

MX-HIV-0395 PROTEASE FRAGMENT (Fwd & Rev)

>395_PR_F

GTCaAaATTTGGGGAGGAGACAACAATTCCTTCTCAGAAGCAGGGGACAATGGACAAGGAGGGGTATCCTCCTTTAGCTTCCCTCAGATCACTCTTTGGCAACGACCCATTGTC
ACAATAAAGACAGGGGGCAACTAAAGGAAGCTCTACTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGGAGATGGAAACAAAAATGATAGGGG
AATGGAGGTTTTATCAAGGTAAGACAGTATGAAGAAGTATCCGTAGACATCTGCGGGCATAAAGCTATAGGTACAGTATTGGTAGGGCTACACCTGTCAACATAATGGAA
GAAATCTGTTGACTCAGCTGGTTGCACCTTAAATTTCCCATTAGCCCTATTGAAACTGTACCAGTAAAAATTAAGCCAGGAGTGGATGGCCAAAAGTTAAACAATGGCCA
TT

>395_PR_R

CCAGAGCCAACAGCCCCACCAGAGGAGAGTGTCAAATTTGGGGAGGAGACAACAATTCCTTCTCAGAAGCAGGGGACAATGGACAAGGAGGGGTATCCTCCTTTAGCTTCCCT
CAGATCACTCTTTGGCAACGACCCATTGTCACAATAAAGACAGGGGGCAACTAAAGGAAGCTCTACTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGCC
AGGGAGATGGAAACAAAAATGATAGGGGGAATTTGGAGGTTTTATCAAGGTAAGACAGTATGAAGAAGTATCCGTAGACATCTGCGGGCATAAAGCTATAGGTACAGTATTGG
TAGGGCCTACACCTGTCAACATAAATTTGAAGAAGTCTGTTGACTCAGCTGGTTGCACCTTAAATTTCCCATTAGCCCTATTGAAACTGTACCAGTAAAAATTAAGCC

Nucleotide Alignments

```

      1
      |
395_PR_F *****GTCAAATTTGGGGAGGAGACAACAATTCCTTCTCAGAAGCAGGGG
395_PR_R CCAGAGCCAACAGCCCCACCAGAGGAGAGT-----

     101
     |
395_PR_F ACAATGGACAAGGAGGGGTATCCTCCTTTAGCTTCCCTCAGATCACTCTTTGGCAACGACCCATTGTCACAATAA
395_PR_R -----

     201
     |
395_PR_F AGACAGGGGGCAACTAAAGGAAGCTCTACTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGC
395_PR_R -----

     301
     |
395_PR_F CAGGGAGATGGAAACAAAAATGATAGGGGAATTTGGAGGTTTTATCAAGGTAAGACAGTATGAAGAAGTATCCG
395_PR_R -----

     401
     |
395_PR_F TAGACATCTGCGGGCATAAAGCTATAGGTACAGTATTGGTAGGGCTACACCTGTCAACATAAATTTGAAGAATC
395_PR_R -----

     501
     |
395_PR_F TGTTGACTCAGCTGGTTGCACCTTAAATTTCCCATTAGCCCTATTGAAACTGTACCAGTAAAAATTAAGCCAG
395_PR_R -----**

     601
     |
395_PR_F GAGTGGATGGCCAAAAGTTAAACAATGGCCATT
395_PR_R *****
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>395_PR

CCAGAGCCAACAGCCCCACCAGAGGAGAGTGTCAaATTTGGGGAGGAGACAACAATTCCTTCTCAGAAGCAGGGGACAATGGACAAGGAGGGGTATCCTCCTTTAGCTTCCCT
CAGATCACTCTTTGGCAACGACCCATTGTCACAATAAAGACAGGGGGCAACTAAAGGAAGCTCTACTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGCC
AGGGAGATGGAAACAAAAATGATAGGGGGAATTTGGAGGTTTTATCAAGGTAAGACAGTATGAAGAAGTATCCGTAGACATCTGCGGGCATAAAGCTATAGGTACAGTATTGG
TAGGGCCTACACCTGTCAACATAAATTTGAAGAAGTCTGTTGACTCAGCTTGGTTGCACCTTAAATTTCCCATTAGCCCTATTGAAACTGTACCAGTAAAAATTAAGCCAGGA
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MX-HIV-0395 REVERSE TRANSCRIPTASE FRAGMENT A (Fwd & Rev)

>395_RTa_F

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AAAGACAGTACTAAATGGAGAAAAGTACTAGATTTTCCAGAGAAGTAAATAAGAGAAGTCAAGACTTCTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGGTTAAAAAGAA
CAGATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCTTTAGATAAAGACTTCAGGAAGTATACTGCATTCACCATACTAGTACAAAACAATGAGACACCAG
GAATTAGGTATCAGTACAATGTACTTCCACAAGGATGGAAAGGATCACCAGCAATATTTCCAAAAGTAGCATGACAAAAGATCTTAGAGCCTTTTAGAAAAGAAAATCCAGACATA
GTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGCATTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAACTAAGACAACATCTGTTGAGGTGGGGATTTACCAC
ACCAGACAAAAACATCAGAAAAGAACCTCCATTTCTTTGGATGGGTTATGAACTCCACCCCGATAAAATGGaCAGTACAGCCTATAATGCTGCCAGAAAAGGACGGCTGgACTG
TCAATGACATACAGAAGTTAGTGGGAAAAGTGAATTGGGCAAGTCAGATTTATTCaGGGATTAAGTAAAGCAATTATGTAAACTCCTTcGGGGAGCCaAAGCaCTAACAGAA
GTAGTAC

>395_RTa_R

AAAaggaAGgAAAAATTTcAAAAttGGGCCTGAAAATCCATAcAaTACTcCAGTatTTGCCaTAAAGAAAAAGACAGTACTAAATGgagAAAaCTaGTAGATTTTCAGAGAA
CTTAATAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGGTTAAAAAAGAACAGATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTC
AGtTCCCTTAGATAAAGACTTCAGGAAGTATACTGCATTCACCATACCTAGTACAAACAATGAGACACCAGGAATTAGGTATCAGTACAATGTACTTCCACAAGGATGGAAAG
GATCACCAGCAATATTTCCAAAAGTAGCATGACAAAAGATCTTAGAGCCTTTTAGAAAAGAAAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGAC
TTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAACTAAGACAACATCTGTTGAGGTGGGGATTTACCACACCAGACAAAAACATCAGAAAAGAACCTCCATTTCTTTGGAT
GGGTTATGAAGTCCACCCGATAAAATGGACAGTACAGCCTATAATGCTGCCAGAAAAGGACGGCTGGACTGTCAATGACATACAGAAGTTAGTGGGAAAAGTGAATTGGGCAA
GTCAGATTTATTCAGGGATTAAGTAAAGCAATTATGTAAACTCCTTcGGGGAGCCaAAGCActAACAGAAGTAGTACCActAACAGCAGAAGCAGAGTTAGAACTGGCAGAA
AACAGGGAGAT

Nucleotide Alignments

```

      1
      |
395_RTa_F  GTTAACTCAGATTGGTTGCACTTTAAATTTTCCCATTTAGTCCTATTGAACTGTACCAGTAAAATAAGCCAGG
395_RTa_R  *****

     101
     |
395_RTa_F  AATGGATGGCCAAAAGTTAAACAATGGCCATTGACAGAAGAAAAATAAAAGCATTAGTAGAAATTTGTACAGA
395_RTa_R  *****

     201
     |
395_RTa_F  AATGGAAAAGGAAGGAAAAATTTCAAAAATTTGGGCCTGAAAATCCATAACAATACTCCAGTATTTGCCATAAAGAA
395_RTa_R  *****

     301
     |
395_RTa_F  AAAAGACAGTACTAAATGGAGAAAAGTACTAGATTTTCAGAGAAGTAAATAAGAGAACTCAAGACTTCTGGGAAGT
395_RTa_R  -----

     401
     |
395_RTa_F  TCAATTAGGAATACCACACCCAGCAGGGTTAAAAAAGAACAGATCAGTAACAGTACTGGATGTGGGTGATGCATA
395_RTa_R  -----

     501
     |
395_RTa_F  TTTTTCAGTTCCTTTAGATAAAGACTTCAGGAAGTATACTGCATTCACCATACCTAGTACAAAACAATGAGACACC
395_RTa_R  -----

     601
     |
395_RTa_F  AGGAATTAGGTATCAGTACAATGTACTTCCACAAGGATGGAAAGGATCACCAGCAATATTTCCAAAGTAGCATGAC
395_RTa_R  -----

     701
     |
395_RTa_F  AAAGATCTTAGAGCCTTTTAGAAAAGAAAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGG
395_RTa_R  -----

     801
     |
395_RTa_F  ATCTGACTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAACTAAGACAACATCTGTTGAGGTGGGGATTTAC
395_RTa_R  -----
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901
|
395_RTa_F CACACCAGACAAAAACATCAGAAAAGAACCTCCATTTCTTTGGATGGGTTATGAACTCCACCCCGATAAATGGAC
395_RTa_R -----

1001
|
395_RTa_F AGTACAGCCTATAATGCTGCCAGAAAAGGACGGCTGGACTGTCAATGACATACAGAAGTTAGTGGGAAAAC TGAA
395_RTa_R -----

1101
|
395_RTa_F TTGGGCAAGTCAGATTTATTCAGGGATTAAAGTAAAGCAATTATGTAAACTCCTTCGGGGAGCCAAAGCACTAAC
395_RTa_R -----

1201
|
395_RTa_F AGAAGTAGTAC*****
395_RTa_R -----CACTAACAGCAGAAGCAGAGTTAGAAGTGGCAGAAAACAGGGAGAT

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

>395_RTa
GTTAACTCAGATTGGTTGCACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAC TAAAGCCAGGAA TGGATGGCCAAAAGTTAAACAATGGCCATTGACAG
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AAAGACAGTACTAAATGGAGAAAAC TAGTAGATTTTCAGAGA ACTTAATAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGGTTAAAAAGAA
CAGATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTCAGTTCCCTTAGATAAAGACTTCAGGAAGTATACTGCATTCCACATACCTAGTACAAAACAATGAGACACCAG
GAATTAGGTATCAGTACAATGTACTTCCACAAGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGACAAAGATCTTAGAGCCTTTTAGAAAAGAAAATCCAGACATA
GTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGAAAATAGGGCAGCATAGAACA AAAATAGAGGAACTAAGACAACATCTGTGAGGTGGGGATTTACCAC
ACCAGACAAAAACATCAGAAAAGAACCTCCATTTCTTTGGATGGGTTATGAACTCCACCCCGATAAATGGaCAGTACAGCCTATAATGCTGCCAGAAAAGGACGGCTGGaCTG
TCAATGACATACAGAAGTTAGTGGGAAAAC TGAATTTGGGCAAGTCAGATTTATTCaGGGATTAAGTAAAGCAATTATGTAAACTCCTTCGGGGAGCCaAAGCaCTAACAGAA
GTAGTACC ACTAACAGCAGAAGCAGAGTTAGAAGTGGCAGAAAACAGGGAGAT

MX-HIV-0395 REVERSE TRANSCRIPTASE FRAGMENT B (Fwd & Rev)

>395_RTb_F

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AAACAGGGAGATTCTAAAGAACCAGTACATGGGGTGTACTATGACCCATCAAAAGACTTGATAGCAGAAGTACAGAAGCAGGGGCAAGATCAATGGACATATCAAATTTATC
AAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATGCAAAAATGAGGGGTACCCACACTAATGATGCAAAAACAATTAACAGAGGCAGTGCAAAAAATAGCCACAGAAAGCATA
GTAATATGGGAAAAGACTCCTAAATTTAAATTTACCCATACAAAAGGAAAACATGGGAAGCATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGTCAA
TACCCACCCCTTAGTGAATTTAGGTACCAGTTAGAAAAAGAACCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAG
GATATGTTACTGACAAAGGAAGACAAGAGGTTGTTTCTCTAACTGACACAACCAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCTTTGCAGGATTCGGGATCAGAAGTA
AACATAGTAACAGACTCACGATATGCATTAGGAATCATTCATGCACAACCAGATAAGAGTGAATTCAGATTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGAT
CTACCTAGCATGGGTTCCAGCACACAAAGGAATTGGagGAAATGAACAAGTAGATAAAATTAGTCAGTTCGGGAATCAGgAaAGTTCTATTTTGGATGGaATAGAtaAgqCCC
A

>395_RTb_R

CAAGTCAGATTTATTTCAGGGATtAAAGTAAAGCAATTATGTAAACTCCTTCGGGGAGCCAAAGCACTAACAGAAGTAGTACCACCTAACAGCAGAAGCAGAGTTAGAACTGGCA
GAAAACAGGGAGATTCTAAAGAACCAGTACATGGGGTGTACTATGACCCATCAAAAGACTTGATAGCAGAAGTACAGAAGCAGGGGCAAGATCAATGGACATATCAAATTTA
TCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATGCAAAAATGAGGGGTACCCACACTAATGATGCAAAAACAATTAACAGAGGCAGTGCAAAAAATAGCCACAGAAAGCA
TAGTAATATGGGAAAAGACTCCTAAATTTAAATTTACCCATACAAAAGGAAAACATGGGAAGCATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGT
AATACCCACCCCTTAGTGAATTTAGGTACCAGTTAGAAAAAGAACCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGC
AGGATATGTTACTGACAAAAGGAAGACAAGAGGTTGTTTCTCTAACTGACACAACCAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCTTTGCAGGATTCGGGATCAGAAG
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ATCTACCTAGCATGGGTTCCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAAATTAGTCAGTTCGGGAATCAGGAAAAGTTCTATTTTGGATggg

Nucleotide Alignments

```

      1
      |
395_RTb_F  **AGTCAGATTTATTTCAGGGATTAAGTAAAGCAATTATGTAAACTCCTTCGGGGAGCCAAAGCACTAACAGAAG
395_RTb_R  CA-----

      101
      |
395_RTb_F  TAGTACCACCTAACAGCAGAAGCAGAGTTAGAACTGGCAGAAAACAGGGAGATTCTAAAGAACCAGTACATGGGG
395_RTb_R  -----

      201
      |
395_RTb_F  TGTACTATGACCCATCAAAAGACTTGATAGCAGAAGTACAGAAGCAGGGGCAAGATCAATGGACATATCAAATTT
395_RTb_R  -----

      301
      |
395_RTb_F  ATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATGCAAAAATGAGGGGTACCCACACTAATGATGCAAAAC
395_RTb_R  -----

      401
      |
395_RTb_F  AATTAACAGAGGCAGTGCAAAAAATAGCCACAGAAAGCATAGTAATATGGGAAAAGACTCCTAAATTTAAATTC
395_RTb_R  -----

      501
      |
395_RTb_F  CCATACAAAAGGAAAACATGGGAAGCATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTG
395_RTb_R  -----

      601
      |
395_RTb_F  TCAATACCCACCCCTTAGTGAATTTATGGTACCAGTTAGAAAAAGAACCATAGTAGGAGCAGAAACTTTCTATG
395_RTb_R  -----

      701
      |
395_RTb_F  TAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAAAGGAAGACAAGAGGTTG
395_RTb_R  -----

      801
      |
395_RTb_F  TTTCTCTAACTGACACAACCAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCTTTGCAGGATTCGGGATCAG
395_RTb_R  -----
```

901
|
395_RTb_F AAGTAAACATAGTAACAGACTCACGATATGCATTAGGAATCATTTCATGCACAACCAGATAAGAGTGATTTCAGATT
395_RTb_R -----

1001
|
395_RTb_F TAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGATCTACCTAGCATGGGTTCAGCACACAAAGGAA
395_RTb_R -----

1101
|
395_RTb_F TTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTTCGGGAATCAGGAAAGTTCATTTTTGGATGGAATAGATA
395_RTb_R -----*****

1201
|
395_RTb_F AGGCCCA
395_RTb_R *****

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

>395_RTb
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AAGAGCCATTTAAAAATCTGAAAACAGGAAAGTATGCAAAAATGAGGGGTACCCACACTAATGATGCAAAACAATTAACAGAGGCAGTGCAAAAATAGCCACAGAAAGCATA
GTAATATGGGGAAAGACTCCTAAATTTAAATTACCCATACAAAAGGAAACATGGGAAGCATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCCTGAGTGGGAGTTTGTCAA
TACCCACCCCTTAGTGAAATTATGGTACCAGTTAGAAAAGAACCATAGTAGGAGCAGAACTTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAG
GATATGTTACTGACAAAGGAAGACAAGAGGTTGTTTCTCTAACTGACACAACCAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCTTTGCAGGATTCGGGATCAGAAGTA
AACATAGTAACAGACTCACGATATGCATTAGGAATCATTTCATGCACAACCAGATAAGAGTGATTCAGATTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGAT
CTACCTAGCATGGGTTCAGCACACAAAGGAATTGGagGAAATGAACAAGTAGATAAATTAGTCAGTTCGGGAATCAGgAaAGTTCTATTTTGGATGGaATAGAtaAggCCC
A

MX-HIV-0395 INTEGRASE FRAGMENT (Fwd & Rev)

>395_IN_F

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AACCTGCTGTGATAAAATGTCAGCAAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCCTGG
TAGCGGTTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGACAGGAAACAGCATACTTCATCTTAAATTAGCAGGAAGATGGCCAGTAAAAACA
ATACATACAGACAATGGCAGCAATTTCCACGACTGTCAGTTAAGGCCGCCCTGTTGGTGGGGGGGATCAAGCAGGAATTTGGCATTCCCTACAACCCCAAAGTCAAGGAGT
AGTGGAGTCCATGAATAAAGAATTAAAGAAAAATATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAGAA
AAGGGGGGATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCATCAGACATACAAACTAAAGCATTACAAAAACACATTACAAAAATTCAAAATTTTCGGGTT
TATTACAGGGACAGCAGAGATCCACTTTGGAAAGGGCCAGCAAACTTCTCTGGAAAGGTGAAGGGGCAGTAGTGATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAG
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>395_IN_R

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GCAAAAGAAATAGTAACCTGCTGTGATAAAATGTCAGCAAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAGAAG
AAAAATTTATCCTGGTAGCGGTTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTcCAGCAGAGACAGGACAGGAAACAGCATACTTCATCTTAAATTAGCAGGAAGAT
GGCCAGTAAAAACAATACATACAGACAATGGCAGCAATTTCCACGACTGTCAGTTAAGGCCGCCCTGTTGGTGGGGGGGATCAAGCAGGAATTTGGCATTCCCTACAACCC
CAAAGTCAAGGAGTAGTGGAGTCCATGAATAAAGAATTAAAGAAAAATATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCATCCA
CAATTTTAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCATCAGACATACAACTAAAGCATTACAAAAACACATTACAAAAATTC
AAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGGCCAGCAAACTTCTCTGGAAAGGTGAAGGGGCAGTAGTGATAACAAGATAATAGTGACATAAAA
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Nucleotide Alignments

```

      1
      |
395_IN_F *****CTATTTTGGATGGAATAGATAAAGCCCAAGAAGACCATGAAAAATATCACAGTAATTGGA
395_IN_R GAATCAGGAAAGTT-----

      101
      |
395_IN_F GGGCAATGGCCAGTGATTTTAACTGCCACCTGTAGTAGCAAAAGAAATAGTAACCTGCTGTGATAAAATGTCAGC
395_IN_R -----

      201
      |
395_IN_F AAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAGAAG
395_IN_R -----

      301
      |
395_IN_F GAAAAATTATCCTGGTAGCGGTTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGAC
395_IN_R -----

      401
      |
395_IN_F AGGAAACAGCATACTTCATCTTAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGCA
395_IN_R -----

      501
      |
395_IN_F ATTTACCAGTACTGCAGTTAAGGCCGCCCTGTTGGTGGGGGGGATCAAGCAGGAATTTGGCATTCCTACAACC
395_IN_R -----

      601
      |
395_IN_F CCCAAAGTCAAGGAGTAGTGGAGTCCATGAATAAAGAATTAAAGAAAAATATAGGACAGGTAAGAGATCAGGCTG
395_IN_R -----

      701
      |
395_IN_F AACACCTTAAGACAGCAGTACAAATGGCAGTATTTCATCCACAATTTTAAAGAAAAGGGGGGATTGGGGGGTAC
395_IN_R -----

      801
      |
395_IN_F GTGCAGGGGAAAGAATAGTAGACATAATAGCATCAGACATACAACTAAAGCATTACAAAAACACATTACAAAA
395_IN_R -----
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901
|
395_IN_F TTCAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGGCCAGCAAACTTCTCTGAAAAG
395_IN_R -----

1001
|
395_IN_F GTGAAGGGGCAGTAGTGATAACAAGATAATAGTGACATAAAAAGTAGTGCCAAGAAGAAAGGCAAAGATCATTAGGG
395_IN_R -----

1101
|
395_IN_F ATTATGAAAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACATGGA
395_IN_R -----*****

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

>395_IN
GAATCAGGAAAGTTCTATTTTTGGATGGaATAGATAAGGCCCAAGAAGACCATGAAAAATATCACAGTAATTGGAGGGCAATGGCCAGTGATTTAACCTGCCACCTGTAGTA
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GGCCAGTAAAAACAATACATACAGACAATGGCAGCAATTCACCAGTACTGCAGTTAAGGCCGCTGTGGTGGGCGGGGATCAAGCAGGAATTTGGCATTCCCTACAACCC
CAAAGTCAAGGAGTAGTGGAGTCCATGAATAAAGAATTAAAGAAAATTTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCATCCA
CAATTTTAAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCATCAGACATACAACTAAAGCATTACAAAAACATTACAAAAATTC
AAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGGCCAGCAAACTTCTCTGAAAGGTGAAGGGGCAGTAGTGATAACAAGATAATAGTGACATAAAA
GTAGTGCCAAGAAGAAAGGCAAAGATCATTAGGGATTATGGA AAAACAGATGGCAGGTGATGATTGTGTGGCAGGTAGACAGGATGAGGATTAGAACATGGA

MX-HIV-0395 CONTIG ASSEMBLY (4 Fragments)

Nucleotide Alignments

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2085 2159
|-----|
B.FR.83.HXB2 TTT TTT AGG GAA GAT CTG GCC TTC CTA CAA GGG AAG GCC AGG GAA TTT TCT TCA GAG CAG ACC AGA GCC AAC AGC
395_PR      *** **
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          F  F  R  E  D  L  A  F  L  Q  G  K  A  R  E  F  S  S  E  Q  T  R  A  N  S
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2160 2234
|-----|
B.FR.83.HXB2 CCC ACC AGA AGA GAG CTT CAG GTC TGG GGT AGA GAC AAC AAC TCC CCC TCA GAA GCA GGA GCC GAT AGA CAA GGA
395_PR      --- --- G-- --- TG- --A A-T --- --A G-- --- --T --- TT- --- --- --G --A- A-- G-- --- ---
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          P  T  R  R/G E L/C Q V/I W G R/G D N N S P/F S E A G A/D D/N R/G Q G
```

```
2235 2253 2306
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
B.FR.83.HXB2 ACT GTA *** TCC TTT AAC TTC CCG CAG GTC ACT CTT TGG CAA CGA CCC CTC GTC ACA ATA AAG ATA GGG GGG CAA
395_PR      GGG --- TCC --- --- -G- --- --- --- A-- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          T/G V S S F N/S F P Q V/I T L W Q R P L/I V T I K I/T G G Q
```

```
2307 2381
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
B.FR.83.HXB2 CTA AAG GAA GCT CTA TTA GAT ACA GGA GCA GAT GAT ACA GTA TTA GAA GAA ATG AGT TTG CCA GGA AGA TGG AAA
395_PR      --- --- --- --- --- C-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          L  K  E  A  L  L  D  T  G  A  D  D  T  V  L  E  E  M  S/N L  P  G  R  W  K
```

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2382 2456
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
B.FR.83.HXB2 CCA AAA ATG ATA GGG GGA ATT GGA GGT TTT ATC AAA GTA AGA CAG TAT GAT CAG ATA CTC ATA GAA ATC TGT GGA
395_PR      *** **
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          P  K  M  I  G  G  I  G  G  F  I  K  V  R  Q  Y  D/E Q/E I/V L/S I/V E/D I  C  G
```

```
2457 2531
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
B.FR.83.HXB2 CAT AAA GCT ATA GGT ACA GTA TTA GTA GGA CCT ACA CCT GTC AAC ATA ATT GGA AGA AAT CTG TTT ACT CAG ATT
395_PR      --- --- --- --- --- --G --G --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          H  K  A  I  G  T  V  L  V  G  P  T  P  V  N  I  I  G  R  N  L  L  T  Q  I/L
```

```
2532 2549 2550 2606
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
B.FR.83.HXB2 GGT TGC ACT TTA AAT TTT CCC ATT AGC CCT ATT GAG ACT GTA CCA GTA AAA TTA AAG CCA GGA ATG GAT GGC CCA
395_PR      --- --- --C --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          G  C  T  L  N  F  I  S  P  I  E  T  V  P  V  K  L  K  P  G  M/V D  G  P
```

```
2607 2681
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
B.FR.83.HXB2 AAA GTT AAA CAA TGG CCA TTG ACA GAA GAA AAA ATA AAA GCA TTA GTA GAA ATT TGT ACA GAG ATG GAA AAG GAA
395_PR      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
395_RTa     *** **
395_RTb     *** **
395_IN      *** **
          K  V  K  Q  W  P  L  T  E  E  K  I  K  A  L  V  E  I  C  T  E  M  E  K  E
```


4482 4556
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
GAA GCA GAA GTT ATT CCA GCA GAA ACA GGG CAG GAA ACA GCA TAT TTT CTT TTA AAA TTA GCA GGA AGA TGG CCA
*** **
*** **
*** **
---G---A---C---A-C---
E A E V I P A E T G Q E T A Y F L/I L K L A G R W P

4557 4631
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
GTA AAA ACA ATA CAT ACT GAC AAT GGC AGC AAT TTC ACC GGT GCT ACG GTT AGG GCC GCC TGT TGG TGG GCG GGA
*** **
*** **
*** **
---A---G---A---G---A---
V K T I H T D N G S N F T G/S A/T T/A V R/K A A C W W A G

4632 4706
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
ATC AAG CAG GAA TTT GGA ATT CCC TAC AAT CCC CAA AGT CAA GGA GTA GTA GAA TCT ATG AAT AAA GAA TTA AAG
*** **
*** **
*** **
---C---C---G---G---G---
I K Q E F G I P Y N P Q S Q G V V E S M N K E L K

4707 4781
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
AAA ATT ATA GGA CAG GTA AGA GAT CAG GCT GAA CAT CTT AAG ACA GCA GTA CAA ATG GCA GTA TTC ATC CAC AAT
*** **
*** **
*** **
---C---
K I I G Q V R D Q A E H L K T A V Q M A V F I H N

4782 4856
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
TTT AAA AGA AAA GGG GGG ATT GGG GGG TAC AGT GCA GGG GAA AGA ATA GTA GAC ATA ATA GCA ACA GAC ATA CAA
*** **
*** **
*** **
---C---T---
F K R K G G I G G Y S A G E R I V D I I A T/S D I Q

4857 4931
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
ACT AAA GAA TTA CAA AAA CAA ATT ACA AAA ATT CAA AAT TTT CGG GTT TAT TAC AGG GAC AGC AGA AAT CCA CTT
*** **
*** **
*** **
---C---C---G---
T K E/A L Q K Q/H I T K I Q N F R V Y Y R D S R N/D P L

4932 5006
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
TGG AAA GGA CCA GCA AAG CTC CTC TGG AAA GGT GAA GGG GCA GTA GTA ATA CAA GAT AAT AGT GAC ATA AAA GTA
*** **
*** **
*** **
---G---A---T---G---
W K G P A K L L W K G E G A V V I Q D N S D I K V

5007 5081
B.FR.83.HXB2
395_PR
395_RTa
395_RTb
395_IN
GTG CCA AGA AGA AAA GCA AAG ATC ATT AGG GAT TAT GGA AAA CAG ATG GCA GGT GAT GAT TGT GTG GCA AGT AGA
*** **
*** **
*** **
---G---S---
V P R R K A K I I R D Y G K Q M A G D D C V A S R

```

5082          5096
|---Integrase end---|
B.FR.83.HXB2 CAG GAT GAG GAT TAG *** **
395_PR      *** **
395_RTa     *** **
395_RTb     *** **
395_IN      --- --- --- --- AAC ATG GA*
           Q  D  E  D  X

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Protein Alignments

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1      10      20      30      40      50      60      70      80      90      100
B.FR.83.HXB2 FFREDLAFLO GKAREFSSEQ TRANSPTRRE LQVWGRDNNS PSEAGADROG TV.SFNFGQV TLWQRPLVTI KIGGQLKEAL LDTGADDTVL EEMSLPGRWK
395_PR      *****
395_RTa     *****
395_RTb     *****
395_IN      *****

101     110     120     130     140     150     160     170     180     190     200
B.FR.83.HXB2 PKMIGGIGGF IKVRQYDQIL TEICGHKAIG TVLVGPTPVN IIGRNLLTQI GCTLNFISP IETVPVKLKP GMDGPKVKQW PLTEEKIKAL VEICTEMEKE
395_PR      -----EEVS VD-----
395_RTa     *****
395_RTb     *****
395_IN      *****

201     210     220     230     240     250     260     270     280     290     300
B.FR.83.HXB2 GKISKIGPEN PYNTPVFAIK KKDSTKWRKL VDFRELNKRT QDFWEVQLGI PHPAGLKKKK SVTVLDVGDA YFSVPLDEDF RKYTAFTIPS INNETPGIRY
395_PR      *****
395_RTa     *****
395_RTb     *****
395_IN      *****

301     310     320     330     340     350     360     370     380     390     400
B.FR.83.HXB2 QYNVLPQGWK GSPAIFQSSM TKILEPFRQK NPDIVIYQYM DDLVYGSdle IGQHRKIEE LRQHLLRWGL TTPDKKHQKE PPFLWMGYEL HPAKHTVQPI
395_PR      *****
395_RTa     *****
395_RTb     *****
395_IN      *****

401     410     420     430     440     450     460     470     480     490     500
B.FR.83.HXB2 VLPEKDSWTV NDIQKLVGKL NwasQIYPGI KVRQLCKLLR GTKALTEVIP LTBAAELELA ENREILKEPV HGVYDPSKD LIAEIQKQGG GQWTYQIYQE
395_PR      *****
395_RTa     M-----G-----S-----K-----A-----V-----A-----
395_RTb     *****
395_IN      *****

501     510     520     530     540     550     560     570     580     590     600
B.FR.83.HXB2 PFKNLKTGKY ARMRGAHTND VKQLTEAVQK ITTESIVIWG KTKPKFLPIQ KETWETWTE YWQATWIPEW EfvNTPPLVK LWYQLEKEPI VgaETfYVDG
395_PR      *****
395_RTa     *****
395_RTb     *****
395_IN      *****

601     610     620     630     640     650     660     670     680     690     700
B.FR.83.HXB2 AANRETKLKG AGYVTNRGRQ KVVTLTDTTN QKTELQAIYL ALQDSGLEVN IVTDSYALG IQAQPDQSE SELVNQIIEQ LIKKEKVYLA WvPAHKGIGG
395_PR      *****
395_RTa     *****
395_RTb     *****
395_IN      *****

701     710     720     730     740     750     760     770     780     790     800
B.FR.83.HXB2 NEQVDKLVSA GIRKVLILDG IDKAQDEHEK YHSNWRAMAS DFNLPpVvAK EIVASCDKcQ LKGEAMHGQV DCSPGIWQLD CTHLEKGVIL VAVHVASGYI
395_PR      *****
395_RTa     *****
395_RTb     *****
395_IN      *****

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801      810      820      830      840      850      860      870      880      890      900
B.FR.83.HXB2  EAEVIPAETG QETAYFLLKL AGRWPVKTIH TDNGSNFTGA TVRAACWWAG IKQEFGIPYN PQSQGVVESH NKLKKIIGQ VRDQAEHLKT AVQMAVFIHN
395_PR       *****
395_RTa      *****
395_RTb      *****
395_IN       -----I-----ST-----A-----K-----

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901      910      920      930      940      950      960      970      980      990      1000
B.FR.83.HXB2  FKRRGGIGGY SAGERIVDII ATDIQTKELQ KQITKIQNFR VYYRDSRNPL WKGPAKLLWK GEGAVVIQDN SDIKVPPRRK AKIIRDYGKQ MAGDDCVASR
395_PR       *****
395_RTa      *****
395_RTb      *****
395_IN       -----S-----A-----H-----D-----G-----

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1001
B.FR.83.HXB2  QDEDX
395_PR       *****
395_RTa      *****
395_RTb      *****
395_IN       -----

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

>395_pol

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CCAGAGCCAACAGCCCCACCAGAGGAGAGTGTCAaATTGGGGAGGAGACAACAATTCCTTCTCAGAAGCAGGGGACAAATGGACAAGGAGGGGTATCCTCCTTTAGCTTC CCN
CAGATCACTCTTTGGCAACGACCCATTGTCACAATAAAGACAGGGGGCAACTAAAGGAAGCTTACTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGCC
AGGGAGATGGAAACCAAAAATGATAGGGGAAATGGAGGTTTTATCAAGGTAAGACAGTATGAAGAAGTATCCGTAGACATCTGCGGGCATAAAGCTATAGGTACAGTATTGG
TAGGGCCTACACCTGTCAACATAATTGGAAGAAATCTGTTRACTCAGMTTGGTTGCAC YTTAAATTTT CCCATTAG YCCATTGAAACTGTACCAGTAAAA YTAAAGCCAGGA
RTGGATGGCCAAAAGTTAAACAATGGCCATTGACAGAAAGAAAAATAAAGCATTAGTAGAAATTTGACAGAAATGGAAAAGGAAGAAAAATTTCAAAAATTTGGCCTGA
AAATCCATACAATACTCCAGTATTGGCCATAAAGAAAAAGACAGTACTAAATGGAGAAAACTAGTAGATTTTCAGAGAACTTAATAAGAGAACCAAGACTTCTGGGAAGTTC
AATTAGGAATACCACACCAGCAGGGTTAAAAAAGAACAGATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCCTTAGATAAAGACTTCAGGAAGTATACT
GCATTCACCATACTAGTACAAAATGAGACACCAGGAATTAGGTATCAGTACAATGTACTTCCACAAGGATGGAAAGGATCACCAGCAATATTCAAAAGTAGCATGACAAA
GATCTTAGAGCCTTTTAGAAAAGAAAATCCAGACATAGTTATCTATCAATACATGGATGatTTGTATGTAGGATCTGACTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGG
AACTAAGACAACATCTGTTGAGGTGGGGATTTACCACACCAGACAAAAACATCAGAAAAGAACTCCATTTCTTTGGATGGGTATGAACTCCACCCGATAAATGGaCAGTA
CAGCCTATAATGCTGCCAGAAAAGGACGGCTGGaCTGTCAATGACATACAGAAGTTAGTGGGAAAACGAATTTGGGCAAGTCAGATTTATTCaGGGaTTAAAGTAAAGCAATT
ATGTAAACTCCTTcGGGGAGCCaAAGCaCTAACAGAAGTAGTACCCTAACAGCAGAAGCAGAGTTAGAACTGGCAGAAAACAGGGAGATTCATAAGAACCCAGTACATGGGG
TGTAATGACCCATCAAAGACTTGATAGCAGAAGTACAGAAGCAGGGCAAGATCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTAT
GCAAAAATGAGGGGTACCACACTAATGATGCAAAAACAAATTAACAGAGGCAGTGCAAAAAATAGCCACAGAAAAGCATAGTAATATGGGAAAGACTCCTAAATTTAAATTACC
CATACAAAAGGAAAACATGGGAAGCATGGTGGACAGAGTATTGGCAAGCCACCCTGGATTCCTGAGTGGGAGTTTGTCAATACCCACCCTTAGTGAATTTAGGTACCAGTTAG
AAAAAGAACCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAAAAGGAAGACAAGAGGTGTTT
TCTCTAAGTACACAACCAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCTTTCAGGATTCGGGATCAGAAGTAAACATAGTAACAGACTCACGATATGCATTAGGAAT
CATTCATGCACAACCAGATAAGAGTGATTCAGATTTAGTCAGTCAAAATAATAGAGCAGTTAAATAAAAAGGAAAAGATCTACCTAGCATGGGTTCAGCACAAAAGGAATTTG
GagAAAATGAACAAGTAGATAAATTAGTCAGTCCGGGAATCAGgAaAGTTCTA TTTTTGGATGGaATAGAtaAggCCCAAGAAGACCATGAAAAATATCACAGTAATTTGGAGG
GCAATGGCCAGTGATTTTAAACCTGCCACCTGTAGTACAAAAGAAAATAGTAACCTGCTGTGATAAATGTCCAGCAAAAAGGAGAAAGCCATGCATGGCAAGTAGACTGTAGTCC
AGGAATATGGCAACTAGATTGTACACATCTAGAAAGAAAATATCCCTGGTAGCGGTTATGTAGCCAGTGGATATATAAGAAGCAGAAGTTATCCAGCAGAGACAGGACAGG
AAACAGCATACTTCATCTTAAATTAGCAGGAAGATGCCAGTAAAAACAATACATACAGACAAATGGCAGCAATTTCCAGTACTGCAGTTAAGGCCCGCTGTGGTGGGG
GGGATCAAGCAGGAATTTGGCATTCCTTACAACCCCAAAGTCAAGGAGTAGTGGAGTCCATGAATAAAGAATTAAGAAAATATAGGACAGGTAAGAGATCAGGCTGAACA
CCTTAAGACAGCAGTACAAATGGCAGTATTTCATCCACAATTTTAAAAGAAAAGGGGGGATTTGGGGGTACAGTGCAGGGGAAAAGAAATAGTAGACATAATAGCATCAGACATAC
AACTAAAGCATTACAAAACACATTACAAAATTTCAAATTTTCGGGTTTATACAGGGACAGCAGAGATCCACTTTGGAAAAGGGCCAGCAAACTTCTCTGGAAAAGGTGAA
GGGGCAGTAGTGATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGGCAAAAGATCATTAGGGATTTATGGAAAACAGATGGCAGGTGATGATGTGTGGCAGGTAG
ACAGGATGAGGAT TAGAACATGGA

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