

Resource Summary Report

Generated by T1D on Jul 29, 2026

PaVE

RRID:SCR_016599

Type: Tool

Proper Citation

PaVE (RRID:SCR_016599)

Resource Information

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

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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: service resource, web application, data or information resource, data analysis service, database, software resource, production service resource, analysis 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: 20260729T044418+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 125 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Jiang X, et al. (2025) Depletion of Effector Regulatory T Cells Associates with Major Response to Induction Dual Immune Checkpoint Blockade. *Cancer discovery*, 15(8), 1569.

Liu H, et al. (2025) The long noncoding RNA Inc-FANCI-2 intrinsically restricts RAS signaling in human papillomavirus type 16-infected cervical cancer cells. *eLife*, 13.

Liu H, et al. (2025) High-Throughput Targeted Sequencing Identifies an HPV Methylation Panel for Detecting Cervical Lesion Progression. *Journal of medical virology*, 97(12), e70739.

Munabi IG, et al. (2025) Nanopore sequencing of non-oncogenic oral Papillomaviruses from people living with HIV. *Research square*.

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. *Briefings in bioinformatics*, 26(2).

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.

Parida P, et al. (2025) Precise identification of viral-host integration events in HPV-positive cervical cancers by targeted long-read sequencing. *Tumour virus research*, 20, 200325.

Intan NS, et al. (2025) Urinary detection of high-risk HPV DNA to enhance cervical cancer screening in developing countries. *Microbiology spectrum*, 13(9), e0193824.

Munabi IG, et al. (2025) Changes in Oral Papilloma Virus Infections Over Six Months in People Living with HIV. *Research square*.

Sasivimolrattana T, et al. (2025) Virome capture sequencing for comprehensive HPV genotyping in cervical samples. *Science progress*, 108(2), 368504251334515.

Majerciak V, et al. (2025) Identification and Characterization of MmuPV1 Causing Papillomatosis Outbreak in an Animal Research Facility. *Viruses*, 17(9).

Porter VL, et al. (2025) Rearrangements of viral and human genomes at human papillomavirus integration events and their allele-specific impacts on cancer genome regulation. *Genome research*, 35(4), 653.

Liu Y, et al. (2025) Human papillomavirus in canine serum: evidence from a Chinese study. *Frontiers in veterinary science*, 12, 1511289.

Regney M, et al. (2025) Diversity of polyomaviruses and papillomaviruses in penguins from eastern and western Antarctica. *Microbial genomics*, 11(11).

Khan N, et al. (2025) Human Papillomavirus Integration Induces Oncogenic Host Gene Fusions in Oropharyngeal Cancers. *Cancer discovery*, 15(9), 1927.

Vieira Alves M, et al. (2025) Intratype variants and high genotypic diversity of human papillomavirus with polymorphisms in the antigenic hypervariable loops of the L1 protein from women living with human immunodeficiency virus in Northeastern Brazil. *Journal of medical microbiology*, 74(3).

Tamai K, et al. (2025) Elucidating Alterations in Viral and Human Gene Expression Due to Human Papillomavirus Integration by Using Multimodal RNA Sequencing. *Viruses*, 17(10).

Solis-Ponce L, et al. (2025) Genotype distribution and molecular characterization of HPV in the Peruvian amazon: insights into prevalence, lineage diversity, and viral integration. *Scientific reports*, 15(1), 32535.

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.

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