# Resource Summary Report

Generated by RRID on Aug 5, 2026

## 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 application, software resource

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

**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:** 20260805T044121+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 199 mentions in open access literature.

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


Varadarajan K, et al. (2025) Efficacy of ATR Kinase Inhibitor Elimusertib Monotherapy or Combination in Tumors with DNA Damage Response Pathway and Other Genomic Alterations. Molecular cancer therapeutics, 24(9), 1402.

Peng T, et al. (2025) Individualized patient tumor organoids faithfully preserve human brain tumor ecosystems and predict patient response to therapy. Cell stem cell, 32(4), 652.

Diamond B, et al. (2025) Mutagenic Impact and Evolutionary Influence of Chemoradiotherapy in Hematologic Malignancies. Blood cancer discovery, 6(5), 450.

Pareja F, et al. (2024) A Genomics-Driven Artificial Intelligence-Based Model Classifies Breast Invasive Lobular Carcinoma and Discovers CDH1 Inactivating Mechanisms. Cancer research, 84(20), 3478.

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.

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

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).

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.

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.

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.

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

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

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

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

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.

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.

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

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