G Q/P E T A Y F L L K L A G R W P V

```

4560 4634

```

|-----|
B.FR.83.HXB2 AAA ACA ATA CAT ACT GAC AAT GGC AGC AAT TTC ACC GGT GCT ACG GTT AGG GCC GCC TGT TGG TGG GCG GGA ATC
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --A --- --T G--- -- --T- A-- AA- G-A --- --A- --- --- --A --G ---
K T I H T D N G S/G N F T/I G/S A/N T/A V R/K A A C W W A G I

```

4635 4709

```

|-----|
B.FR.83.HXB2 AAG CAG GAA TTT GGA ATT CCC TAC AAT CCC CAA AGT CAA GGA GTA GTA GAA TCT ATG AAT AAA GAA TTA AAG AAA
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --- --- --C --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
K Q E F G I P Y N P Q S Q G V V E S M/I N K E L K K

```

4710 4784

```

|-----|
B.FR.83.HXB2 ATT ATA GGA CAG GTA AGA GAT CAG GCT GAA CAT CTT AAG ACA GCA GTA CAA ATG GCA GTA TTC ATC CAC AAT TTT
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --- --- --A --- --A- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
I I G Q V R/K D Q A E H L K T A V Q M A V F I H N F

```

4785 4859

```

|-----|
B.FR.83.HXB2 AAA AGA AAA GGG GGG ATT GGG GGG TAC AGT GCA GGG GAA AGA ATA GTA GAC ATA ATA GCA ACA GAC ATA CAA ACT
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
K R K G G I G G Y S A G E R I V D I I A T D I Q T

```

4860 4934

```

|-----|
B.FR.83.HXB2 AAA GAA TTA CAA AAA CAA ATT ACA AAA ATT CAA AAT TTT CGG GTT TAT TAC AGG GAC AGC AGA AAT CCA CTT TGG
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --- --- --- --C --- --- --- --- --- TC- --A --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
K E L Q K/N Q I T K I Q/S N/K F R V Y Y R D S R N/D P L W

```

4935 5009

```

|-----|
B.FR.83.HXB2 AAA GGA CCA GCA AAG CTC CTC TGG AAA GGT GAA GGG GCA GTA GTA ATA CAA GAT AAT AGT GAC ATA AAA GTA GTG
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --- --- --- --- --T --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
K G P A K L L W K G E G A V V I Q D N S D/E I K V V

```

5010 5084

```

|-----|
B.FR.83.HXB2 CCA AGA AGA AAA GCA AAG ATC ATT AGG GAT TAT GGA AAA CAG ATG GCA GGT GAT GAT TGT GTG GCA AGT AGA CAG
86_PR *** **
86_RTa *** **
86_RTb *** **
86_IN --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
P R R K A K I I R D Y G K Q M A G D D C V A S R Q

```

```

5084          5096
|Integrase end|
B.FR.83.HXB2  GAT GAG GAT TAG *** ** *
86_PR         *** ** *
86_RTa        *** ** *
86_RTb        *** ** *
86_IN         --- --- --- CAA ATG GAA AA
              D E D X

```

Protein Alignments

```

1      10      20      30      40      50      60      70      80      90      100
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  FFREDLAFLO GKAREFSSEQ TRANSPTRRE LQVWGRDNNS PSEAGADRQG TVSFNFPOVT LWQRPPLVTK IGGQLKEALL DTGADDTVLE EMSLPGRWKP
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              *-----G-----L--T-. . . .-AI-S-L--I-----V-----N-----

```

```

101     110     120     130     140     150     160     170     180     190     200
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  KMIGGIGGFI KVRQYDQILI EICGHKAIGT VLVGPTPVNI IGRNLLTQIG CTLNFPISPI ETVVPVKLPG MDGPKVKQWP LTEEKIKALV EICTEMEKEG
86_PR         -----VP-----TV-----I-----
86_RTa        *****
86_RTb        *****
86_IN         *****
              -----L-----

```

```

201     210     220     230     240     250     260     270     280     290     300
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  KISKIGPENP YNTPVFAIKK KDSTKWRKLV DFRELNKRTQ DFWEVQLGIP HPAGLKKKKS VTVLDVGDAY FSVPLDEDFR KYTAFTIPSI NNETPGIRYQ
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              -----KG-----

```

```

301     310     320     330     340     350     360     370     380     390     400
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  YNVLPOGWKG SPAIFQSSMT KILEPFRKQN PDIVIQYMD DLYVGSLEI GQHRTKIEEL RQHLLRWGLT TPKKKHKEPE PFLWMGYELH PDKWTVQPIV
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              -----FD-----E-----E

```

```

401     410     420     430     440     450     460     470     480     490     500
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  LPEKDSWTVN DIQKLVGKLN WASQIYPGK VRQLCKLLRG TKALTEVIPL TEEAELELAE NREILKEPVH GVIYDPSKDL IAEIQKQGQG QWTYQIQEPE
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              -----A--Q--K-----A-----A-----H-----

```

```

501     510     520     530     540     550     560     570     580     590     600
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  FKNLKTGKYA RMRGAHTNDV KQLTEAVQKI TTESIIVWIK TPKFKLPIQK ETWETWWEY WQATWIPEWE FVNTPLPLVKL WYQLEKEPIV GAETFYVDGA
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              ---S---I-----SI-A-----V---R-----V-----

```

```

601     610     620     630     640     650     660     670     680     690     700
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  ANRETKLGKA GYVTRNGRQK VVTLTDTNTQ KTELQAIYLA LQDSGLEVNI VTDSQYALGI IQAQPDSQES ELVNQIIEQL IKKEKVYLAW VPAHKGIGGN
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              -----D-----P-----L-----K-----M-----I-----

```

```

701     710     720     730     740     750     760     770     780     790     800
|      |      |      |      |      |      |      |      |      |
B.FR.83.HXB2  EQVDKLVSAG IRKVLFLDGI DKAQDEHEKY HSNWRAMASD FNLPPVVAKE IVASCDCQCL KGEAMHGQVD CSPGIWQLDC THLEKGVILV AVHVASGYIE
86_PR         *****
86_RTa        *****
86_RTb        *****
86_IN         *****
              -----I-----

```

