

Resource Summary Report

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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 [dkNET](#) .

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.