

# Human Immunodeficiency Virus Type 1 Integrase (p32) aminoacid sequence unanimity alignments.

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<-----N terminal domain-----><-----Catalytic core domain----->
1      10      20      30      40      50      60      70      80      90      100
|      |      |      |      |      |      |      |      |      |
HXB2   FLDGIDKAQD EHEKYHSNWR AMASDFNLPP VVAKEIVASC DKCQLKGEAM HGQVDCSPGI WQLDCTHLEG KVILVAVHVA SGYIEAEVIP AETGQETAYF
MXHIV00086 -----E D----- ---E--I-- I----- I----- I----- I----- I----- P-----L
MXHIV00327 -----E D----- ---E--I-- I----- I----- I----- I----- I----- P-----L
MXHIV00395 -----E D----- ---E--I-- I----- I----- I----- I----- I----- P-----L
MXHIV00401 -----E D----- T----- ---TC- ---Q----- I----- I----- I----- I----- P-----L
MXHIV00422 -----E D----- T----- ---TC- ---Q----- I----- I----- I----- I----- P-----L
1K6Y_A -----E -----T----- ---TC- ---Q----- I----- I----- I----- I----- P-----L

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-----Catalytic core domain-----
101     110     120     130     140     150     160     170     180     190     200
|      |      |      |      |      |      |      |      |      |
HXB2   LLKLAGRWPV KTIHTDNGSN FTGATVRAAC WWAGIKQEFG IPYNPQSQGV VESMNKELKK IIGQVRDQAE HLKTAVQMAV FIHNFKRKGG IGGYSAGERI
MXHIV00086 -----G -ISNA-K--- I----- I----- I----- I----- I----- I----- K-----
MXHIV00327 I----- ---P- --SN--K--- ---Q----- ---L----- I----- I----- I----- I----- K-----
MXHIV00395 I----- ---P- --STA-K--- I----- I----- I----- I----- I----- I----- K-----
MXHIV00401 -----M----- P- -ISNA-K--- I----- I----- I----- I----- I----- I----- K-----
MXHIV00422 I----- ---P- --ST--K--- I----- I----- I----- I----- I----- I----- K-----
1K6Y_A -----V----- --ST--K--- D----- I----- I----- I----- I----- I----- K-----

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Catalytic core domain<-----C terminal domain----->
201     210     220     230     240     250     260     270     280     289
|      |      |      |      |      |      |      |      |
HXB2   VDIIATDIQT KELQKQITKI QNFRVYYRDS RNPLWKGPAK LLWKGEHAVV IQDNSDIKVV PRRKAKIIRD YGQMAGDCC VASRQDEDX
MXHIV00086 -----N----- SK----- -D----- ---E----- I----- I----- I----- I-----
MXHIV00327 -----R----- S--- ---D----- ---X----- I----- I----- I----- I-----
MXHIV00395 -----S----- A--H----- ---D----- ---G----- I----- I----- I----- I-----
MXHIV00401 -----S----- X----- I----- I----- I----- I-----
MXHIV00422 -----S----- X----- I----- I----- I----- I-----
1K6Y_A -----S----- X----- I----- I----- I----- I-----

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HXB2 corresponds to the reference nucleotide sequence for HIV-1, 1K6Y\_A corresponds to the PDB ID for the crystallographic model into 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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