

Resource Summary Report

Generated by T1D on Jul 30, 2026

SoftBerry

RRID:SCR_000902

Type: Tool

Proper Citation

SoftBerry (RRID:SCR_000902)

Resource Information

URL: <http://www.softberry.com/>

Proper Citation: SoftBerry (RRID:SCR_000902)

Description: Developer of software tools for genomic research focused on computational methods of high throughput biomedical data analysis, including software to support next generation sequencing technologies, transcriptome analysis with RNASeq data, SNP detection and selection of disease specific SNP subsets. Provides custom genome annotation services.

Synonyms: Linux SoftBerry, Soft berry

Resource Type: data or information resource, portal, software resource

Keywords: genomic, analysis, computation, biomedical, data analysis, rnaseq, sna, snp, transcriptome

Availability: Restricted

Resource Name: SoftBerry

Resource ID: SCR_000902

Alternate IDs: nlx_156881

Old URLs: <http://linux1.softberry.com/>

Record Creation Time: 20220129T080204+0000

Record Last Update: 20260729T044008+0000

Ratings and Alerts

No rating or validation information has been found for SoftBerry.

No alerts have been found for SoftBerry.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 356 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Mulyanti D, et al. (2021) Insertion of prpoD_rpoS fragment enhances expression of recombinant protein by dps auto-inducible promoter in Escherichia coli. Molecular biology reports, 48(8), 5833.

Zou X, et al. (2018) Function analysis of 5'-UTR of the cellulosomal xyl-doc cluster in Clostridium papyrosolvens. Biotechnology for biofuels, 11, 43.

Geng A, et al. (2018) Transcriptome analysis of the digestive system of a wood-feeding termite (Coptotermes formosanus) revealed a unique mechanism for effective biomass degradation. Biotechnology for biofuels, 11, 24.

Dufresne K, et al. (2018) Functional Analysis of the Chaperone-Usher Fimbrial Gene Clusters of Salmonella enterica serovar Typhi. Frontiers in cellular and infection microbiology, 8, 26.

Mukhopadhyaya I, et al. (2018) Sporulation capability and amylosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader Ruminococcus bromii. Environmental microbiology, 20(1), 324.

Kohl C, et al. (2018) Hervey virus: Study on co-circulation with Henipaviruses in Pteropid bats within their distribution range from Australia to Africa. PloS one, 13(2), e0191933.

Dong Y, et al. (2018) Evolution of Darwin's Peloric Gloxinia (Sinningia speciosa) Is Caused by a Null Mutation in a Pleiotropic TCP Gene. Molecular biology and evolution, 35(8), 1901.

Salvador-Guirao R, et al. (2018) The Polycistronic miR166k-166h Positively Regulates Rice Immunity via Post-transcriptional Control of EIN2. Frontiers in plant science, 9, 337.

Taneja M, et al. (2018) Molecular characterization and differential expression suggested diverse functions of P-type II Ca²⁺-ATPases in Triticum aestivum L. BMC genomics, 19(1), 389.

Huang F, et al. (2018) Isolation and Functional Characterization of a Floral Repressor, BcMAF1, From Pak-choi (Brassica rapa ssp. Chinensis). Frontiers in plant science, 9, 290.

Mei T, et al. (2018) Comparative genomics of chemosensory protein genes (CSPs) in twenty-two mosquito species (Diptera: Culicidae): Identification, characterization, and evolution. PloS one, 13(1), e0190412.

Aamir M, et al. (2018) Structural and functional dissection of differentially expressed tomato WRKY transcripts in host defense response against the vascular wilt pathogen (*Fusarium oxysporum* f. sp. *lycopersici*). PloS one, 13(4), e0193922.

Gajewska P, et al. (2018) Forward Genetics Approach Reveals a Mutation in bHLH Transcription Factor-Encoding Gene as the Best Candidate for the Root Hairless Phenotype in Barley. Frontiers in plant science, 9, 1229.

Zhou S, et al. (2018) Investigation of lignocellulolytic enzymes during different growth phases of *Ganoderma lucidum* strain G0119 using genomic, transcriptomic and secretomic analyses. PloS one, 13(5), e0198404.

Papierniak A, et al. (2018) Contribution of NtZIP1-Like to the Regulation of Zn Homeostasis. Frontiers in plant science, 9, 185.

Jiao H, et al. (2018) The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear (*Pyrus bretschneideri*). BMC plant biology, 18(1), 36.

Poidevin M, et al. (2018) Mutation in ESBL Plasmid from *Escherichia coli* O104:H4 Leads Autoagglutination and Enhanced Plasmid Dissemination. Frontiers in microbiology, 9, 130.

Morimoto D, et al. (2018) Transcriptome Analysis of a Bloom-Forming Cyanobacterium *Microcystis aeruginosa* during Ma-LMM01 Phage Infection. Frontiers in microbiology, 9, 2.

Belahbib H, et al. (2018) New genomic data and analyses challenge the traditional vision of animal epithelium evolution. BMC genomics, 19(1), 393.

Nguyen VNT, et al. (2018) OsABCG9 Is an Important ABC Transporter of Cuticular Wax Deposition in Rice. Frontiers in plant science, 9, 960.