

Resource Summary Report

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Bio-Linux

RRID:SCR_005399

Type: Tool

Proper Citation

Bio-Linux (RRID:SCR_005399)

Resource Information

URL: <http://nebc.nerc.ac.uk/tools/bio-linux/bio-linux-7-info>

Proper Citation: Bio-Linux (RRID:SCR_005399)

Description: A free, fully featured, powerful, configurable and easy to maintain bioinformatics workstation that provides more than 500 bioinformatics programs on an Ubuntu Linux 12.04 LTS base. Install it or run it live. There is a graphical menu for bioinformatics programs, as well as easy access to the Bio-Linux bioinformatics documentation system and sample data useful for testing programs. You can run a Bio-Linux system on Amazon EC2 or other cloud computing architectures by using CloudBioLinux.

Abbreviations: Bio-Linux

Synonyms: BioLinux, NEBC Bio-Linux

Resource Type: software resource

Defining Citation: [PMID:16841067](#)

Keywords: ubuntu, cloud computing, workstation, bioinformatics

Availability: Acknowledgement requested, Open unspecified license

Resource Name: Bio-Linux

Resource ID: SCR_005399

Alternate IDs: OMICS_01137

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260815T182314+0000

Ratings and Alerts

No rating or validation information has been found for Bio-Linux.

No alerts have been found for Bio-Linux.

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 [NIF](#) .

Liu H, et al. (2025) Genome-wide identification and functional characterization of the DREB gene family in barley (*Hordeum vulgare* L.) reveal its role in drought and salinity responses. *BMC genomics*, 27(1), 63.

Mu D, et al. (2024) Identification and characterization of soybean phytochrome-interacting factors and their potential roles in abiotic stress. *BMC plant biology*, 24(1), 1273.

Yuan Z, et al. (2022) Systematic identification and expression profiles of the BAHD superfamily acyltransferases in barley (*Hordeum vulgare*). *Scientific reports*, 12(1), 5063.

Chen B, et al. (2021) GhN/AINV13 positively regulates cotton stress tolerance by interacting with the 14-3-3 protein. *Genomics*, 113(1 Pt 1), 44.

Zhang T, et al. (2021) Genome-Wide Identification and Expression Analysis of MYB Transcription Factor Superfamily in *Dendrobium catenatum*. *Frontiers in genetics*, 12, 714696.

Zhang Q, et al. (2021) Genome-Wide Identification and Analysis of the MADS-Box Gene Family in *Theobroma cacao*. *Genes*, 12(11).

Liu H, et al. (2021) The Sugar Transporter family in wheat (*Triticum aestivum*. L): genome-wide identification, classification, and expression profiling during stress in seedlings. *PeerJ*, 9, e11371.

Takahashi M, et al. (2020) Improvement of Psoriasis by Alteration of the Gut Environment by Oral Administration of Fucoidan from *Cladosiphon Okamuranus*. *Marine drugs*, 18(3).

Li J, et al. (2020) Heavy Metal Stress-Associated Proteins in Rice and Arabidopsis: Genome-Wide Identification, Phylogenetics, Duplication, and Expression Profiles Analysis. *Frontiers in genetics*, 11, 477.

Tang D, et al. (2020) The association between microbial community and ileal gene expression on intestinal wall thickness alterations in chickens. *Poultry science*, 99(4), 1847.

Deng H, et al. (2020) Modular engineering of *Shiraia bambusicola* for hypocrellin production through an efficient CRISPR system. *International journal of biological macromolecules*, 165(Pt A), 796.

Diack O, et al. (2020) GWAS unveils features between early- and late-flowering pearl millets. *BMC genomics*, 21(1), 777.

Zhang B, et al. (2019) Variation in Actinobacterial Community Composition and Potential Function in Different Soil Ecosystems Belonging to the Arid Heihe River Basin of Northwest China. *Frontiers in microbiology*, 10, 2209.

Li J, et al. (2019) Genome-Wide Characterization and Identification of Trihelix Transcription Factor and Expression Profiling in Response to Abiotic Stresses in Rice (*Oryza sativa* L.). *International journal of molecular sciences*, 20(2).

Shen S, et al. (2019) Genome-Wide Analysis of the NAC Domain Transcription Factor Gene Family in *Theobroma cacao*. *Genes*, 11(1).

Franceschi S, et al. (2018) Cancer astrocytes have a more conserved molecular status in long recurrence free survival (RFS) IDH1 wild-type glioblastoma patients: new emerging cancer players. *Oncotarget*, 9(35), 24014.

Harumoto T, et al. (2018) Male-killing toxin in a bacterial symbiont of *Drosophila*. *Nature*, 557(7704), 252.

Theotokis PI, et al. (2017) Profiling the Mismatch Tolerance of Argonaute 2 through Deep Sequencing of Sliced Polymorphic Viral RNAs. *Molecular therapy. Nucleic acids*, 9, 22.

Yang J, et al. (2017) Indigenous species barcode database improves the identification of zooplankton. *PloS one*, 12(10), e0185697.

Negro S, et al. (2017) CXCL12^{hi}/SDF-1 from perisynaptic Schwann cells promotes regeneration of injured motor axon terminals. *EMBO molecular medicine*, 9(8), 1000.