Resource Summary Report

Generated by NIF on May 25, 2025

Platypus

RRID:SCR_005389
Type: Tool

Proper Citation

Platypus (RRID:SCR_005389)

Resource Information

URL: http://www.well.ox.ac.uk/platypus

Proper Citation: Platypus (RRID:SCR_005389)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. Software tool designed for efficient and accurate variant detection in high throughput sequencing data. Haplotype based variant caller for next generation sequence data.

Synonyms: Platypus: A Haplotype-Based Variant Caller For Next Generation Sequence Data, PLAYPUS

Resource Type: software resource, software application

Keywords: Haplotype based variant caller, next generation sequence data, gene, genomic, high throughput sequencing data,

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Platypus

Resource ID: SCR_005389

Alternate IDs: SCR_009046, nlx_154021, OMICS_00068

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250525T032453+0000

Ratings and Alerts

No rating or validation information has been found for Platypus.

No alerts have been found for Platypus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 195 mentions in open access literature.

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

Chun D, et al. (2024) Flt3L enhances clonal diversification and selective expansion of intratumoral CD8+ T cells while differentiating into effector-like cells. Cell reports, 43(12), 115023.

Liu Z, et al. (2023) Absence of Lugol staining indicates initiation of esophageal squamous cell carcinoma: A combined genomic and epidemiologic study. Cell reports. Medicine, 4(9), 101168.

Feltin N, et al. (2023) Metrological Protocols for Reaching Reliable and SI-Traceable Size Results for Multi-Modal and Complexly Shaped Reference Nanoparticles. Nanomaterials (Basel, Switzerland), 13(6).

Huebner A, et al. (2023) ACT-Discover: identifying karyotype heterogeneity in pancreatic cancer evolution using ctDNA. Genome medicine, 15(1), 27.

Naz S, et al. (2023) GWAS and functional studies suggest a role for altered DNA repair in the evolution of drug resistance in Mycobacterium tuberculosis. eLife, 12.

Spain L, et al. (2023) Late-Stage Metastatic Melanoma Emerges through a Diversity of Evolutionary Pathways. Cancer discovery, 13(6), 1364.

Seaby EG, et al. (2023) Targeting de novo loss-of-function variants in constrained disease genes improves diagnostic rates in the 100,000 Genomes Project. Human genetics, 142(3), 351.

Agrafiotis A, et al. (2023) Persistent virus-specific and clonally expanded antibody-secreting cells respond to induced self-antigen in the CNS. Acta neuropathologica, 145(3), 335.

Sekine K, et al. (2023) Transposons contribute to the acquisition of cell type-specific cis-elements in the brain. Communications biology, 6(1), 631.

Kang Y, et al. (2022) Cloning and base editing of GFP transgenic rhesus monkey and off-target analysis. Science advances, 8(29), eabo3123.

Ahmad US, et al. (2022) Desmoglein-3 induces YAP phosphorylation and inactivation during collective migration of oral carcinoma cells. Molecular oncology, 16(8), 1625.

Wu Z, et al. (2022) Mapping short tandem repeats for liver gene expression traits helps prioritize potential causal variants for complex traits in pigs. Journal of animal science and biotechnology, 13(1), 8.

Ebler J, et al. (2022) Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature genetics, 54(4), 518.

Yang H, et al. (2022) ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. Nature, 606(7913), 358.

Noyes MD, et al. (2022) Familial long-read sequencing increases yield of de novo mutations. American journal of human genetics, 109(4), 631.

Neumeier D, et al. (2022) Profiling the specificity of clonally expanded plasma cells during chronic viral infection by single-cell analysis. European journal of immunology, 52(2), 297.

Denisova E, et al. (2022) Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. Cancer gene therapy, 29(6), 697.

McGlacken-Byrne SM, et al. (2022) Pathogenic variants in the human m6A reader YTHDC2 are associated with primary ovarian insufficiency. JCI insight, 7(5).

Wang N, et al. (2022) Tool evaluation for the detection of variably sized indels from next generation whole genome and targeted sequencing data. PLoS computational biology, 18(2), e1009269.

Sumazin P, et al. (2022) Hepatoblastomas with carcinoma features represent a biological spectrum of aggressive neoplasms in children and young adults. Journal of hepatology, 77(4), 1026.