

Resource Summary Report

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BioAfrica HIV Informatics in Africa

RRID:SCR_002295

Type: Tool

Proper Citation

BioAfrica HIV Informatics in Africa (RRID:SCR_002295)

Resource Information

URL: <http://bioafrica.mrc.ac.za/index.html>

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Description: The BioAfrica HIV-1 Proteomics Resource is a website that contains detailed information about the HIV-1 proteome and protease cleavage sites, as well as data-mining tools that can be used to manipulate and query protein sequence data, a BLAST tool for initiating structural analyses of HIV-1 proteins, and a proteomics tools directory. HIV Proteomics Resource contains information about each HIV-1 gene product in regard to expression, post-transcriptional / post-translational modifications, localization, functional activities, and potential interactions with viral and host macromolecules. The Proteome section contains extensive data on each of 19 HIV-1 proteins, including their functional properties, a sample analysis of HIV-1HXB2, structural models and links to other online resources. The HIV-1 Protease Cleavage Sites section provides information on the position, subtype variation and genetic evolution of Gag, Gag-Pol and Nef cleavage sites.

Synonyms: HIV Informatics in Africa

Resource Type: data or information resource, portal, topical portal

Keywords: expression, functional, gene, aids, cleavage, database, hiv, hiv/aids databases, interaction, localization, model, modification, post-transcriptional, post-translational, protease, protein, proteome, proteomic, publication, research, sequence, software, structural, journal article

Resource Name: BioAfrica HIV Informatics in Africa

Resource ID: SCR_002295

Alternate IDs: nif-0000-21050

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260808T185749+0000

Ratings and Alerts

No rating or validation information has been found for BioAfrica HIV Informatics in Africa.

No alerts have been found for BioAfrica HIV Informatics in Africa.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Lin SY, et al. (2016) Molecular Evolution and Phylodynamics of Acute Hepatitis B Virus in Japan. PloS one, 11(6), e0157103.

Druce M, et al. (2016) Improving HIV proteome annotation: new features of BioAfrica HIV Proteomics Resource. Database : the journal of biological databases and curation, 2016.

Wilkinson E, et al. (2015) History and origin of the HIV-1 subtype C epidemic in South Africa and the greater southern African region. Scientific reports, 5, 16897.

Harrison A, et al. (2011) Genomic analysis of hepatitis B virus reveals antigen state and genotype as sources of evolutionary rate variation. Viruses, 3(2), 83.

Penn O, et al. (2008) Evolutionary modeling of rate shifts reveals specificity determinants in HIV-1 subtypes. PLoS computational biology, 4(11), e1000214.