

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 analysis software, data processing software, software application, software resource

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: 20260829T182544+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 33 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Santos LBD, et al. (2026) Pangenome analysis of nine soybean cyst nematode genomes reveals hidden variation contributing to diversity and adaptation. BMC genomics, 27(1), 177.

De Vega JJ, et al. (2026) A haplotype-complete chromosome-level assembly of octoploid Urochloa humidicola cv. Tully reveals multiple genomic compositions and evolutionary histories in the species. G3 (Bethesda, Md.), 16(4).

Zadesenets KS, et al. (2026) Mining Differentially Expressed Genes in the Marine Free-Living Flatworm Macrostomum lignano Under Aneuploidy-Driven Ploidy Changes. Cells, 15(3).

Biello R, et al. (2026) One Sea, Different Whales: Genomics Sheds Light on a Small Population of Fin Whales. Genome biology and evolution, 18(4).

Sanchez G, et al. (2026) Rapid mid-Cretaceous diversification of squid and cuttlefish preceded radiation into coastal niches. Nature ecology & evolution, 10(4), 662.

Hoff SNK, et al. (2026) Rapid genome modifications including chromosomal fusions and large-scale inversions are key features in Arctic codfish species. Genome biology, 27(1).

Biello R, et al. (2026) Chromosome-level genome of the Adriatic sturgeon, Acipenser naccarii: A resource for polyploid fish genomics. The Journal of heredity, 117(4), 877.

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.

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

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.

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.

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

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.

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

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

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

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

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).