

MX-HIV-0327 PROTEASE FRAGMENT (Fwd & Rev)

>327_PR_F

agGTTTGGGGAGGAGatAACAAACCCCTCTCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAAATAGGAGG
GCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAGTGAATTTACCAGGAAGATGGAAACCAAAAATGATAAGGGGAATGGAGGTTTTATC
AAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAACTATAGGTACAGTATTAATAGGACCTACACCTGTCAACATAAATGGGAAGAAATCTATTGACTC
AGATTGGCTGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAAGTTAAACAATGGCCATT

>327_PR_R

AGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGATAACAACACCCTCTCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGC
AGCGACCCCTCGTCACAGTAAAAATAGGAGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAGTGAATTTACCAGGAAGATGGAAACC
AAAAATGATAAGGGGAATGGAGGTTTTATCAAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAACTATAGGTACAGTATTAATAGGACCTACACCT
GTCAACATAAATGGGAAGAAATCTATTGACTCAGATTGGCTGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAGCCa

Nucleotide Alignments

```

      1
      |
327_PR_F *****AGGTTTGGGGAGGAGATAACAACACCCTCTCAGAAACAGGAGGA
327_PR_R AGAGCCAACAGCCCCACCAGAAGAGAGCTC-----

     101
     |
327_PR_F GCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTCGTCACAGTAAAAATAGGAGGGCAACTA
327_PR_R -----

     201
     |
327_PR_F AAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAGTGAATTTACCAGGAAGATGGAAACCA
327_PR_R -----

     301
     |
327_PR_F AAAATGATAAGGGGAATGGAGGTTTTATCAAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACAT
327_PR_R -----

     401
     |
327_PR_F AAACTATAGGTACAGTATTAATAGGACCTACACCTGTCAACATAAATGGGAAGAAATCTATTGACTCAGATTGGC
327_PR_R -----

     501
     |
327_PR_F TGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAGCCAGGAATGGATGGCCAAAA
327_PR_R -----*****

     601
     |
327_PR_F GTTAAACAATGGCCATT
327_PR_R *****
```

>327_PR

AGAGCCAACAGCCCCACCAGAAGAGAGCTTCagGTTTGGGGAGGAGatAACAAACACCCTCTCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGC
AGCGACCCCTCGTCACAGTAAAAATAGGAGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAGTGAATTTACCAGGAAGATGGAAACC
AAAAATGATAAGGGGAATGGAGGTTTTATCAAAGTAAGACAGTATGATCAGGTACCCATAGAAATCTGTGGACATAAACTATAGGTACAGTATTAATAGGACCTACACCT
GTCAACATAAATGGGAAGAAATCTATTGACTCAGATTGGCTGTACTTTAAATTTTCCATTAGTCCTATTGAAACTGTACCAGTAAATTAAGCCAGGAATGGATGGCCAA
AAGTTAAACAATGGCCATT

MX-HIV-0327 REVERSE TRANSCRIPTASE FRAGMENT A (Fwd & Rev)

>327_RTa_F

CTGTTGACTCAGATTGGATGCACTTTAAATTTTCCATTAGTCTATTGAAACTGTACCAGTCAAATTTAAACCAGGAATGGATGGCCCAAAGTTAAACAATGGCCATTGACAGAAAGAAAAGATAAAAAGCATTAGTAGAAAATTTGCACAGAAATGGAAAAAGAAGGGAAAAATTTCAAATAATGGGCCTGAAAAATCCATAACAATACTCCAATATTTGCCATAAA
GAAAAAGACAGTACCAATGGAGAAAATAGTAGATTTAGAGAACTTAACAAGAGAACTCAAGACTTCTGGGAGGTTTCAGTTAGGAATACCACATCCCTCAGGGCTAAAA
AAGAAAAAGTCAGTAACAGTACTGGATGTGGGTGATGCATATTTTCAGTTCCTTAGATCCAGACTTCAGGAAGTATACGGCATTCCACATACCTAGTAGAAAACAATGAGA
CACCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAGGATCACCAGCGATATTTCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAAACAATCC
AGACATAGTTATCTATCAATACATGGATGATTGTATGTAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAATAAGATGAAGTACAGAGAAATTTGTTGAGGTGGGGA
TTTGCCACACCAGACAAAAACACCAGAAAGAACCTCCATTCCTTTGGATGGGTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAGTGTGCCAGAAAAAGACA
GCTGGACTGTCAATGACATACAAAAGTTAGTGGGAAAATTAATTTGGGCAAGTCAGATTTATGCAGGGaTCAAAGTAAgGCAATTATGTAAGCTcCTTaGGGGATCCAAaGC
ACTAACAGAAAATAGTACCCTAAcCAGAaAagCAGAGCTAGAA

>327_RTa_R

TGAAACTGTaccCAGtGAAatTaaAaCCAGGAATGGATGGCCCAAAGTTAAACAAtggCCATTGACAgaagaAAAGATAAAAAGCATTAGTAGAAAATtTGCACAGAAATGGAA
AAAGAAGGAAAAATTTCAAATAATGGGCCTGAAAAATCCATACAAATcCCAATATTTGCCATAAAAGAAAAAGACAGTaCCAAATGGAGAAAATTAGTAGATTTAGAGAAC
TTAAACAAGAGAACTCAAGACTTCTGGGAGGTTTCAGTTAGGAATACCACATCCCTCAGGGCTAAAAAAGAAAAAGTCAGTAACAGTACTGGATGTGGGTGATGCATATTTTC
AGTTCCTTAGATCCAGACTTCAGGAAGTATACGGCATTCCACATACCTAGTAGAAAACAATGAGACACCAGGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAA
GGATCACCAGCGATATTTCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACAATAAGTATCTATCAATACATGGATGATTTGTATGTAGGATCTG
ATTTAGAAAATAGGGCAGCATAGAACAATAAGATGAAGTACAGAGAACATTTGTTGAGGTGGGATTTGCCACACCAGACAAAAACACCAGAAAGAACCTCCATTCCTTTG
GATGGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAGTGTGTCAGAAAAGACAGCTGGACTGTCAATGACATACAAAAGTTAGTGGGAAAATTAATTTGG
GCAAGTCAGATTTATGCAGGGATCAAAGTAAAGCAATATATGTAAGCTCCTTAGGGGATCCAAAGCACTAACAGAAAATAGTACCCTAACAGAAGAAGCAGAGCTAGAACTGG
CAGAAAACAGAGAGAT

Nucleotide Alignments

```

1
|
327_RTa_F CTGTTGACTCAGATTGGATGCACTTTAAATTTTCCATTAGTCTATTGAAACTGTACCAGTCAAATTTAAACCA
327_RTa_R *****-----

101
|
327_RTa_F GGAATGGATGGCCCAAAGTTAAACAATGGCCATTGACAGAAAGAAAAGATAAAAAGCATTAGTAGAAAATTTGCACA
327_RTa_R -----

201
|
327_RTa_F GAAATGGAAAAAGAAGGGAAAATTTCAAATAATGGGCCTGAAAAATCCATAACAATACTCCAATATTTGCCATAAAG
327_RTa_R -----

301
|
327_RTa_F AAAAAAGACAGTACCAAATGGAGAAAATTAGTAGATTTTAGAGAACTTAACAAGAGAACTCAAGACTTCTGGGAG
327_RTa_R -----

401
|
327_RTa_F GTTCAGTTAGGAATACCACATCCCTCAGGGCTAAAAAAGAAAAGTCAGTAACAGTACTGGATGTGGGTGATGCA
327_RTa_R -----

501
|
327_RTa_F TATTTTTCAGTTCCTTAGATCCAGACTTCAGGAAGTATACGGCATTACCACATCCTAGTAGAAAACAATGAGACA
327_RTa_R -----

601
|
327_RTa_F CCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAGGATCACCAGCGATATTTCAAAGTAGCATG
327_RTa_R -----

701
|
327_RTa_F ACAAAAATCTTAGAGCCTTTTAGAAAACAATAAGTATCAGCATAGTTATCTATCAATACATGGATGATTTGTATGTA
327_RTa_R -----

801
|
327_RTa_F GGATCTGATTTAGAAAATAGGGCAGCATAGAACAATAAGATGAAGTACAGAGAACATTTGTTGAGGTGGGATTT
327_RTa_R -----
```

901
|
327_RTa_F GCCACACCAGACAAAAAACACCAGAAAGAACCTCCATTCCCTTTGGATGGGTATGAACTCCATCCTGATAAATGG
327_RTa_R -----

1001
|
327_RTa_F ACAGTACAGCCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGTCAATGACATACAAAAGTTAGTGGGAAATTA
327_RTa_R -----

1101
|
327_RTa_F AATTGGGCAAGTCAGATTTATGCAGGGATCAAAGTAAGGCAATTATGTAAGCTCCTTAGGGGATCCAAAGCACTA
327_RTa_R -----

1201
|
327_RTa_F ACAGAAATAGTACCCTAACAGAAGAAGCAGAGCTAGAA*****
327_RTa_R -----CTGGCAGAAAACAGAGAGAT

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

>327_RTa
CTaTTGACTCAGATTGGcTGtACTTTAAATTTTCCATTAGTCTTATTGAAACTGTACCAGTGAATTAAGCCAGGAATGGATGGCCAAAAGTTAAACAATGGCCATTGA
CAGAAGAAAAGATAAAAGCATTAGTAGAAATTTGCACAGAAATGGAAAAAGAGGAAATTTCAAAAATTGGGCCTGAAAATCCATACAATACTCCAATATTTGCCATAAA
GAAAAAGACAGTACCAATGGAGAAAATTAGTAGATTTTAGAGAACTTAACAAGAGAACTCAAGACTTCTGGGAGGTTTCAGTTAGGAATACCACATCCCTCAGGGCTAAAA
AAGAAAAAGTCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCTTAGATCCAGACTTCAGGAAGTATACGGCATTCCACATACCTAGTAGAAACAATGAGA
CACCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAGGATCACCAGCGATATFCCAAAGTAGCATGCAAAAATCTTAGAGCCTTTTAGAAAACAAAATCC
AGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGATGAACTGAGAGAACATTTGTTGAGGTGGGGA
TTTGCCACACCAGACAAAAAACACCAGAAAGAACCTCCATTCCCTTTGGATGGGTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAAGACA
GCTGGACTGTCAATGACATACAAAAGTTAGTGGGAAATTAATTTGGGCAAGTCAGATTTATGCAGGgATCAAAGTAaGGCAATTATGTAAGCTcCTTaGGGGATCCAAaGC
ACTAACAGAAATAGTACCCTAaCAGAaAaGcAGAGCTAGAA

MX-HIV-0327 REVERSE TRANSCRIPTASE FRAGMENT B (Fwd & Rev)

>327_RTb_F

CAaAGTAAGGCAATTATGTAAGCTCCTTAGGGGAACCAAAGCACTAACAGAAATAGTACCCTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAA
GAACCAGTACATGGGGTGTATTATGACCCATCAAAGACTTAATAGCAGAAATACAGAAGCAGGGGTACGGCCAATGGACATACCAAATTTATCAAGAACCATTAAAGAATC
TGAAAACAGGAAAATATGCAAGAATAAGGGGTACCCACACTAATGATGTAACAATTAACAGAGACAGTGCAAAAATAGCCCTAGAAAGCATAGTAATATGGGGAAAAAC
TCCTAAATTTAAATTAACCATACAAAAAGAAACATGGGAAACATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAATGGGAGTTTGTCAATACCCCTCCCTTGGTG
AAATTTATGGTACCAGTTAGAGAAAGATCCCATAGTGGGAGCAGAAACTTCTATGTAGATGGGGCAGCTAACAGGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTAACA
GAGGAAGACAAAAGGTTGTCTCCCTAACTGACACAACAAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCCTTGCAGGATTTCAGGATTAGAAGTAAATATAGTGACAGA
CTCACAATATGCATTAGGAATCATTTCAAGCACACCAGATAAAAAGTGAATCAGAGATAGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGACAAGGTCTACCTGGCATGG
GTACCAGCACACAAAGGAATCGGAGGAAATGAACAAGTAGATAAATTAGTCAGTACTggaatCAGGAAGgTGCTATTTTTAGATGGAATAgATAAGGCCAaGaagACC

>327_RTb_R

TAAcAgaaaTaGTaCCAcTAAcCAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGaacCAGTACATGGGGTGTATTATGACCCATCAAAGACTTAAT
AGCAGAAATACAGAAGCAGGGGTACGgCCAATGGACATACCAAATTTATCAAGAACCATTAAAGAATCTGAAAACAGGAAAATATGCAAGAATAAGGGGTACCCACACTAAT
GATGTAAAACAATTAACAGAGACAGTGCAAAAATAGCCCTAGAAAAGCATAGTAATATGGGGAAAAACTCCTAAATTTAAATTAACCATACAAAAAGAAACATGGGAAACAT
GGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAATGGGAGTTTGTCAATACCCCTCCCTTGGTGAATTTATGGTACCAGTTAGAGAAAAGATCCCATAGTGGGAGCAGA
AACTTTCTATGTAGATGGGGCAGCTAACAGGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTAACAGAGGAAGACAAAAGGTTGTCTCCCTAACTGACACAACAAATCAG
AAGACTGAGTTACAAGCAATTTATCTAGCCTTGCAGGATTTCAGGATTAGAAGTAAATATAGTGACAGACTCACAATATGCATTAGGAATCATTTCAAGCACACCAGATAAAA
GTGAATCAGAGATAGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGACAAGGTCTACCTGGCATGGGTACCAGCACAAAAGGAATCGGAGGAAATGAACAAGTAGATAAA
ATTAGTCAGTACTGGAATCAGGAAGGTGCTATTTTAGatg

Nucleotide Alignments

```

      1
      |
327_RTb_F  CAAAGTAAGGCAATTATGTAAGCTCCTTAGGGGAACCAAAGCACTAACAGAAATAGTACCCTAACAGAAGAAGC
327_RTb_R  *****-----

     101
     |
327_RTb_F  AGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGAACCAGTACATGGGGTGTATTATGACCCATCAAAGA
327_RTb_R  -----

     201
     |
327_RTb_F  CTTAATAGCAGAAATACAGAAGCAGGGGTACGGCCAATGGACATACCAAATTTATCAAGAACCATTAAAGAATCT
327_RTb_R  -----

     301
     |
327_RTb_F  GAAAACAGGAAAATATGCAAGAATAAGGGGTACCCACACTAATGATGTAACAATTAACAGAGACAGTGCAAAA
327_RTb_R  -----

     401
     |
327_RTb_F  AATAGCCCTAGAAAGCATAGTAATATGGGGAAAAACTCCTAAATTTAAATTAACCATACAAAAGAAACATGGGA
327_RTb_R  -----

     501
     |
327_RTb_F  AACATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCTGAATGGGAGTTTGTCAATACCCCTCCCTTGGTGAA
327_RTb_R  -----

     601
     |
327_RTb_F  ATTATGGTACCAGTTAGAGAAAGATCCCATAGTGGGAGCAGAACTTTCATGTAGATGGGGCAGCTAACAGGGA
327_RTb_R  -----

     701
     |
327_RTb_F  GACTAAATTAGGAAAAGCAGGATATGTTACTAACAGAGGAAGACAAAAGGTTGTCTCCCTAACTGACACAACAAA
327_RTb_R  -----

     801
     |
327_RTb_F  TCAGAAGACTGAGTTACAAGCAATTTATCTAGCCTTGCAGGATTTCAGGATTAGAAGTAAATATAGTGACAGACTC
327_RTb_R  -----
```

901
|
327_RTb_F ACAATATGCATTAGGAATCATTCAAGCACACCAGATAAAAAGTGAATCAGAGATAGTCAATCAAATAATAGAGCA
327_RTb_R -----

1001
|
327_RTb_F GTTAATAAAAAAGGACAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATCGGAGGAAATGAACAAGTAGA
327_RTb_R -----

1101
|
327_RTb_F TAAATTAGTCAGTACTGGAATCAGGAAGGTGCTATTTTTAGATGGAATAGATAAGGCCCAAGAAGACC
327_RTb_R -----*****

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

>327_RTb
CaAAGTAAGGCAATTATGTAAGCTCCTTAGGGGatCCAAAGCACTAACAGAAATAGTACCACTAACAGAAGAAGCAGAGCTAGAAGTGGCAGAAAACAGAGAGATTCTAAAA
GAACCAGTACATGGGGTGTATTATGACCCATCAAAGACTTAATAGCAGAAATACAGAAGCAGGGGTACGGCCAATGGACATACCAAATTTATCAAGAACCATTTAAGAATC
TGAAAACAGGAAAATATGCAAGAATAAGGGGTACCCACACTAATGATGTAACAATTAACAGAGACAGTGCAAAAATAGCCCTAGAAAGCATAGTAATATGGGGAAAAAC
TCCTAAATTTAAATTACCATACAAAAAGAAACATGGGAAACATGGTGGACAGAGTATGGCAAGCCACCTGGATTCTGAATGGGAGTTTGTCAATACCCCTCCCTGGTG
AAATTTATGGTACCAGTTAGAGAAAAGATCCCATAGTGGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTAACA
GAGGAAGACAAAAGGTTGTCTCCCTAACGACACAACAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCCTTGCAGGATTCAGGATTAGAAGTAAATATAGTGACAGA
CTCACAATATGCATTAGGAATCATTCAAGCACACCAGATAAAAAGTGAATCAGAGATAGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGACAAGGTCTACCTGGCATGG
GTACCAGCACACAAAGGAATCGGAGGAAATGAACAAGTAGATAAATTAGTCAGTACTggaatCAGGAAGgTGCTATTTTTAGATGGAATAgATAAGGCCCAaGAgACC

MX-HIV-0327 INTEGRASE FRAGMENT (Fwd & Rev)

>327_IN_F

AgGTGCTATTTTTAGATGGaaTAGATAAGGCCCAAGAAGACCATGAGAAGTATCACAGTAATTGGAGAGCAATGGCTAGTGAATTTAACATACCACCTGTAGTAGCAAAAGA
AATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGATTGTAGTCCAGGAATATGGCAGCTAGATTGTACACATTTAGAAGGAAAAATT
ATCTGGTAGCAGTCCATGTAGCTAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGGCAAGAAACAGCATAACCTTATCTTGAAGCTAGCAGGAAGATGGCCAG
TAAAAACAATACACACAGACAATGGCCCAATTTCCACCAGTAATACTGTAAAGGCCGCTTGTGGTGGGCAGGGATCCAGCAGGAATTCGGCATCCCTACAATCCCCAAAG
TCAAGGAGTAGTAGAATCTTTAAATAAAGAATTAAAGAAAATTATAGGACAAGTAAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAGATGGCAGTATTCATCCCAAT
TTTAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAGAGAATTACAAAAACAAATTTCAAAAATTCAAA
ATTTTCGGGTTTATTACAGAGACAGCAGAGATCCACTTTGGAAAAGACCAGCCAAACTCCTCTGGAAAAGGTGAAGGGGCAGTAGTAATATAAGATAAATAGTGACATAAAAGT
AGTGCCAAGAAGAAAAGCAAAGATCATTAGGgATTATGGAAAACAGATGGCAGGTGATGATTGtGTGGCAAGTAGACAGGATGAGGATTAGAACATGGAACAGCCTAG

>327_IN_R

AGTACTGGAaTCAGGAaGTGCTATTTTLAGATGgAaTAqATaAGGCCCAAGAAGacCATGAGAAGTATCACAGTAATTGGAGAGCAATGGCTAGTGAATTTAACATACCAC
CTGTAGTAGCAAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGATTGTAGTCCAGGAATATGGCAGCTAGATTGTACACA
TTTAGAAGGAAAAATTATCCTGGTAGCAGTCCATGTAGCTAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAGACAGGGCAAGAAACAGCATAACCTTATCTTGAAGCTA
GCAGGAAGATGGCCAGTAAAACAATACACACAGACAATGGCCCAATTTCCACCAGTAATACTGTAAAGGCCGCTTGTGGTGGGCAGGGATCCAGCAGGAATTCGGCATCC
CCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTTTAAATAAAGAATTAAAGAAAATTATAGGACAAGTAAGAGATCAGGCTGAACATCTTAAAGACAGCAGTACAGATGGC
AGTATTCATCCCAATTTTAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAGAGAATTACAAAAACAA
ATTTCAAAAATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGATCCACTTTGGAAAAGACCAGCCAAACTCCTCTGGAAAAGGTGAAGGGGCAGTAGTAATATAAGATA
ATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGA

Nucleotide Alignments

```

      1
      |
327_IN_F *****AGGTGCTATTTTTAGATGGAATAGATAAGGCCCAAGAAGACCATGAGAAGTATCACAGT
327_IN_R AGTACTGGAATCAGGA-----

     101
     |
327_IN_F AATTGGAGAGCAATGGCTAGTGAATTTAACATACCACCTGTAGTAGCAAAAAGAAATAGTAGCCAGCTGTGATAAA
327_IN_R -----

     201
     |
327_IN_F TGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGATTGTAGTCCAGGAATATGGCAGCTAGATTGTACACAT
327_IN_R -----

     301
     |
327_IN_F TTAGAAGGAAAAATTATCCTGGTAGCAGTCCATGTAGCTAGTGGATATATAGAAGCAGAAGTTATTCAGCAGAG
327_IN_R -----

     401
     |
327_IN_F ACAGGGCAAGAAACAGCATAACCTTATCTTGAAGCTAGCAGGAAGATGGCCAGTAAAACAATACACACAGACAAT
327_IN_R -----

     501
     |
327_IN_F GGCCCAATTTCCACCAGTAATACTGTAAAGGCCGCTTGTGGTGGGCAGGGATCCAGCAGGAATTCGGCATCCCC
327_IN_R -----

     601
     |
327_IN_F TACAATCCCCAAAGTCAAGGAGTAGTAGAATCTTTAAATAAAGAATTAAAGAAAATTATAGGACAAGTAAGAGAT
327_IN_R -----

     701
     |
327_IN_F CAGGCTGAACATCTTAAGACAGCAGTACAGATGGCAGTATTCATCCCAATTTTAAAGAAAAGGGGGGATTGGG
327_IN_R -----

     801
     |
327_IN_F GGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAACTAGAGAATTACAAAAACAAAT
327_IN_R -----
```

901
|
327_IN_F TCAAAAATTCAAAAATTTTCGGGTTTATTACAGAGACAGCAGAGATCCACTTTGGAAAGGACCAGCCAAACTCCTC
327_IN_R -----

1001
|
327_IN_F TGGAAAGGTGAAGGGGCAGTAGTAATATAAGATAAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAGATC
327_IN_R -----

1101
|
327_IN_F ATTAGGGATTATGGAAAACAGATGGCAGGTGATGATTTGTGTGGCAAGTAGACAGGATGAGGATTAGAACATGGAA
327_IN_R -----*****

1201
|
327_IN_F CAGCCTAG
327_IN_R *****

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

>327_IN
AGTACTGGAATCAGGAAGGTGCTATTTTTAGATGGaaTAGATAAGGCCCAAGAAGACCATGAGAAGTATCACAGTAATTGGAGAGCAATGGCTAGTGAATTTAACATACCAC
CTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGATTGTAGTCCAGGAATATGGCAGCTAGATTGTACACA
TTTAGAAGGAAAAATTTATCCTGGTAGCAGTCCATGTAGCTAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGGCAAGAAACAGCATAACCTTATCTTGAAGCTA
GCAGGAAGATGGCCAGTAAAAACAATACACACAGACAATGGCCCAATTCACCAGTAATACGTAAAGGCCGTTGTGGTGGGCAGGATCCAGCAGGAATTCGGCATCC
CCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTTTAAATAAAGAATTAAAGAAAAATTATAGGACAAGTAAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAGATGGC
AGTATTCATCCACAATTTTAAAAGAAAAGGGGGATTGGGGGTACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAGAGAATTACAAAAACAA
ATTTCAAAAATTCAAAAATTTTCGGGTTTATTACAGAGACAGCAGAGATCCACTTTGGAAAGGACCAGCCAAACTCCTCTGGAAGGTGAAGGGGCAGTAGTAATATAAGATA
ATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGgATTATGGAAAACAGATGGCAGGTGATGATTGtGGCAAGTAGACAGGATGAGGATTAGAACAT
GGAACAGCCTAG

MX-HIV-0327 CONTIG ASSEMBLY (4 Fragments)

Nucleotide Alignments

```
                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
327_PR          *** **
327_RTa         *** **
327_RTb         *** **
327_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
```

```
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
327_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTa         *** **
327_RTb         *** **
327_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
```

```
2232                                                    2253                                                    2306
B.FR.83.HXB2    GGA ACT GTA TCC TTT AAC TTC CCC CAG GTC ACT CTT TGG CAA CGA CCC CTC GTC ACA ATA AAG ATA GGG GGG CAA
327_PR          --- G-- A-- --- --- G-- C-- --- --A A-- --- --- --- --G --- --- --- G-- --A --- --A --- ---
327_RTa         *** **
327_RTb         *** **
327_IN          *** **
                G T/A V/I S F N/D F/L P Q V/I T L W Q R P L V T I/V K I G G Q
                -----Protease start-----
```

```
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
327_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTa         *** **
327_RTb         *** **
327_IN          *** **
                L K E A L L D T G A D D T V L E E M/V S/N L P G R W K
```

```
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
327_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTa         *** **
327_RTb         *** **
327_IN          *** **
                P K M I G/R G I G G F I K V R Q Y D Q I/V L/P 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
327_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTa         *** **
327_RTb         *** **
327_IN          *** **
                H K A/T I G T V L V/I G P T P V N I I G R N L L T Q I
```

```
2533                                                    2549 2550                                                    2606
B.FR.83.HXB2    |-----Protease end-----| |-----Pol p66 and p51 start-----|
GGT TGC ACT TTA AAT TTT CCC ATT AGC CCT ATT GAG ACT GTA CCA GTA AAA TTA AAG CCA GGA ATG GAT GC CCA
327_PR          --C --T --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTa         *** **
327_RTb         *** **
327_IN          *** **
                G C T L N F P I S P I E T V P V K L K P G M 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
327_PR          --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTa         *** **
327_RTb         *** **
327_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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- A--- --- --- --- --- --- --- --- --- --- ---C
327_RTb *** ** *
327_IN *** ** *
G K I S K I G P E N P Y N T P V 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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- --T --- --- --- --- --- --- --- --- --- --- ---G --- --G --- --- ---
327_RTb *** ** *
327_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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- --T --- --- --- --- --- --- --- --- --- --- ---C --- --- --- ---
327_RTb *** ** *
327_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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- --G --- --- --- --- --- --- --- --- --- --- ---G --- --- --- ---
327_RTb *** ** *
327_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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- --A --- --- --- --- --- --- --- --- --- --- ---G --- --- --- ---
327_RTb *** ** *
327_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
327_PR *** ** *
327_RTa ---T --- --- --- ---
327_RTb *** ** *
327_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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- --T --A --- --- --- --- --- --- --- --- --- --- ---T --- G--- --- --- ---
327_RTb *** ** *
327_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
327_PR *** ** *
327_RTa --- --- --- --- --- --- --- --- --- --- --- --C --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
327_RTb *** ** *
327_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
 327_PR 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
 327_RTa ***
 327_RTb ---
 327_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
 327_PR 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
 327_RTa ***
 327_RTb --- --T G-- --- --C ---
 327_IN ***
 I Y P/A G I K 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
 327_PR 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
 327_RTa ***
 327_RTb ---
 327_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
 327_PR 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
 327_RTa ***
 327_RTb ---
 327_IN ***
 D P S K D L I A E I Q K Q G Q/Y G Q W T Y Q I Y Q E

3582 |-----| 3656
 B.FR.83.HXB2
 327_PR 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
 327_RTa ***
 327_RTb --- --- --G ---
 327_IN ***
 P F K N L K T G K Y A R M/I R G A/T H T N D V K Q L T

3657 |-----| 3731
 B.FR.83.HXB2
 327_PR 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
 327_RTa ***
 327_RTb --- A-- --- --- --- G-- CT- ---
 327_IN ***
 E A/T V Q K I T/A T/L E S I V I W G K T P K F K L P I Q

3732 |-----| 3806
 B.FR.83.HXB2
 327_PR 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
 327_RTa ***
 327_RTb --- A-- --- --- --- G-- CT- ---
 327_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 |-----p51 end and p66 RT continue-----| |RNase H start| 3881
 B.FR.83.HXB2
 327_PR 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
 327_RTa ***
 327_RTb --- --- --G ---
 327_IN ***
 P P L V K L W Y Q L E K E/D P I V G A E T F Y V D G

4482 4556
B.FR.83.HXB2
327_PR
327_RTa
327_RTb
327_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---C---
E A E V I P A E T G Q E T A Y F/L L/I L K L A G R W P

4557 4631
B.FR.83.HXB2
327_PR
327_RTa
327_RTb
327_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
*** **
*** **
*** **
---C---A---CC---A---T---A---
V K T I H T D N G S/P N F T G/S A/N T V R/K A A C W W A G

4632 4706
B.FR.83.HXB2
327_PR
327_RTa
327_RTb
327_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---C---
I K/Q Q E F G I P Y N P Q S Q G V V E S M/L N K E L K

4707 4781
B.FR.83.HXB2
327_PR
327_RTa
327_RTb
327_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---G---
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
327_PR
327_RTa
327_RTb
327_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
327_PR
327_RTa
327_RTb
327_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
*** **
*** **
*** **
---G---T---A---G---
T K/R E L Q K Q I T/S K I Q N F R V Y Y R D S R N/D P L

4932 5006
B.FR.83.HXB2
327_PR
327_RTa
327_RTb
327_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
*** **
*** **
*** **
---C---A---T---
W K G P A K L L W K G E G A V V I Q/X D N S D I K V

5007 5081
B.FR.83.HXB2
327_PR
327_RTa
327_RTb
327_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 *** ** * ** * ** * ** *
 327_PR *** ** * ** * ** * ** * ** * ** * ** * ** *
 327_RTa *** ** * ** * ** * ** * ** * ** * ** * ** *
 327_RTb *** ** * ** * ** * ** * ** * ** * ** * ** *
 327_IN --- --- --- --- AAC ATG GAA CAG CCT AG*
 Q D E D X

Protein Alignments

1 10 20 30 40 50 60 70 80 90 99
 B.FR.83.HXB2 *FFREDLAFQ GKAREFSSEQ TRANSPTRRE LQVWRDNNNS PSEAGADRQG TVSFNFPQVT LWQRPLVTIK IGGQLKEALL DTGADDTVLE EMSLPGRWK
 327_PR _*****|*****|*-----|-----G-T L-T-----|A-I--D-I-I-----|V-----|-----|-----|-----VN-----
 327_RTa _*****|*****|*-----|-----G-T L-T-----|A-I--D-I-I-----|V-----|-----|-----|-----VN-----
 327_RTb _*****|*****|*-----|-----G-T L-T-----|A-I--D-I-I-----|V-----|-----|-----|-----VN-----
 327_IN _*****|*****|*-----|-----G-T L-T-----|A-I--D-I-I-----|V-----|-----|-----|-----VN-----

100 110 120 130 140 150 160 170 180 190 199
 B.FR.83.HXB2 PKMI^GGIGGF IKVRQYDQ^{LI} EICGHKA^IIGT VLVGPTPVNI IGRNLLTQIG CTLNF^GISPI ETVPVKLPG MDGPKVKQWP L^TEEKIKALV EICTEMEKE
 327_PR -----R-----|-----V^P-----|-----T-----|-----I-----|-----|-----|-----|-----|-----|-----|-----
 327_RTa -----R-----|-----V^P-----|-----T-----|-----I-----|-----|-----|-----|-----|-----|-----|-----
 327_RTb -----R-----|-----V^P-----|-----T-----|-----I-----|-----|-----|-----|-----|-----|-----|-----
 327_IN -----R-----|-----V^P-----|-----T-----|-----I-----|-----|-----|-----|-----|-----|-----|-----

200 210 220 230 240 250 260 270 280 290 299
 B.FR.83.HXB2 GKISKIGPEN PYNTPVFAIKK KDSTKWRKLV DFRELNKRTQ DFWEVQLGIP HPAGLKKKKS VTVLDVGDAY FSVPLDEDFR KYTAF^TTIPSI NNETPG^IIRY
 327_PR *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTa *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTb *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_IN *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****

300 310 320 330 340 350 360 370 380 390 399
 B.FR.83.HXB2 QYNVLPQGWK GSPAIFQSSMT KILEPFRKQN PDIVIQYQMD DLYVGSDELI GQHRTKIEEL RQHL^LRWGLT TPKKHQKEP PFLWMGYELH PDKWT^VQPI
 327_PR *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTa *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTb *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_IN *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****

400 410 420 430 440 450 460 470 480 490 499
 B.FR.83.HXB2 VLPEKDSWTV NDIQKLVGKLN WASQIY^PGIK VRQLCKLLRG TKALTE^VVIPL TEEAELELAE NREILKEPVH GVIYDPSKDL IAEIQKGG^G QWTYQIYQE
 327_PR *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTa *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTb *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_IN *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****

500 510 520 530 540 550 560 570 580 590 599
 B.FR.83.HXB2 PFKNLKTGKY ARMRGAHTNDV KQLTEAVQKI TTESI^VIWGK TPKFKLPIQK ETWETWTEY WQATWIPEWE FVNT^PPLVKL WYQLEKE^PIV GAETFYVDG
 327_PR *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTa *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTb *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_IN *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****

600 610 620 630 640 650 660 670 680 690 699
 B.FR.83.HXB2 AANRETKLGK AGYV^TNRGRQK VVTLTDTT^NQK TELQAIYLA LQDSGLEVNI VTDSQYALGI IQAQP^DQSES ELVNQ^IIEQL IKKEKVYLAW VPAK^HGIGG
 327_PR *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTa *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTb *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_IN *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****

700 710 720 730 740 750 760 770 780 790 799
 B.FR.83.HXB2 NEQVDKLVSA GIRKVL^LLDGI DKAQ^DDEHEKY HSNWRAMAS^D FN^LPPVVAKE IVASC^DKCQL KGEAMHGQVD CSPGI^WQLDC THLE^GKVILV AVH^VVASGYI
 327_PR *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTa *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_RTb *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****
 327_IN *****|*****|*****|*****|*****|*****|*****|*****|*****|*****|*****

	800	810	820	830	840	850	860	670	880	890	899
B.FR.83.HXB2	EAEVIPAETG	QETAYFLKLA	GRWPVKTIHT	DNGSNFTGAT	VRAACWVAGI	KQEFQIPYNP	QSQGVVESMN	KELKKIIGQV	RDQAEHLKTA	VQMAVFIHN	
327_PR	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
327_RTa	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
327_RTb	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
327_IN	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		LI		P	SN	K	Q		L		

	900	910	920	930	940	950	960	970	980	990	999
B.FR.83.HXB2	FKRKGIGGYS	AGERIVDIIA	TDIQTKELOK	QITKIQNFRV	YYRDSRNPLW	KGPAKLLWKG	EGAVVIQDNS	DIKVVPRRKA	KIIRDYGKQM	AGDDCVASR	
327_PR	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
327_RTa	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
327_RTb	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
327_IN	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
			R	S		D		X			

	1000
B.FR.83.HXB2	QDEDX
327_PR	*****
327_RTa	*****
327_RTb	*****
327_IN	*****

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

>327_pol

AGAGCCAACAGCCCCACCAGAAGAGAGCTTCagGTTTGGGGAGGAGAtAAACAACCCCTCTCAGAAACAGGAGGAGCTATATCCTTTGACCTCCCTCAAATCACTCTTTGGC
AGCGACCCCTCGTACAGTAAAAATAGGAGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAGTGAATTTACCAGGAAGATGGAACCC
AAAAATGATAAGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAGGTACCATAGAAATCTGTGGACATAAACTATAGGTACAGTATTAATAGGACCTACACCT
GTCAACATAATTGGAAGAAATCTATTGACTCAGATTGGCTGTACTTTAAATTTTCCCATTAGTCTTATGAAACTGTACCAGTAAATTAAGCCAGGAATGGATGGCCCAA
AAGTTAAACAATGGCCATTGACAGAAGAAAAGATAAAAGCATTAGTAGAAAATTTGCACAGAAATGGAAGAAAGGGAAAATTTCAAAAATTTGGGCCGAAAATCCATACAA
TACTCCAATATTTGCCATAAAGAAAAAGACAGTACCAAATGGAGAAAATTAGTAGAATTTTAGAGAACTTAACAAGAGAAGCTCAAGACTTCTGGGAGGTTTCAGTTAGGAATA
CCACATCCCTCAGGGCTAAAAAGAAAAGTACAGTAACTGATGTTGGTGTGCATATTTTTTCAGTTCCTTAGATCCAGACTTCAGGAAGTATACGGCATTACCA
TACCTAGTAGAAAACAAATGAGACACCAGGGTTAGATATCAGTACAATGTGCTTCCACAAGGATGGAAAGGATACCAGCGATATCCAAAGTAGCATGACAAAATCTTAGA
GCCTTTTAGAAAACAAAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGATTTAGAAATAGGGCAGCATAGAACAAAATAGATGAACGTGAGA
GAACATTTGTTGAGGTGGGGATTTGCCACACCAGACAAAAAACACAGAAAAGAACCTCCATTCTTTGGATGGGTTATGAACCTCCATCTGATAAATGGACAGTACAGCCTA
TAGTGTCTGCCAGAAAAGACAGCTGGACTGTCAATGACATACAAAAGTTAGTGGGAAAATTAATTTGGGCAAGTTCAGATTTATGCGAGGATCAAAAGTAAAGCAATTATGTAA
GCTCCTTaGGGGATCCAAAGCACTAACAGAAATAGTACCCTAaCAGAAgAaGAGACTAGAACTGGCAGAAAACAGAGAGATTTCTAAAAGAACAGTACATGGGGTGTAT
TATGACCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGGTACGGCCAAATGGACATACCAAATTTATCAAGAACCATTTAAGAACTGAAAACAGGAAAATATGCAA
GAATAAGGGGTACCACACTAATGATGTAAAACAATTAACAGAGACAGTGCAAAAATAGCCCTAGAAAAGCATAGTAATATGGGGAAAAAATCTCAAATTTAAATACCCT
ACAAAAGAAAACATGGGAAACATGGTGGACAGAGTATTGGCAAGCCACTGGATTCCGTAATGGGAGTTTGTCAATACCCCTCCCTTGGTGAATTTATGGTACCAGTTAGAG
AAAGATCCCATAGTGGGAGCAGAACTTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTAACAGAGGAAGACAAAAGTTGTCT
CCCTAACAGCACACAACAAATCAGAAGACTGAGTTACAAGCAATTTATCTAGCCTTGCAGGATTCAGGATTAGAAAGTAAATATAGTGCAGACTCACAATATGCATTAGGAAT
CATTCAGCACAAACAGATAAAAAGTGAATCAGAGATAGTCAATCAAAATAATAGAGCAGTTAATAAAAAAGGACAAGGTCTACCTGGCATGGGTACCAGCACAAAAGGAATC
GGAGGAAATGAACAAGTAGATAAATAGTCACTACTgaaTCAGGAAGgTGCTATTTTTAGATGGAATAgATAAGGCCCAaGaaGACATGAGAAGTATCACAGTAATTTGGA
GAGCAATGGCTAGTGAATTTAACATACCACCTGTAGTAGCAAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGATTGTAG
TCCAGGAATATGGCAGCTAGATTGTACACATTTAGAAGGAAAAATTTATCCGGTAGCAGTCCATGTAGCTAGTGGATATATAGAAGCAGAAGTTATCCAGCAGAGACAGGG
CAAGAAACAGCATACTTTATCTTGAAGCTAGCAGGAAGATGGCCAGTAAAAACAATACACACAGACAATGGCCCAATTTACCAGTAAATCTGTTAAGGCCGCTTGTGGT
GGCAGGGATCCAGCAGGAATTCGGCATCCCTTACAATCCCAAGTCAAGGAGTAGTAGAATCTTTAAATAAAGAAATTAAGAAAATTTATAGGACAAGTAAGAGATCAGGC
TGAACATCTTAAGACAGCAGTACAGATGGCAGTATTCATCCACAATTTAAAAGAAAAGGGGGGATTGGGGGTACAGTGCAGGGGAAAAGAAATAGTAGACATAATAGCAACA
GACATACAAACTAGAGAATTAACAAAACAATTTCAAAAATTTCAAAAATTTTCGGGTTTATTACAGAGACAGCAGAGATCCACTTTGGAAAGGACCAGCCAAACTCCTCTGGA
AAGGTGAAGGGCAGTAGTAATATAAGATAATAGTGACATAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGgATTATGGAAAACAGATGGCAGGTGATGTTgtG
GGCAAGTAGACAGGATGAGGATTAGAACATGGAACAGCCTAG