

# Human Immunodeficiency Virus Type 1 Protease (p15) aminoacid sequence unanimity alignments.

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Terminal domain--->|<-----Core domain----->|<-----Flat domain----->|<-----Core domain
                    |          10          20          30          |          40          50          60          |          70
HXB2                PQVTLWQRP| LVTIKIGGQL| KEALLDTGAD| DTV| LEEMSLP| GRWKPKMIGG| IGGFIKVRQY| DQI| LIEICGH| KAIGTVLVGP
MXHIV00086          --I-----| ---V-----| -----| ---| ---N---| -----R-| -----V| P-----| -TV---I--
MXHIV00327          --I-----| ---V-----| -----| ---| ---VN--| -----R-| -----V| P-----| -T---I--
MXHIV00395          --I-----| I---T-----| -----| ---| ---N---| -----| -----EEV| SVD---| -V-----
MXHIV00401          --I-----| -----| -----| ---| ---N-L| -----| -----V| P-----| -V-----
MXHIV00422          --I-----| ---V-----| -----| ---| ---N---| ---X-----| -----| I---A---
30XC                --I---K---| -----| -----| ---| I-----| -----| -----| I---A---

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----->|<---Terminal domain
        |          80          90
HXB2    TPVNII| GRNL| LTOIGCTLNF
MXHIV00086  -----| -----| -----
MXHIV00327  -----| -----| -----
MXHIV00395  -----| -----| ---L-----
MXHIV00401  ---T-  | -----| -----
MXHIV00422  -----| -----| -----
30XC       -----| -----| ---AT---

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Residues that form the catalytic domain are shown in yellow highlight. HXB2 corresponds to the reference nucleotide sequence for HIV-1, 30XC corresponds to the PDB ID for the crystallographic model unto which the polymorphic residues were mapped to. Alignments produced from partial overlapping clones of viral RNA sequences obtained from human blood samples. Clones, contigs, alignments, annotations and maps produced by Pedro Gerardo Hernández Sánchez, Viral & Human Genomics Laboratory UASLP, México. Unanimity reformatting script written by James Robinson, Anthony Nolan Research Institute, London.

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