

Resource Summary Report

Generated by T1D on Aug 27, 2026

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

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: 20260821T194057+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 156 mentions in open access literature.

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

Aldana-Caballero A, et al. (2026) A LAMP-Assay for the Detection and Genotyping of HPV Causing Plantar Warts From Skin Scrapes Samples. Journal of medical virology, 98(5), e70975.

Wang Z, et al. (2026) Development and clinical validation of an ERA-CRISPR/Cas12a assay for the rapid detection of 14 high-risk HPV types. Microbiology spectrum, 14(2), e0303625.

Shadang M, et al. (2026) The R2TP complex stabilises E7 to drive human papillomavirus-mediated pathogenesis in cellular models of cervical cancer. Virology journal, 23(1).

Talpe-Nunes V, et al. (2026) GATA3 Inhibits the Expression of Viral E6/E7 Genes, and Its Expression Is Compromised During HPV-Mediated Cervical Carcinogenesis. Journal of medical virology, 98(7), e71034.

Nakamura H, et al. (2026) Prevalence and genotype distribution of human papillomavirus in cervical cancer and precancer in Japan between 2012 and 2025: a retrospective single-center study. Frontiers in public health, 14, 1857364.

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.

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).

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.

Baranda-??vila N, et al. (2025) Translational regulation of human papillomavirus mRNAs in carcinogenesis: old questions and new insights. Frontiers in cell and developmental

biology, 13, 1676001.

Lyu Y, et al. (2025) Skin microbiome engineering: Challenges and opportunities in skin diseases treatment. *iMetaOmics*, 2(2), e70012.

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.

Derveniz V, et al. (2025) The Role of HPV in the Development of Cutaneous Squamous Cell Carcinoma-Friend or Foe? *Cancers*, 17(7).

Munday JS, et al. (2025) First Detection and Genetic Characterization of *Felis catus* Papillomavirus Type 11, the First Treisetapapillomavirus Type to Infect Domestic Cats. *Animals : an open access journal from MDPI*, 15(10).

Liu H, et al. (2025) The long noncoding RNA lnc-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.

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

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.

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