Old protease page
(http://www.bioafrica.net/proteomics2005/POL-PRprot.html)

# bioafrica *HIV bioinformatics in Africa*

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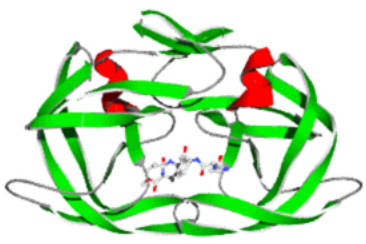
## PR - Protease - Retropepsin

HIV **PR** is an aspartyl protease and is required for cleavage of Gag, Gag-Pol, Pol and Nef precursors.

- p15 Protease GO!

Reference Sequences GO!



[animated gif: 320x240 ]

**ViralZone:** HIV-1
**PDB:** 1AAQ (HIV-1 Protease)
**SwissProt:** P04585 (HIV-1 HXB2 POL)
**Chime Tutorial:** Online Macromolecular Museum
**Los Alamos HIV structure DB:** Protease
**EMBL:** K03455 [EMBL/GenBank/DDBJ]
**BioAfrica:** Pol Protein Data Mining Tool

### Isoforms:

- p15 (99 amino acids)

### Cleavage site:

- HIV-1 Pol cleavage site details

### Localization:

- Virion

### Function:

- Viral enzyme
- Protease activity initiates virion maturation
- Processes Gag and Gag-pol polyproteins into mature chains

### Additional Information:

- Protease is an aspartyl protease
- Protease functions while in a homodimer

## Genomic Location: [TOP]

### Reference Sequences:

**HIV-1 (HXB2):**

```
         10         20         30         40         50         60         70
          |          |          |          |          |          |          |
PQVTLWQRPL VTIKIGGQLK EALLDTGADD TVLEEMSLPG RWKPKMIGGI GGFIKVRQYD QILIEICGHK
         80         90         99
          |          |          |
AIGTVLVGPT PVNIIGRNLL TQIGCTLNF
    [download in fasta format]
```

**Length:** 99 amino acids (residues 57 to 155)
**Molecular Weight:** 10779 Da
**Theoretical pI:** 8.83

## Protein Domains/Folds/Motifs: [TOP]

**InterPro signature for active site Aspartic Peptidase** - IPR001969
**InterPro signature for Retrovirus Peptidase A2A** - IPR001995
**InterPro signature for Aspartic Peptidase Family** - IPR009007

**Secondary Structure** prediction:

Antigenic Sites - EMBOSS:
5 potential sites

**Predicted Motifs:** Printer-friendly version

| | |
|---|---|
| **N-glycosylation:** | none |
| **N-myristoylation:** | 3 potential sites |
| **Amidation:** | none |
| **Protein kinase C:** | 1 potential site |
| **Casein kinase II:** | 2 potential sites |
| **Tyrosine kinase:** | none |
| **cAMP / cGMP kinase:** | none |
| **Cell attachment motif:** | none |
| **Asp Protease motif:** | 1 potential site |
| **Asp Prot Retro motif:** | 1 potential site |
| **Cysteine-rich Region:** | none |
| **Tryptophan-rich Region:** | none |
| **Zinc-finger CCHC motif:** | none |
| **Leucine Zipper motif:** | none |

## Protein-Protein Interactions: [TOP]

- Protease cleaves the HIV **Gag polyprotein**
- Protease cleaves the HIV **Gag-Pol polyprotein**
- Protease cleaves the HIV **Nef protein**

## Primary and Secondary Database Entries: [TOP]

### Identifiers:

**ViralZone:** HIV-1
**PDB/MMDB:** Search for HIV-1 & Protease
**SwissProt:** P04585 (HIV-1 HXB2 POL)
**EC:** 3.4.23.16
**EMBL:** K03455; AAB50259.1 [EMBL/GenBank/DDBJ]
**PIR:** UNKNOWN
**HIV:** K03455; UNKNOWN$HXB2
**InterPro:** IPR001969 / IPR001995
**Pfam:** PF00558;UNKNOWN
**Prints:** none
**ProDom:** PD186096 (1 - 16)
**SCOP:** SSF50630 Acid protease
**BLOCKS:** P04585
**Prosite:** P04585
**ProtoNet:** P04585
**ProtoMap:** P04585
**PRESAGE:** P04585
**Database of Interacting Proteins:** P04585
**ModBase:** P04585
**Swiss-2DPAGE:** 2D gel

**BioAfrica Tools:**
- Pol Protein Data Mining Tool provides real-time analysis of HIV-1 Pol isolates
- HIV Structure BLAST searches for similar HIV sequences that have known structures
- HIV Proteomics Resource contains protein sequence and structure analysis tools

## Reviews and References: [TOP]

**Cite the resource by citing the following paper:**
**Doherty R et al. BioAfrica's HIV-1 Proteomics Resource: Combining protein data with bioinformatics tools. Retrovirology (2005), 9;2(1):18.**


1 - **HIV Sequence Compendium 2000**
Kuiken CL, Foley B, Hahn B, Korber B, Marx PA, McCutchan F, Mellors JW, Mullins JI, Sodroski J, Wolinksy S.
Theoretical Biol. & Biophys. Group, Los Alamos Nat Lab, LA-UR 01-3860 [Read it online: Compendium]

2 - **Retroviruses**
Coffin JM, Hughes SH, Varmus HE.
CD-ROM ed. (2002) Cold Spring Harbor Laboratory Press [Read it online: NCBI Bookshelf]

3 - **Molecular Characteristics of HIV-1 Subtype C Viruses from KwaZulu-Natal, South Africa: Implications for Vaccine and Antiretroviral Control Strategies.**
Gordon M, De Oliveira T, Bishop K, Coovadia HM, Madurai L, Engelbrecht S, Janse van Rensburg E, Mosam A, Smith A, Cassol S.
Journal of Virology 77(4): 2587-2599 (2003) [pubmed: 12551997]

4 - **An inhibitor of the protease blocks maturation of human and simian immunodeficiency viruses and spread of infection.**
Ashorn P, McQuade TJ, Thaisrivongs S.
Proc Natl Acad Sci USA 87: 7472-7476 (1990) [pubmed: 2217178]

5 - **Crystal structure of a retroviral protease proves relationship to aspartic protease family.**
Miller M, Jaskolski M, Rao JK.
Nature 337: 576-579 (1989) [pubmed: 2536902]

6 - **Three-dimensional structure of aspartyl protease from human immunodeficiency virus HIV-1.**
Navia MA, Fitzgerald PM, McKeever BM.
Nature 337: 615-620 (1989) [pubmed: 2645523]

7 - **[HIV Protease Drug Design - Review] Aspartic proteinases in disease: a structural perspective.**
Cooper JB.
Curr Drug Targets 3(2):155-173 (2002) [pubmed: 11958298]

8 - **[Website] HIV Drug Resistance Database**
Stanford
Website: http://hivdb.stanford.edu

9 - **[Website] HIV Drug Resistance Database**
Los Alamos National Labs
Website: http://resdb.lanl.gov/Resist_DB/default.htm

10 - **[Website] HIVdb: a database of the structures of human immunodeficiency virus protease.**
NIST
Website: http://srdata.nist.gov/hivdb/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