Resource Summary Report

Generated by NIF on May 10, 2025

HPV Sequence Database

RRID:SCR_008154
Type: Tool

Proper Citation

HPV Sequence Database (RRID:SCR_008154)

Resource Information

URL: http://ncv.unl.edu/Angelettilab/HPV/Database.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute''s (NCI''s) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester''s questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone., documented August 23, 2016. The Human Papillomaviruses Database collects, curates, analyzes, and publishes genetic sequences of papillomaviruses and related cellular proteins. It includes molecular biologists, sequence analysts, computer technicians, post-docs and graduate research assistants. This Web site has two main branches. The first contains our four annual data books of papillomavirus information, called Human

Papillomaviruses: A Compilation and Analysis of Nucleic Acid and Amino Acid Sequences. and the second contains papillomavirus genetic sequence data. There is also a New Items location where we store the latest changes to the database or any other current news of interest. Besides the compendium, we also provide genetic sequence information for papilloma viruses and related cellular proteins. Each year they publish a compendium of papillomavirus information called Human Papillomaviruses: A Compilation and Analysis of Nucleic Acid and Amino Acid Sequences. which can now be downloaded from this Web site.

Synonyms: HPVSD

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

Keywords: gene, genetic, alignment, amino acid, biologist, cellular protein, genome, human, molecular, papilloma, papillomavirus, phylogenetic, sequence, virus

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HPV Sequence Database

Resource ID: SCR_008154

Alternate IDs: nif-0000-21000

Old URLs: http://www.stdgen.lanl.gov/

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250508T065127+0000

Ratings and Alerts

No rating or validation information has been found for HPV Sequence Database.

No alerts have been found for HPV Sequence Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Flores R, et al. (2015) The Chlamydia pneumoniae Inclusion Membrane Protein Cpn1027 Interacts with Host Cell Wnt Signaling Pathway Regulator Cytoplasmic Activation/Proliferation-Associated Protein 2 (Caprin2). PloS one, 10(5), e0127909.

Meza-Menchaca T, et al. (2013) A low density microarray method for the identification of human papillomavirus type 18 variants. Sensors (Basel, Switzerland), 13(10), 12975.

Chen T, et al. (2010) The Human Oral Microbiome Database: a web accessible resource for investigating oral microbe taxonomic and genomic information. Database : the journal of biological databases and curation, 2010, baq013.

Kiselev AO, et al. (2007) Expression, processing, and localization of PmpD of Chlamydia trachomatis Serovar L2 during the chlamydial developmental cycle. PloS one, 2(6), e568.