

MX-HIV-0422 PROTEASE FRAGMENT (Fwd & Rev)

>422_PR_F

ACAACACcctctCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAAATAGGAGGGCAACTAAAGGAAGCTCT
ATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTACCAGGAAGATGGTAACCAAAAATGATAAGGGGAATTGGAGGTTTATCAAAGTAAGACAGTATGAT
CAGTACCCATAGAAATCTGTGGACATAAAACTATAGGTACAGTATTAATAGGACCTACACCTGTCAACATAATGGGAAGAAATCTATGACTCAGATTGGCTGTACTTTAA
ATTTTCCCATTAGTCTATTGAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGTTAAACAATGGCCATT

>422_PR_R

GCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATAACAACACCCCTCTCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGCAGC
GACCCCTCGTCACAGTAAAAATAGGAGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTACCAGGAAGATGGTAACCAAAA
AATGATAAGGGGAATTGGAGGTTTATCAAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAAACTATAGGTACAGTATTAATAGGACCTACACCTGTCT
AACATAATTGGAAGAAATCTATTGACTCAGATTGGCTGTACTTTAAATTTTCCCATTAGTCTATTGAACTGTACCAGTAAAATTAAGCCa

Nucleotide Alignments

```

      1
      |
422_PR_F *****ACAACACCCCTCTCAGAAACAGGAGGAGCT
422_PR_R GCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATA-----

     101
     |
422_PR_F ATATCCTTTGACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAAATAGGAGGGCAACTAAAG
422_PR_R -----

     201
     |
422_PR_F GAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTACCAGGAAGATGGTAACCAAAA
422_PR_R -----

     301
     |
422_PR_F ATGATAAGGGGAATTGGAGGTTTATCAAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAA
422_PR_R -----

     401
     |
422_PR_F ACTATAGGTACAGTATTAATAGGACCTACACCTGTCAACATAATGGGAAGAAATCTATTGACTCAGATTGGCTGT
422_PR_R -----

     501
     |
422_PR_F ACTTTAAATTTTCCCATTAGTCTATTGAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGTT
422_PR_R -----*****

     601
     |
422_PR_F AAACAATGGCCATT
422_PR_R *****
```

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

>422_PR

GCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATAACAACACcctctCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGCAGC
GACCCCTCGTCACAGTAAAAATAGGAGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTACCAGGAAGATGGTAACCAAAA
AATGATAAGGGGAATTGGAGGTTTATCAAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAAACTATAGGTACAGTATTAATAGGACCTACACCTGTCT
AACATAATTGGAAGAAATCTATTGACTCAGATTGGCTGTACTTTAAATTTTCCCATTAGTCTATTGAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAG
TTAAACAATGGCCATT

MX-HIV-0422 REVERSE TRANSCRIPTASE FRAGMENT A (Fwd & Rev)

>422_RTa_F

GAGAATCTGTTGACTCAGATTGGATGCACTTTAAATTTTCCCATTTAGTCTTATTGAAACTGTACCAGTGAAATTAACCAGGAATGGATGGCCAAAAGTTAAACAATGGC
CATTTGACAGAAGAAAAGATAAAAAGCATTAGTAGAAAATTTGCACAGAAATGGAAAAAGGGAAAATTTCAAAAATTTGGGCCTGAAAATCCATACAATACTCCAATATTTGC
CATAAAGAAAAAGACAGTACCAAATGGAGAAAATTTAGTAGATTTTAGAGAACTTAACAAGAGAACTCAAGACTTCTGGGAGGTTTCAGTTAGGAATACCACATCCCTCAGGG
CTAAAAAGAAAAAGTCACTAGTAACAGTACTGGATGTGGGTGATGCATATTTTTTCAGTTCCCTTAGATCCAGACTTCAGGAAGTATACGGCATTACCATACTAGTAGAAACA
ATGAGACACCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAAGGATCACCAGCGATATCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAAACA
AAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGATGAACAGAGAGAACATTTGTTGAGG
TGGGATTTGCCACACCAGACAAAAACACCAGAAaGAACTCCATTCTTTGGATGGGTTATGAACCCATCTGATAAATGGACAGTACAGCCTATAGTCTGCCAGAAA
AAGACAGCTGGACTGTCAATGACaTACAAAAGTTAGTGGGAAAATTAATTTGGGCAAGTCAGATTTATGCaGGGATCAAAGTAAGGCAATTaTGTAAGCTcCtTaGGGGATC
CaAAGCACTAACAgAAATAGTACCACTA

>422_RTa_R

AtgGCCatTGaCAGAAGAAAAGATAAAAAGCaTTAGTAGAAAATTTGCACAGAAATGGAAAAGAAAGGGAAAATTTCAAAAATTTGGGCCTGAAAATCCATaCAaTACTCCAATA
TTTGCCATAAAGAAAAAGACAGTaCCAAATGGAGAAAATTTAGTAGATTTTAGAGAACTTaaCAAGAGAACTCAAGACTTCTGGGAGGTTTCAGTTAGGAATACCACATCCCT
CAGGGCTAAAAAGAAAAAGTCACTAGTAACAGTACTGGATGTGGGTGATGCATATTTTTTCAGTTCCCTTAGATCCAGACTTCAGGAAGTATACGGCATTACCATACTAGTAG
AAACAATGAGACACCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAAGGATCACCAGCGATATCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGA
AAACAAAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGATGAACAGAGAGAACATTTGT
TGAGGTGGGATTTGCCACACCAGACAAAAACACCAGAAAAGAACCTCCATTCTTTGGATGGGTTATGAACCCATCTGATAAATGGACAGTACAGCCTATAGTCTGCC
AGAAAAGACAGCTGGACTGTCAATGACATACAAAAGTTAGTGGGAAAATTAATTTGGGCAAGTCAGATTTATGCAGGGATCAAAGTAAGGCAATTATGTAAGCTCCTTAGG
GGATCCAAAGCACTAACAGAAATAGTACCACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATt

Nucleotide Alignments

```

      1
      |
422_RTa_F  GAGAATCTGTTGACTCAGATTGGATGCACTTTAAATTTTCCCATTTAGTCTTATTGAAACTGTACCAGTGAAATTA
422_RTa_R  *****

     101
     |
422_RTa_F  AAACCAGGAATGGATGGCCAAAAGTTAAACAATGGCCATTGACAGAAGAAAAGATAAAAAGCATTAGTAGAAAT
422_RTa_R  *****-----

     201
     |
422_RTa_F  TGCACAGAAATGGAAAAGAAGGGAAAATTTCAAAAATTTGGGCCTGAAAATCCATACAATACTCCAATATTTGCC
422_RTa_R  -----

     301
     |
422_RTa_F  ATAAAGAAAAAGACAGTACCAAATGGAGAAAATTTAGTAGATTTTAGAGAACTTAACAAGAGAACTCAAGACTTC
422_RTa_R  -----

     401
     |
422_RTa_F  TGGGAGGTTTCAGTTAGGAATACCACATCCCTCAGGGCTAAAAAGAAAAGTCAAGTAACTGATGATGTTGGGT
422_RTa_R  -----

     501
     |
422_RTa_F  GATGCATATTTTTTCAGTTCCCTTAGATCCAGACTTCAGGAAGTATACGGCATTACCATACTAGTAGAAACAAT
422_RTa_R  -----

     601
     |
422_RTa_F  GAGACACCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAAGGATCACCAGCGATATCCAAAGT
422_RTa_R  -----

     701
     |
422_RTa_F  AGCATGACAAAAATCTTAGAGCCTTTTAGAAAACAAAATCCAGACATAGTTATCTATCAATACATGGATGATTTG
422_RTa_R  -----

     801
     |
422_RTa_F  TATGTAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGATGAACAGAGAGAACATTTGTTGAGGTGG
422_RTa_R  -----
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```

901
|
422_RTa_F  GGATTTGCCACACCAGACAAAAAACACCAGAAAGAACCTCCATTCTTTGGATGGGTTATGAACTCCATCCTGAT
422_RTa_R  -----

1001
|
422_RTa_F  AAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGTCAATGACATACAAAAGTTAGTGGGA
422_RTa_R  -----

1101
|
422_RTa_F  AAATTAATTTGGGCAAGTCAGATTTATGCAGGGATCAAAGTAAGGCAATTATGTAAGCTCCTTAGGGGATCCAAA
422_RTa_R  -----

1201
|
422_RTa_F  GCACCTAACAGAAATAGTACCCTA*****
422_RTa_R  -----ACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATT

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

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>422_RTa
AATCTGTTGACTCAGATTGGATGCACTTTAAATTTCCCTATTAGTCCTATTGAAACTGTACCAGTGAAATTAATAACAGGAATGGATGGCCCAAAAGTTAAACAATGGCCAT
TGACAGAAGAAAAGATAAAAGCATTAGTAGAAATTTGCACAGAAATGGAAAAAGAGGAAAATTTCAAAAATTTGGCCTGAAAATCCATACATACTCCAATATTTGCCAT
AAAGAAAAAAGACAGTACCAAATGGAGAAAATTAGTAGATTTTAGAGAACTTAACAAGAGAAGTCAAGACTTCTGGGAGGTTTCAGTTAGGAATACCACATCCCTCAGGGCTA
AAAAGAAAAAGTCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCTTAGATCCAGACTTCAGGAAGTATACGGCATTCCCATACCTAGTAGAAACAATG
AGACACCAGGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAGGATCACCAGCGATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAAACAAA
TCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGATTTAGAAATAGGGCAGCATAGAACAAAAATAGATGAACTGAGAGAACATTTGTTGAGGTGG
GGATTTGCCACACCAGACAAAAAACACCAGAAaGAACCTCCATTCCTTTGGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAAG
ACAGCTGGACTGTCAATGACaTACAAAAGTTAGTGGGAAAATTAATTTGGGCAAGTCAGATTTATGCAGGGATCAAGTAAGGCAATTaTGTAAGCTcCtTagGGATCCaA
AGCACTAACAgaaTAGTACCCTAACAGAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATT

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MX-HIV-0422 REVERSE TRANSCRIPTASE FRAGMENT B (Fwd & Rev)

>422_RTb_F

TAAGTAAGGCAATTATGTTAACTCCTTAGAGGAGCTAAAGCACTAACAGAAGTAGTACCCTAACAAAAGAAGCAGAACTAGAACTGGCAGAAAACAGGGAGATTCTAAAAG
AACCAAGTACATGGGGTGTATTATGACCCATCAAAAAGACTTAATAGCAGAAAATACAGAAAACAGGAGCTAGGCCAATGGACATATCAAATTTATCAAGAGCCACTTAAGAATCT
GAAAACAGGAAAATATGCAAGAATGAGGGGTGCCCACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCACAGAAAAGCATAGTGATATGGGAAAAGACT
CCTAAATTTAGACTACCCATACAAAAGGAAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCCACTTGGATTCCTGAATGGGAATTTGTCAATACCCCTCCCTTAGTGA
AATTTATGGTACCAGTTAGAGAAAACCCCATAGTAGGAGCAGAACTTTCTATGTAGATGGAGCAGCTAATAGGGACACTAACTAGGAAAAGCAGGGTATGTTACTGACAG
AGGAAGACAAAAGTAGTCTCCCTGACTGACACAACAAGTCAGAAGACTGAGTTACAGGCAATTAATCTAGCTTTACAGGATTCAGGGCCAGAAGTAAACATAGTAACAGAC
TCACAATATGCATTAGGAATAATCAAGCGCAACCAGATAAGAGTGAATCAGAGGTAGTCAGTCAAATAATAGAACAATTAATAAAAAAGGAAAAGTCTACCTGACATGGG
TACCAGCACAAAAGGaaTTGGaGAAAATGAAAAGAGTAGATAAGTTAGTCAGTGCTGGaATCAGAAAAGTACTATTTTGGATGGAATAGATA

>422_RTb_R

AGAGGAGCTAAAGCActaACAGAAGTAGTAcCaCTAaCAAAAAGAAGCAGAACTAGaACTGGCAGAAAACAGGGAGATTCTAAAAGaaCCAGTACATGGGGTGTATTATGACC
CATCAAAAGACTTAATAGCAGAAAATACAGAAAACAGGAGCTAGgcCAATGGACATATCAAATTTATCAAGAGCCACTTAAGAATCTGAAAACAGGAAAATATGCAAGAATGAG
GGGTGCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCACAGAAAAGCATAGTGATATGGGGAAAAGACTCCTAAATTTAGACTACCCATACAAAAG
GAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCCACTTGGATTCCTGAATGGGAATTTGTCAATACCCCTCCCTTAGTGAATTTATGGTACCAGTTAGAGAAAAGACC
CCATAGTAGGAGCAGAAAATTTCTATGTAGATGGAGCAGCTAATAGGGACACTAAACTAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGACAAAAGTAGTCTCCCTGAC
TGACACAACAAGTCAGAAGACTGAGTTACAGGCAATTAATCTAGCTTTACAGGATTCAGGGCCAGAAGTAAACATAGTAACAGACTACAATATGCATTAGGAATAATCAA
GCCAACCCAGATAAGAGTGAATCAGAGGTAGTCAGTCAAATAATAGAACAATTAATAAAAAAGGAAAAGTCTACCTGACATGGGTACCAGCACAAAAGGAAATGGAGGAA
ATGAAAAGAGTAGATAAGTTAGTCAGTGCTGGAATCAGAAAAGTACTATTTTGGatggaatAGATA

Nucleotide Alignments

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      1
      |
422_RTb_F  TAAGTAAGGCAATTATGTTAACTCCTTAGAGGAGCTAAAGCACTAACAGAAGTAGTACCCTAACAAAAGAAGCA
422_RTb_R  *****-----

     101
     |
422_RTb_F  GAACTAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCAGTACATGGGGTGTATTATGACCCATCAAAAGAC
422_RTb_R  -----

     201
     |
422_RTb_F  TTAATAGCAGAAAATACAGAAAACAGGAGCTAGGCCAATGGACATATCAAATTTATCAAGAGCCACTTAAGAATCTG
422_RTb_R  -----

     301
     |
422_RTb_F  AAAACAGGAAAATATGCAAGAATGAGGGGTGCCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAAA
422_RTb_R  -----

     401
     |
422_RTb_F  ATAGCCACAGAAAGCATAGTGATATGGGAAAAGACTCCTAAATTTAGACTACCCATACAAAAGGAAACATGGGAA
422_RTb_R  -----

     501
     |
422_RTb_F  GCATGGTGGATGGAGTATTGGCAAGCCACTTGGATTCCTGAATGGGAATTTGTCAATACCCCTCCCTTAGTGAAA
422_RTb_R  -----

     601
     |
422_RTb_F  TTATGGTACCAGTTAGAGAAAAGACCCCATAGTAGGAGCAGAACTTTCTATGTAGATGGAGCAGCTAATAGGGAC
422_RTb_R  -----

     701
     |
422_RTb_F  ACTAAACTAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGACAAAAGTAGTCTCCCTGACTGACACAACAAGT
422_RTb_R  -----

     801
     |
422_RTb_F  CAGAAGACTGAGTTACAGGCAATTAATCTAGCTTTACAGGATTCAGGGCCAGAAGTAAACATAGTAACAGACTCA
422_RTb_R  -----

     901
     |
422_RTb_F  CAATATGCATTAGGAATAATCAAGCGCAACCAGATAAGAGTGAATCAGAGGTAGTCAGTCAAATAATAGAACAA
422_RTb_R  -----
```

```
1001
|
422_RTb_F  TTAATAAAAAAGGAAAAAGTCTACCTGACATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAAAGAGTAGAT
422_RTb_R  -----
```

```
1101
|
422_RTb_F  AAGTTAGTCAGTGCTGGAATCAGAAAAGTACTATTTTTGGATGGAATAGATA
422_RTb_R  -----
```

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

```
>422_RTb
TAAGTAAGGCAATTATGTAACTCCTTAGAGGAGCTAAAGCACTAACAGAACTAGTACCACTAACAAAGAAGCAGAACTAGAACTGGCAGAAAACAGGAGATTCTAAAAG
AACCAGTACATGGGGTGTATTATGACCCATCAAAGACTTAATAGCAGAAATACAGAAACAGGAGCTAGGCCAATGGACATATCAAATTTATCAAGAGCCACTTAAGAATCT
GAAAACAGGAAAATATGCAAGAATGAGGGGTGCCACACTAATGATGTAACAGTTAAACAGAGGCAGTGCAAAAAATAGCCACAGAAAGCATAAGTATATGGGGAAAGACT
CCTAAATTTAGACTACCCATACAAAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCCACTGGATTCCTGAATGGGAATTTGTCAATACCCCTCCCTTAGTGA
AATTATGGTACCAGTTAGAGAAAGACCCCATAGTAGGAGCAGAACTTCTATGTAGATGGAGCAGCTAATAGGGACACTAACTAGGAAAAGCAGGGTATGTTACTGACAG
AGGAAGACAAAAGTAGTCTCCCTGACTGACACAACAAGTCAGAAGACTGAGTTACAGGCAATTAATCTAGCTTTACAGGATTCAGGGCCAGAAGTAAACATAGTAACAGAC
TCACAATATGCATTAGGAATAATCAAGCGCAACCAGATAAGAGTGAATCAGAGGTAGTCAGTCAAATAATAGAACAATTAATAAAAAAGGAAAAAGTCTACCTGACATGGg
TACCAGCACACAAAGGaaTTGGaGGAAATGAAAGAGTAGATAAGTTAGTCAGTGCTGGaATCAGAAAAGTACTATTTTTGGATGGAATAGATa
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MX-HIV-0422 INTEGRASE FRAGMENT (Fwd & Rev)

>422_IN_F

GATAAAGCCaAAGAAGACATGAGAAGTATCACAGTAATTTGGAGAGCAATGGCTAGTGATTTTAACTACCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAGT
GTCAGTTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGCCCAGGAATATGGCAGCTAGATTGTACACACTTAGAAGGAAAAATTTCTGGTAGCAGTTCATGTAGC
CAGTGGATATATAGAAGCAGAAGTTATCCAGCAGAGACAGGGCAAGAAACAGCATACTTTATTTAACTAGCCGGGAGATGGCCAGTAAAAACAATACATACAGACAAT
GGCAGCAATTTTACCAGTACTACAGTTAAGGCCGCCCTGTGGTGGGGCGGGATCAAACAGGAATTTGGTATTCCCTACAATCCTCAAAGTCAAGGAGTAGTAGAATCTATGA
ATAAAGAATTAAGAAAAATAATAGAACAGGTAAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATTCACAATTTTAAAAAGAAAAGGGGGATTGG
GGGTACAGTGCAGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAATAAAGAATTACAAAAACAATTACAAAAATTTAAATTTTCGGGTTTATTACAGGGAC
AGCAGAGATCCACTTTGGAAAGGACCAGCAAAGCTTCTTTGGaAAGGTGAAGGGGCAGTAGTGATACAGATAATAGTGACATAAAAGTAGTGCCAAAGAAGAAAAGCAAAGA
TCATTAGGGACTATGAAAAACAGATGGCAGGTGATGATTTGTgGCAAGTAGACAGGATGAGGATTAGGACATG

>422_IN_R

GAAAAGTACTATTTTAGATGGAaTAGATaAAGCCCAAGAAGaCaTAGAGAAGTATCACAGTAATtGgaGAGCaATGGCTAGTGATTTTAACTaCCACCTGTAGTAGCAAA
AGAAATAGTAGCCAGCTGTGATAAGTGTCAAGTTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGCCCAGGAATATGGCAGCTAGATTGTACACACTTAGAAGGAAAA
ATTATTTCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGGCAAGAAACAGCATACTTTATTTAACTAGCCGGGAGATGGC
CAGTAAAAACAATACATACAGACAATGGCAGCAATTTTACCAGTACTACAGTTAAGGCCGCCCTGTGGTGGGGCGGGATCAAACAGGAATTTGGTATTCCCTACAATCCTCA
AAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTAAGAAAAATAATAGAACAGGTAAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATTCAC
AATTTTAAAGAAAAGGGGGATTTGGGGGTACAGTGCAGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAAACAATTACAAAAATTT
AAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGACCAGCAAAGCTTCTTTGGAAAGGTGAAGGGGCAGTAGTGATACAAAGATAATAGTGACATAAA
AGTAGTGCCAAAGAAGAAAAGCAAAGATCATTAGGGACTATGAAAAACAGATGGCAGGTg

Nucleotide Alignments

```

      1
      |
422_IN_F *****GATAAAGCCCAAGAAGACATGAGAAGTATCACAGTAATTTGGAGAGCAAA
422_IN_R GAAAAGTACTATTTTAGATGGAATA-----

      101
      |
422_IN_F TGGCTAGTGATTTTAACTACCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAGTGTCAAGTTAAAAG
422_IN_R -----

      201
      |
422_IN_F GAGAAGCCATGCATGGACAAGTAGACTGTAGCCCAGGAATATGGCAGCTAGATTGTACACACTTAGAAGGAAAAA
422_IN_R -----

      301
      |
422_IN_F TTATTTCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGGCAAGAAA
422_IN_R -----

      401
      |
422_IN_F CAGCATACTTTATTTTAACTAGCCGGGAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGCAATTTTA
422_IN_R -----

      501
      |
422_IN_F CCAGTACTACAGTTAAGGCCGCCCTGTGGTGGGGCGGGATCAAACAGGAATTTGGTATTCCCTACAATCCTCAA
422_IN_R -----

      601
      |
422_IN_F GTCAAGGAGTAGTAGAATCTATGAATAAAGAATTAAGAAAAATAATAGAACAGGTAAGAGATCAGGCTGAACATC
422_IN_R -----

      701
      |
422_IN_F TTAAGACAGCAGTACAAATGGCAGTATTCATTCACAATTTTAAAGAAAAGGGGGATTGGGGGTACAGTGCAG
422_IN_R -----

      801
      |
422_IN_F GGGAAAGAATAGTAGACATAATAGCAACAGACATACAAATAAAGAATTACAAAAACAATTACAAAAATTTAA
422_IN_R -----

      901
      |
422_IN_F ATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGACCAGCAAAGCTTCTTTGGAAAGGTGAAG
422_IN_R -----
```

```
1001
|
422_IN_F GGGCAGTAGTGATACAAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGGACTATG
422_IN_R -----
```

```
1101
|
422_IN_F GAAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGGACATG
422_IN_R -----*****
```

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

```
>422_IN
GAAAAGTACTATTTTTAGATGGAATAGATAAAAGCCcAAGAAGAACATGAGAAGTATCAGTAATTGGAGAGCAATGGCTAGTGATTTAACCTACCACCTGTAGTAGCAAA
AGAAATAGTAGCCAGCTGTGATAAGTGTGAGTTAAAAGGAGAAAGCCATGCATGGACAAGTAGACTGTAGCCCAGGAATATGGCAGCTAGATTGTACACACTTAGAAGGAAAA
ATTATTCCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGGCAAGAAACAGCATACTTTATTTTAAAAC TAGCCGGGAGATGGC
CAGTAAAAACAATACATACAGACAATGGCAGCAATTTTACCAGTACTACAGTTAAGGCCGCTGTTGGTGGGCGGGGATCAAACAGGAATTTGGTATTCCCTACAATCCTCA
AAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTAAGAAAAATAATAGAACAGGTAAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCATTCAC
AATTTTAAAAGAAAAGGGGGGATGGGGGTACAGTGCAGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAAACAATTAACAAAAATTT
AAAATTTTCGGGTTTATTACAGGGACAGCAGAGATCCACTTTGGAAAGGACCAGCAAAGCTTCTTTGGaAAGGTGAAGGGGCAGTAGTGATACAAAGATAATAGTGACATAAA
AGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGGACTATGGAAAACAGATGGCAGGTGATGATTGTGTgCAAGTAGACAGGATGAGGATTAGGACATG
```

MX-HIV-0422 CONTIG ASSEMBLY (4 Fragments)

Nucleotide Alignments

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                2085                                     2156
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
422_PR          *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTa         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTb         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_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
    
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                2157                                     2231
B.FR.83.HXB2    AGC CCC ACC AGA AGA GAG CTT CAG GTC TGG GGT AGA GAC AAC AAC TCC CCC TCA GAA GCA GGA GCC GAT AGA CAA
422_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTb         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_IN          *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
                S P T R R E L Q V W G R/G D N N S/T P/L S E A/T G A D R Q
    
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                2232                                     2253                                     2306
B.FR.83.HXB2    GGA ACT GTA TCC TTT AAC TTC CCG CAG GTC ACT CTT TGG CAA CGA CCC CTC GTC ACA ATA AAG ATA GGG GGG CAA
422_PR          --- G-- A-- --- --- G-- C-- --- --A A-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTb         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_IN          *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
                G T/A V/I S F N/D F/L E Q V/I T L W Q R P L V T I/V K I G G Q
    
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-----Protease start-----

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                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
422_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTb         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_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/X
    
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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
422_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTb         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_IN          *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
                P K M I G G I G G F I K V R Q Y D Q I L I E 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 TTG ACT CAG ATT
422_PR          --- --- A-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_RTb         *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
422_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
    
```

```

                2533                                     2549 2550                                     2606
B.FR.83.HXB2    GGT TGC ACT TTA AAT TTT CCG ATT AGC CCT ATT GAG ACT GTA CCA GTA AAA TTA AAG CCA GGA ATG GAT GGC CCA
422_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** *** ---T--- ---A--- --- --- --- --- --- --- --- --- --- ---
422_RTb         *** *** *** *** *** *** *** *** *** *** ---T--- ---A--- --- --- --- --- --- --- --- --- --- ---
422_IN          *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
                G C T L N F E I S P I E T V P V K L K P G M D G P
    
```

-----Protease end----- | -----Pol p66 and p51 start-----

```

                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
422_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTa         *** *** *** *** *** *** *** *** *** ---G--- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTb         *** *** *** *** *** *** *** *** *** ---G--- --- --- --- --- --- --- --- --- --- --- --- ---
422_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
    
```


2682 |-----| 2756
B.FR.83.HXB2 GGG AAA ATT TCA AAA ATT GGG CCT GAA AAT CCA TAC AAT ACT CCA GTA TTT GCC ATA AAG AAA AAA GAC AGT ACT
422_PR *** ** A--
422_RTa ---C
422_RTb
422_IN
G K I S K I G P E N P Y N T P V/I F A I K K K D S T

2757 |-----| 2831
B.FR.83.HXB2 AAA TGG AGA AAA TTA GTA GAT TTC AGA GAA CTT AAT AAG AGA ACT CAA GAC TTC TGG GAA GTT CAA TTA GGA ATA
422_PR *** **
422_RTa ---T ---C ---G ---G
422_RTb
422_IN
K W R K L V D F R E L N K R T Q D F W E V Q L G I

2832 |-----| 2906
B.FR.83.HXB2 CCA CAT CCC GCA GGG TTA AAA AAG AAA AAA TCA GTA ACA GTA CTG GAT GTG GGT GAT GCA TAT TTT TCA GTT CCC
422_PR *** **
422_RTa ---T---C---G
422_RTb
422_IN
P H P A/S G L K K K K S V T V L D V G D A Y F S V P

2907 |-----|
2981 B.FR.83.HXB2 TTA GAT GAA GAC TTC AGG AAG TAT ACT GCA TTT ACC ATA CCT AGT ATA AAC AAT GAG ACA CCA GGG ATT AGA TAT
422_PR *** **
422_RTa ---CC---G---C---G---G
422_RTb
422_IN
L D E/P D F R K Y T A F T I P S I/R N N E T P G I/V R Y

2982 |-----| 3056
B.FR.83.HXB2 CAG TAC AAT GTG CTT CCA CAG GGA TGG AAA GGA TCA CCA GCA ATA TTC CAA AGT AGC ATG ACA AAA ATC TTA GAG
422_PR *** **
422_RTa ---A---G
422_RTb
422_IN
Q Y N V L P Q G W K G S P A I F Q S S M T K I L E

3057 |-----| 3131
B.FR.83.HXB2 CCT TTT AGA AAA CAA AAT CCA GAC ATA GTT ATC TAT CAA TAC ATG GAT GAT TTG TAT GTA GGA TCT GAC TTA GAA
422_PR *** **
422_RTa ---T
422_RTb
422_IN
P F R K Q N P D I V I Y Q Y M D D L Y V G S D L E

3132 |-----| 3206
B.FR.83.HXB2 ATA GGG CAG CAT AGA ACA AAA ATA GAG GAG CTG AGA CAA CAT CTG TTG AGG TGG GGA CTT ACC ACA CCA GAC AAA
422_PR *** **
422_RTa ---T---A---G---T---T---G
422_RTb
422_IN
I G Q H R T K I E/D E L R Q/E H L L R W G L/F T/A T P D K

3207 |-----| 3281
B.FR.83.HXB2 AAA CAT CAG AAA GAA CCT CCA TTC CTT TGG ATG GGT TAT GAA CTC CAT CCT GAT AAA TGG ACA GTA CAG CCT ATA
422_PR *** **
422_RTa ---C
422_RTb
422_IN
K H Q K E P P F L W M G Y E L H P D K W T V Q P I

```
3282-----3356
|-----|
B.FR.83.HXB2 GTG CTG CCA GAA AAA GAC AGC TGG ACT GTC AAT GAC ATA CAG AAG TTA GTG GGG AAA TTG AAT TGG GCA AGT CAG
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTb *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          V  L  P  E  K  D  S  W  T  V  N  D  I  Q  K  L  V  G  K  L  N  W  A  S  Q
```

```
3357-----3431
|-----|
B.FR.83.HXB2 ATT TAC CCA GGG ATT AAA GTA AGG CAA TTA TGT AAA CTC CTT AGA GGA ACC AAA GCA CTA ACA GAA GTA ATA CCA
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa --- --T G-- --- --C--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTb *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          I  Y  P/A  G  I  K/X  V  R  Q  L  C  K  L  L  R  G  T/S  K  A  L  T  E  V/I  I/V  P
```

```
3432-----3506
|-----|
B.FR.83.HXB2 CTA ACA GAA GAA GCA GAG CTA GAA CTG GCA GAA AAC AGA GAG ATT CTA AAA GAA CCA GTA CAT GGA GTG TAT TAT
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_RTb --- --- A--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          L  T  E  E  A  E  L  E  L  A  E  N  R  E  I  L  K  E  P  V  H  G  V  Y  Y
```

```
3507-----3581
|-----|
B.FR.83.HXB2 GAC CCA TCA AAA GAC TTA ATA GCA GAA ATA CAG AAG CAG GGG CAA GGC CAA TGG ACA TAT CAA ATT TAT CAA GAG
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTb --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          D  P  S  K  D  L  I  A  E  I  Q  K  Q  G  Q  G  Q  W  T  Y  Q  I  Y  Q  E
```

```
3582-----3656
|-----|
B.FR.83.HXB2 CCA TTT AAA AAT CTG AAA ACA GGA AAA TAT GCA AGA ATG AGG GGT GCC CAC ACT AAT GAT GTA AAA CAA TTA ACA
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTb --- C-- --G--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          P  F  K  N  L  K  T  G  K  Y  A  R  M  R  G  A  H  T  N  D  V  K  Q  L  T
```

```
3657-----3731
|-----|
B.FR.83.HXB2 GAG GCA GTG CAA AAA ATA ACC ACA GAA AGC ATA GTA ATA TGG GGA AAG ACT CCT AAA TTT AAA CTG CCC ATA CAA
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTb --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          E  A  V  Q  K  I  T  T  E  S  I  V  I  W  G  K  T  P  K  F  K  L  P  I  Q
```

```
3732-----3806
|-----|
B.FR.83.HXB2 AAG GAA ACA TGG GAA ACA TGG TGG ACA GAG TAT TGG CAA GCC ACC TGG ATT CCT GAG TGG GAG TTT GTT AAT ACC
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTb --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          K  E  T  W  E  T  W  W  T  E  Y  W  Q  A  T  W  I  P  E  W  E  F  V  N  T
```

```
3807-----3881
|-----p51 end and p66 RT continue-----| |RNase H start|
B.FR.83.HXB2 CCT CCC TTA GTG AAA TTA TGG TAC CAG TTA GAG AAA GAA CCC ATA GTA GGA GCA GAA ACC TTC TAT GTA GAT GGG
422_PR *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTa *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
422_RTb --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
          P  P  L  V  K  L  W  Y  Q  L  E  K  E  P  I  V  G  A  E  T  F  Y  V  D  G
```

3882 3956
|-----|
B.FR.83.HXB2 GCA GCT AAC AGG GAG ACT AAA TTA GGA AAA GCA GGA TAT GTT ACT AAT AGA GGA AGA CAA AAA GTT GTC ACC CTA
422_PR *** ** *
422_RTa *** ** *
422_RTb --- --- -T --- -C --- --- C-- --- --- --- -G --- --- --- G-C --- --- --- --- -A --- T-- -G
422_IN *** ** *
A A N R E T K L G K A G Y V T N R G R Q K V V T L

3957 4031
|-----|
B.FR.83.HXB2 ACT GAC ACA ACA AAT CAG AAG ACT GAG TTA CAA GCA ATT TAT CTA GCT TTG CAG GAT TCG GGA TTA GAA GTA AAC
422_PR *** ** *
422_RTa *** ** *
422_RTb --- --- --- -G- --- --- --- --- -G --- --- A-- --- --- -A --- --- -A ---G CC- --- --- ---
422_IN *** ** *
T D T T N Q K T E L Q A I Y L A L Q D S G L E V N

4032 4106
|-----|
B.FR.83.HXB2 ATA GTA ACA GAC TCA CAA TAT GCA TTA GGA ATC ATT CAA GCA CAA CCA GAT CAA AGT GAA TCA GAG TTA GTC AAT
422_PR *** ** *
422_RTa *** ** *
422_RTb --- --- --- --- --- --- --- --- --- -A --- --- -G --- --- A-G --- --- --- G-- --- -G-
422_IN *** ** *
I V T D S Q Y A L G I I Q A Q P D Q S E S E L V N

4107 4181
|-----|
B.FR.83.HXB2 CAA ATA ATA GAG CAG TTA ATA AAA AAG GAA AAG GTC TAT CTG GCA TGG GTA CCA GCA CAC AAA GGA ATT GGA GGA
422_PR *** ** *
422_RTa *** ** *
422_RTb --- --- --- -A -A --- --- --- -A --- -C --- A-- --- --- --- --- --- --- --- --- --- --- ---
422_IN *** ** *
Q I I E Q L I K K E K V Y L A W V P A H K G I G G

4182 4229 4230 4256
|-----Pol p66 and RNase H end-----| |-----Pol p31 Integrase start-----|
B.FR.83.HXB2 AAT GAA CAA GTA GAT AAA TTA GTC AGT GCT GGA ATC AGG AAA GTA CTA GTT TTA GAT GGA ATA GAT AAG GCC CAA
422_PR *** ** *
422_RTa *** ** *
422_RTb --- --- AG- --- --- -G --- --- --- --- -A --- --- --- -G --- --- --- --- --- -A --- ** ** * ** *
422_IN *** ** *
N E Q V D K L V S A G I R K V L L L D G I D K A Q

4257 4331
|-----|
B.FR.83.HXB2 GAT GAA CAT GAG AAA TAT CAC AGT AAT TGG AGA GCA ATG GCT AGT GAT TTT AAC CTG CCA CCT GTA GTA GCA AAA
422_PR *** ** *
422_RTa *** ** *
422_RTb *** ** *
422_IN -A --- --- --- -G --- --- --- --- --- --- --- --- --- -A --- --- --- --- ---
D/E E H E K Y H S N W R A M A S D F N L P P V V A K

4332 4406
|-----|
B.FR.83.HXB2 GAA ATA GTA GCC AGC TGT GAT AAA TGT CAG CTA AAA GGA GAA GCC ATG CAT GGA CAA GTA GAC TGT AGT CCA GGA
422_PR *** ** *
422_RTa *** ** *
422_RTb *** ** *
422_IN --- --- --- --- --- -G --- --- T-- --- --- --- --- --- --- --- --- -C --- --- --- ---
E I V A S C D K C Q L K G E A M H G Q V D C S P G

4407 4481
|-----|
B.FR.83.HXB2 ATA TGG CAA CTA GAT TGT ACA CAT TTA GAA GGA AAA GTT ATC CTG GTA GCA GTT CAT GTA GCC AGT GGA TAT ATA
422_PR *** ** *
422_RTa *** ** *
422_RTb *** ** *
422_IN --- --- -G --- --- --- -C --- --- --- A-- -T --- --- --- --- --- --- --- --- --- --- ---
I W Q L D C T H L E G K V/I I L V A V H V A S G Y I

4482 4556

B.FR.83.HXB2
 422_PR
 422_RTa
 422_RTb
 422_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 --G ---
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
 422_PR
 422_RTa
 422_RTb
 422_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 --- --T --- A-- A-- --A --- -A- ---
V K T I H T D N G S N F T G/S A/T T V R/K A A C W W A G
  
```

4632 4706

B.FR.83.HXB2
 422_PR
 422_RTa
 422_RTb
 422_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
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
--- --A --- --T --- --T ---
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
 422_PR
 422_RTa
 422_RTb
 422_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
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
--- --A --- -A- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
K I I G/E 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
 422_PR
 422_RTa
 422_RTb
 422_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
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
F K R K G G I G G Y S A G E R I V D I I A T D I Q
  
```

4857 4931

B.FR.83.HXB2
 422_PR
 422_RTa
 422_RTb
 422_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
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
T K E L Q K Q I T K I Q/X N F R V Y Y R D S R N P L
  
```

4932 5006

B.FR.83.HXB2
 422_PR
 422_RTa
 422_RTb
 422_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
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
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
 422_PR
 422_RTa
 422_RTb
 422_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
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
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 *** **
422_PR      *** ** *
422_RTa     *** ** *
422_RTb     *** ** *
422_IN      --- --- --- --- GAC ATG
           Q  D  E  D  X

```

Protein Alignments

```

      1      10      20      30      40      50      60      70      80      90      99
B.FR.83.HXB2 *FFREDLAFLO GKAREFSSEQ TRANSPTRRE LQVWGRDNNS PSEAGADROG TVSFNFPOVT LWQRPLVTIK IGGQLKEALL DTGADDTVLE EMSLPGRWK
422_PR      _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_RTa     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_RTb     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_IN      _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_

      100     110     120     130     140     150     160     170     180     190     199
B.FR.83.HXB2 PKMIGGIGGFIK VRQYDQILI EICGHKAIGT VLVGPTPVNI IGRNLLTQIG CTLNFIISPI ETVVPVKLKP MDGPKVKQWP LTEEKIKALV EICTEMEKE
422_PR      *****
422_RTa     *****
422_RTb     *****
422_IN      *****

      200     210     220     230     240     250     260     270     280     290     299
B.FR.83.HXB2 GKISKIGPENPY NTPVFAIKK KDSTKWRKLV DFRELNKRTO DFWEVQLGIP HPAGLKKKKS VTVLDVGDAY FSVPLDEDFR KYTAFPTIPSI NNETPGIRY
422_PR      -----
422_RTa     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_RTb     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_IN      _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_

      300     310     320     330     340     350     360     370     380     390     399
B.FR.83.HXB2 QYNVLPQGWKGS PAIFQSSMT KILEPFRKQN PDIVIQYQMD DLYVGSLEI GQHRTKIEEL RQHLLRWGLT TPKKKHQKEP PFLWMGYELH PDKWTVQPI
422_PR      -----
422_RTa     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_RTb     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_IN      _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_

      400     410     420     430     440     450     460     470     480     490     499
B.FR.83.HXB2 VLPEKDSWTVND IQKLVGKLN WASQIYPGIK VRQLCKLLRG TKALTEVIPL TEEAELELAE NREILKEPVH GVIYDPSKDL IAEIQKGGQ GWTYQIYQE
422_PR      -----
422_RTa     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_RTb     _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_
422_IN      _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_ _*****_

      500     510     520     530     540     550     560     570     580     590     599
B.FR.83.HXB2 PFKNLKTGKYAR MRGAHTNDV KQLTEAVQKI TTESIVIWGK TPKFKLPIQK ETWETWWTQY WQATWIPEWE FVNTPLPKL WYQLEKEPIV GAETFYVDG
422_PR      *****
422_RTa     *****
422_RTb     *****
422_IN      *****

      600     610     620     630     640     650     660     670     680     690     699
B.FR.83.HXB2 AANRETKLGKAG YVTNRGRQK VVTLTDTTNO KTELQAIYLA LQDSGLEVNI VTDSQYALGI IQAQPDQSES ELVNQIIEQL IKKEKVYLAV VPAHKGIGG
422_PR      *****
422_RTa     *****
422_RTb     *****
422_IN      *****

      700     710     720     730     740     750     760     770     780     790     799
B.FR.83.HXB2 NEQVDKLVSAGI RKLVLGDI DKAODEHEKY HSNWRAMASD FNLPPVVAKE IVASCDCQQL KGEAMHGQVD CSPGIWQLDC THLEKVIILV AVHVASGYI
422_PR      *****
422_RTa     *****
422_RTb     *****
422_IN      *****

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      800      810      820      830      840      850      860      670      880      890      899
B.FR.83.HXB2  EAEVIPAETGQE TAYFLLKLA GRWPVKTIHT DNGSNFTGAT VRAACWVAGI KQEFGIPYNP QSQGVVESMN KELKKIIGQV RDQAEHLKTA VQMAVFIHN
422_PR      *****
422_RTa      *****
422_RTb      *****
422_IN      -----I-----ST--K-----E-----

      900      910      920      930      940      950      960      970      980      990      999
B.FR.83.HXB2  FKRKGGIGGYSAG ERIVDIIA TDIQTKELQK QITKIQNFRV YYRDSRNPLW KGPAPKLLWKG EGAVVIQDNS DIKVVPRRKA KIIRDYQKQM AGDDCVASR
422_PR      *****
422_RTa      *****
422_RTb      *****
422_IN      -----X-----

      1001
B.FR.83.HXB2  QDEDX
422_PR
422_RTa      *****
422_RTb
422_IN

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

>422_pol

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