

Resource Summary Report

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Biowulf at the NIH

RRID:SCR_007169

Type: Tool

Proper Citation

Biowulf at the NIH (RRID:SCR_007169)

Resource Information

URL: <https://hpc.nih.gov/systems/>

Proper Citation: Biowulf at the NIH (RRID:SCR_007169)

Description: The NIH Biowulf cluster is a GNU/Linux parallel processing system designed and built at the National Institutes of Health and managed by the Helix Systems Staff. The system is designed for large numbers of simultaneous jobs common in bioinformatics as well as large-scale distributed memory tasks such as molecular dynamics. Sponsor: This work was supported by the National Institutes of Health Intramural Research Program through the Center for Information Technology and the National Institute of Neurological Disorders and Stroke, and by the Internal National Institute of Standards and Technology Research Fund. Keywords: Software, Program, Processing, System, Simulatenous, Bioinformatics, Memory, Molecular, Dynamics,

Synonyms: NIH Biowulf

Resource Type: systems interoperability software, software application, data processing software, software resource

Resource Name: Biowulf at the NIH

Resource ID: SCR_007169

Alternate IDs: nif-0000-30204

Old URLs: <http://biowulf.nih.gov>

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260811T043303+0000

Ratings and Alerts

No rating or validation information has been found for Biowulf at the NIH.

No alerts have been found for Biowulf at the NIH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 120 mentions in open access literature.

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

Song HB, et al. (2025) Sex-specific attenuation of photoreceptor degeneration by reserpine in a rhodopsin P23H rat model of autosomal dominant retinitis pigmentosa. *eLife*, 14.

Benner L, et al. (2025) Female germline expression of OVO transcription factor bridges *Drosophila* generations. *G3* (Bethesda, Md.), 15(2).

Valencia EM, et al. (2024) Mock community taxonomic classification performance of publicly available shotgun metagenomics pipelines. *Scientific data*, 11(1), 81.

Choi J, et al. (2024) Molecular targets of glucocorticoids that elucidate their therapeutic efficacy in aggressive lymphomas. *Cancer cell*, 42(5), 833.

Trovão NS, et al. (2021) Molecular characterization of respiratory syncytial viruses circulating in a paediatric cohort in Amman, Jordan. *Microbial genomics*, 7(6).

Tawa GJ, et al. (2021) Transcriptomic profiling in canines and humans reveals cancer specific gene modules and biological mechanisms common to both species. *PLoS computational biology*, 17(9), e1009450.

Peng Y, et al. (2021) Binding of regulatory proteins to nucleosomes is modulated by dynamic histone tails. *Nature communications*, 12(1), 5280.

Maruyama SR, et al. (2021) Total Ortholog Median Matrix as an alternative unsupervised approach for phylogenomics based on evolutionary distance between protein coding genes. *Scientific reports*, 11(1), 3791.

Patel H, et al. (2020) SAVI, in silico generation of billions of easily synthesizable compounds through expert-system type rules. *Scientific data*, 7(1), 384.

Corso-Díaz X, et al. (2020) Genome-wide Profiling Identifies DNA Methylation Signatures of Aging in Rod Photoreceptors Associated with Alterations in Energy Metabolism. *Cell reports*, 31(3), 107525.

Eccles D, et al. (2018) De novo assembly of the complex genome of *Nippostrongylus brasiliensis* using MinION long reads. *BMC biology*, 16(1), 6.

Aoki M, et al. (2017) A novel central nervous system-penetrating protease inhibitor overcomes human immunodeficiency virus 1 resistance with unprecedented aM to pM potency. *eLife*, 6.

Jansen IE, et al. (2017) Discovery and functional prioritization of Parkinson's disease candidate genes from large-scale whole exome sequencing. *Genome biology*, 18(1), 22.

Si H, et al. (2016) TNF- α modulates genome-wide redistribution of α Np63 β /TAp73 and NF- κ B cREL interactive binding on TP53 and AP-1 motifs to promote an oncogenic gene program in squamous cancer. *Oncogene*, 35(44), 5781.

Hoenen T, et al. (2016) Nanopore Sequencing as a Rapidly Deployable Ebola Outbreak Tool. *Emerging infectious diseases*, 22(2), 331.

Takeda T, et al. (2016) Structural insights of a PI3K/mTOR dual inhibitor with the morpholino-triazine scaffold. *Journal of computer-aided molecular design*, 30(4), 323.

Lubbe SJ, et al. (2016) Rare variants analysis of cutaneous malignant melanoma genes in Parkinson's disease. *Neurobiology of aging*, 48, 222.e1.

Shaytan AK, et al. (2016) Trajectories of microsecond molecular dynamics simulations of nucleosomes and nucleosome core particles. *Data in brief*, 7, 1678.

Guay MD, et al. (2016) Compressed Sensing Electron Tomography for Determining Biological Structure. *Scientific reports*, 6, 27614.

Molloy AM, et al. (2016) A Common Polymorphism in HIBCH Influences Methylmalonic Acid Concentrations in Blood Independently of Cobalamin. *American journal of human genetics*, 98(5), 869.