

Resource Summary Report

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Portcullis

RRID:SCR_016442

Type: Tool

Proper Citation

Portcullis (RRID:SCR_016442)

Resource Information

URL: <https://github.com/maplesond/portcullis>

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Description: Software for filtering invalid Splice junctions from pre-aligned RNA-seq data. It takes as input a BAM file generated by an RNAseq mapper, then analyses and quantifies all splice junctions in the file before filtering (culling) those which are unlikely to be genuine.

Resource Type: data processing software, software application, software resource, data analysis software

Keywords: filter, invalid, splicing, rnaseq, sequence, sequencing, bam, junction, rna

Funding: Biotechnology and Biological Sciences Research Council (BBSRC)

Availability: Free, Available for download

Resource Name: Portcullis

Resource ID: SCR_016442

License: GNU GPL V3

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260805T044354+0000

Ratings and Alerts

No rating or validation information has been found for Portcullis.

No alerts have been found for Portcullis.

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](#) .

Riquier S, et al. (2025) RNA-Seq analysis reveals the long noncoding RNAs associated with immunity in wild *Myotis myotis* bats. *BMC genomics*, 26(1), 345.

Ryan C, et al. (2025) A haplotype-resolved chromosome-level genome assembly of *Urochloa decumbens* cv. Basilisk resolves its allopolyploid ancestry and composition. *G3 (Bethesda, Md.)*, 15(4).

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Hill R, et al. (2025) Evolutionary genomics reveals variation in structure and genetic content implicated in virulence and lifestyle in the genus *Gaeumannomyces*. *BMC genomics*, 26(1), 239.

McMullan M, et al. (2025) Developing a crop- wild-reservoir pathogen system to understand pathogen evolution and emergence. *eLife*, 14.

Grewal S, et al. (2025) Chromosome-level haplotype-resolved genome assembly of bread wheat's wild relative *Aegilops mutica*. *Scientific data*, 12(1), 438.

Benoit M, et al. (2025) *Solanum* pan-genetics reveals paralogues as contingencies in crop engineering. *Nature*, 640(8057), 135.

Han H, et al. (2025) Chromosome-level genome assembly of cultivated strawberry 'Seolhyang' (*Fragaria* × *ananassa*). *Scientific data*, 12(1), 1002.

Piovani L, et al. (2025) The genomic origin of the unique chaetognath body plan. *Nature*, 645(8082), 964.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

Kim IV, et al. (2025) Chromatin loops are an ancestral hallmark of the animal regulatory genome. *Nature*, 642(8069), 1097.

Gavriouchkina D, et al. (2025) A single-cell atlas of the bobtail squid visual and nervous system highlights molecular principles of convergent evolution. *Nature ecology & evolution*, 9(7), 1245.

Cicconardi F, et al. (2024) Novel Sex-Specific Genes and Diverse Interspecific Expression in the Antennal Transcriptomes of Ithomiine Butterflies. *Genome biology and evolution*, 16(10).

Sarre LA, et al. (2024) DNA methylation enables recurrent endogenization of giant viruses in an animal relative. *Science advances*, 10(28), eado6406.

Marlétaz F, et al. (2024) The hagfish genome and the evolution of vertebrates. *Nature*, 627(8005), 811.

Grewal S, et al. (2024) Chromosome-scale genome assembly of bread wheat's wild relative *Triticum timopheevii*. *Scientific data*, 11(1), 420.

Phillips AR, et al. (2023) A happy accident: a novel turfgrass reference genome. *G3 (Bethesda, Md.)*, 13(6).

Backer R, et al. (2023) The expression of the NPR1-dependent defense response pathway genes in *Persea americana* (Mill.) following infection with *Phytophthora cinnamomi*. *BMC plant biology*, 23(1), 548.

Marlétaz F, et al. (2023) The hagfish genome and the evolution of vertebrates. *bioRxiv : the preprint server for biology*.

McGowan J, et al. (2023) Identification of a non-canonical ciliate nuclear genetic code where UAA and UAG code for different amino acids. *PLoS genetics*, 19(10), e1010913.