

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, data analysis software, software resource, software application

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: 20260813T055134+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 [dkNET](#) .

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).

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.

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

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.

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

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).

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.

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.

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

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).