Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

PLAYPUS

RRID:SCR_009046
Type: Tool

Proper Citation

PLAYPUS (RRID:SCR_009046)

Resource Information

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

Proper Citation: PLAYPUS (RRID:SCR_009046)

Description: Software application that is an integrated variant caller (entry from Genetic Analysis Software)

Abbreviations: PLAYPUS

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: PLAYPUS

Resource ID: SCR_009046

Alternate IDs: nlx_154021

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260903T234953+0000

Ratings and Alerts

No rating or validation information has been found for PLAYPUS.

No alerts have been found for PLAYPUS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Rota IA, et al. (2021) FOXN1 forms higher-order nuclear condensates displaced by mutations causing immunodeficiency. Science advances, 7(49), eabj9247.

Xu Y, et al. (2021) Technological advances in cancer immunity: from immunogenomics to single-cell analysis and artificial intelligence. Signal transduction and targeted therapy, 6(1), 312.

Huang M, et al. (2020) The fine-scale genetic structure and selection signals of Chinese indigenous pigs. Evolutionary applications, 13(2), 458.

Florian RT, et al. (2019) Unstable TTTTA/TTTCA expansions in MARCH6 are associated with Familial Adult Myoclonic Epilepsy type 3. Nature communications, 10(1), 4919.

Yang W, et al. (2019) Immunogenic neoantigens derived from gene fusions stimulate T cell responses. Nature medicine, 25(5), 767.

Wang W, et al. (2019) A comprehensive multiplex PCR based exome-sequencing assay for rapid bloodspot confirmation of inborn errors of metabolism. BMC medical genetics, 20(1), 3.

Seth S, et al. (2019) Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. Cell reports, 26(6), 1518.

Pitt JJ, et al. (2018) Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. Nature communications, 9(1), 4181.

Madanecki P, et al. (2018) High-Throughput Tabular Data Processor - Platform independent graphical tool for processing large data sets. PloS one, 13(2), e0192858.

Stammnitz MR, et al. (2018) The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. Cancer cell, 33(4), 607.

Mahamdallie S, et al. (2018) The Quality Sequencing Minimum (QSM): providing comprehensive, consistent, transparent next generation sequencing data quality assurance. Wellcome open research, 3, 37.

Siersbæk R, et al. (2017) Dynamic Rewiring of Promoter-Anchored Chromatin Loops during Adipocyte Differentiation. Molecular cell, 66(3), 420.

Scales M, et al. (2017) Search for rare protein altering variants influencing susceptibility to multiple myeloma. Oncotarget, 8(22), 36203.

Koyama S, et al. (2017) Whole-exome sequencing and digital PCR identified a novel compound heterozygous mutation in the NPHP1 gene in a case of Joubert syndrome and related disorders. BMC medical genetics, 18(1), 37.

Koyama S, et al. (2017) Clinical and radiological diversity in genetically confirmed primary familial brain calcification. Scientific reports, 7(1), 12046.

Palmer EE, et al. (2017) A Recurrent De Novo Nonsense Variant in ZSWIM6 Results in Severe Intellectual Disability without Frontonasal or Limb Malformations. American journal of human genetics, 101(6), 995.

Trück J, et al. (2016) Variable phenotype and discrete alterations of immune phenotypes in CTP synthase 1 deficiency: Report of 2 siblings. The Journal of allergy and clinical immunology, 138(6), 1722.

Hintzsche JD, et al. (2016) A Survey of Computational Tools to Analyze and Interpret Whole Exome Sequencing Data. International journal of genomics, 2016, 7983236.

Howard MF, et al. (2014) Mutations in PGAP3 impair GPI-anchor maturation, causing a subtype of hyperphosphatasia with mental retardation. American journal of human genetics, 94(2), 278.

Glusman G, et al. (2014) Whole-genome haplotyping approaches and genomic medicine. Genome medicine, 6(9), 73.