Resource Summary Report

Generated by dkNET on Apr 16, 2025

PaVE

RRID:SCR_016599
Type: Tool

Proper Citation

PaVE (RRID:SCR_016599)

Resource Information

URL: https://pave.niaid.nih.gov

Proper Citation: PaVE (RRID:SCR_016599)

Description: Collection of curated papillomavirus genomic sequences, accompanied by web-based sequence analysis tools. Database and web applications support the storage, annotation, analysis, and exchange of information.

Abbreviations: PaVE

Synonyms: PapillomaVirus Episteme, Papillomavirus Episteme

Resource Type: database, software resource, data analysis service, data or information resource, web application, service resource, analysis service resource, production service resource

Defining Citation: PMID:28053164

Keywords: data, curated, papilloma, virus, genomic, sequence, analysis, storage, annotation, FASEB list

Funding: NIAID ZIA AI001071

Availability: Open source

Resource Name: PaVE

Resource ID: SCR_016599

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250416T063803+0000

Ratings and Alerts

No rating or validation information has been found for PaVE.

No alerts have been found for PaVE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 108 mentions in open access literature.

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

Smith NJ, et al. (2025) Differentiation signals induce APOBEC3A expression via GRHL3 in squamous epithelia and squamous cell carcinoma. The EMBO journal, 44(1), 1.

Rahmoun M, et al. (2024) Genomic diversity of HPV6 and HPV11 in recurrent respiratory papillomatosis: Association with malignant transformation in the lungs and clinical outcomes. Tumour virus research, 18, 200294.

He X, et al. (2024) A retrospective study revealing complex viral diversity and a substantial burden of HPV infection in SARS-CoV-2 positive individuals, Sierra Leone. Virology journal, 21(1), 201.

Jönsson J, et al. (2024) A novel HPV16 splicing enhancer critical for viral oncogene expression and cell immortalization. Nucleic acids research, 52(1), 316.

de Sanjosé S, et al. (2024) Design of the HPV-automated visual evaluation (PAVE) study: Validating a novel cervical screening strategy. eLife, 12.

Wang Y, et al. (2024) Alternative splicing in the genome of HPV and its regulation. Frontiers in cellular and infection microbiology, 14, 1443868.

Smith NJ, et al. (2024) Differentiation signals induce APOBEC3A expression via GRHL3 in squamous epithelia and squamous cell carcinoma. Research square.

Buigues J, et al. (2024) Full-genome sequencing of dozens of new DNA viruses found in Spanish bat feces. Microbiology spectrum, 12(8), e0067524.

Ghouneimy A, et al. (2024) CRISPR-Based Multiplex Detection of Human Papillomaviruses for One-Pot Point-of-Care Diagnostics. ACS synthetic biology, 13(3), 837.

Yu L, et al. (2024) HPV oncogenes expressed from only one of multiple integrated HPV DNA copies drive clonal cell expansion in cervical cancer. mBio, 15(5), e0072924.

Siqueira JD, et al. (2024) Comparison of four different human papillomavirus genotyping methods in cervical samples: Addressing method-specific advantages and limitations. Heliyon, 10(3), e25474.

Galati L, et al. (2024) HPV16 Phylogenetic Variants in Anogenital and Head and Neck Cancers: State of the Art and Perspectives. Viruses, 16(6).

La Frazia S, et al. (2024) Viral Oncogenesis: Synergistic Role of Genome Integration and Persistence. Viruses, 16(12).

Starrett GJ, et al. (2023) Evidence for virus-mediated oncogenesis in bladder cancers arising in solid organ transplant recipients. eLife, 12.

Favilli L, et al. (2023) High-throughput Saccharomyces cerevisiae cultivation method for credentialing-based untargeted metabolomics. Analytical and bioanalytical chemistry, 415(17), 3415.

Ritsch M, et al. (2023) Navigating the Landscape: A Comprehensive Review of Current Virus Databases. Viruses, 15(9).

Farhadi A, et al. (2023) Type distribution of human papillomaviruses in ThinPrep cytology samples and HPV16/18 E6 gene variations in FFPE cervical cancer specimens in Fars province, Iran. Cancer cell international, 23(1), 166.

Burk RD, et al. (2023) Distinguishing Genetic Drift from Selection in Papillomavirus Evolution. Viruses, 15(8).

Li T, et al. (2023) Broad-Spectrum Detection of HPV in Male Genital Samples Using Target-Enriched Whole-Genome Sequencing. Viruses, 15(9).

Kusakabe M, et al. (2023) Cells with stem-like properties are associated with the development of HPV18-positive cervical cancer. Cancer science, 114(3), 885.