Resource Summary Report

Generated by dkNET on Apr 24, 2025

Preseq

RRID:SCR_018664
Type: Tool

Proper Citation

Preseq (RRID:SCR_018664)

Resource Information

URL: http://smithlabresearch.org/software/preseq/

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Description: Software package for predicting library complexity and genome coverage in high throughput sequencing. Aimed at predicting yield of distinct reads from genomic library from initial sequencing experiment. Predicting molecular complexity of sequencing libraries.

Resource Type: data analysis software, software resource, software application, data processing software, software toolkit

Defining Citation: PMID:23435259

Keywords: Genome, high throughput sequencing, predicting library complexity, distinct yield prediction, genomic library, initial sequencing experiment, molecular complexity prediction, sequencing libraryb, bio.tools

Funding:

Availability: Free, Freely available

Resource Name: Preseq

Resource ID: SCR_018664

Alternate IDs: biotools:preseq

Alternate URLs: https://github.com/smithlabcode/preseq, https://bio.tools/preseq

License: GPL

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250424T065556+0000

Ratings and Alerts

No rating or validation information has been found for Preseq.

No alerts have been found for Preseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Kalef-Ezra E, et al. (2024) Single-cell somatic copy number variants in brain using different amplification methods and reference genomes. Communications biology, 7(1), 1288.

Russo T, et al. (2024) The SATB1-MIR22-GBA axis mediates glucocerebroside accumulation inducing a cellular senescence-like phenotype in dopaminergic neurons. Aging cell, 23(4), e14077.

Pham VC, et al. (2024) Epigenetic regulation by polycomb repressive complex 1 promotes cerebral cavernous malformations. EMBO molecular medicine, 16(11), 2827.

Viel KCMF, et al. (2024) Shared and distinct interactions of type 1 and type 2 Epstein-Barr Nuclear Antigen 2 with the human genome. BMC genomics, 25(1), 273.

Russo T, et al. (2023) The SATB1-MIR22-GBA axis mediates glucocerebroside accumulation inducing a cellular senescence-like phenotype in dopaminergic neurons. bioRxiv : the preprint server for biology.

Yazar V, et al. (2023) Impaired ATF3 signaling involves SNAP25 in SOD1 mutant ALS patients. Scientific reports, 13(1), 12019.

West C, et al. (2023) nf-core/clipseq - a robust Nextflow pipeline for comprehensive CLIP data analysis. Wellcome open research, 8, 286.

Ziff OJ, et al. (2023) Nucleocytoplasmic mRNA redistribution accompanies RNA binding

protein mislocalization in ALS motor neurons and is restored by VCP ATPase inhibition. Neuron, 111(19), 3011.

Hanlon VCT, et al. (2022) Construction of Strand-seq libraries in open nanoliter arrays. Cell reports methods, 2(1), 100150.

Horibata S, et al. (2021) Host gene expression modulated by Zika virus infection of human-293 cells. Virology, 552, 32.

Barlow A, et al. (2021) Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. Current biology : CB, 31(8), 1771.

Lu B, et al. (2020) Transposase-assisted tagmentation of RNA/DNA hybrid duplexes. eLife, 9.

Rodrigues AF, et al. (2020) Size-Dependent Pulmonary Impact of Thin Graphene Oxide Sheets in Mice: Toward Safe-by-Design. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 7(12), 1903200.

Riessland M, et al. (2019) Loss of SATB1 Induces p21-Dependent Cellular Senescence in Post-mitotic Dopaminergic Neurons. Cell stem cell, 25(4), 514.

Cruz-Dávalos DI, et al. (2018) In-solution Y-chromosome capture-enrichment on ancient DNA libraries. BMC genomics, 19(1), 608.