

Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 2026

python-bx

RRID:SCR_024202

Type: Tool

Proper Citation

python-bx (RRID:SCR_024202)

Resource Information

URL: <https://github.com/bxlab/bx-python>

Proper Citation: python-bx (RRID:SCR_024202)

Description: Software Python library and associated set of scripts for rapid implementation of genome scale analyses.

Resource Type: software resource, software toolkit, software library

Keywords: rapid implementation of genome scale analyses,

Resource Name: python-bx

Resource ID: SCR_024202

Alternate IDs: OMICS_18239

Old URLs: <https://sources.debian.org/src/python3-bx/>

License: MIT license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260729T044606+0000

Ratings and Alerts

No rating or validation information has been found for python-bx.

No alerts have been found for python-bx.

Data and Source Information

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mogi M, et al. (2026) Pan-cancer analysis of RNA expression signatures associated with cancer tissue architecture. *British journal of cancer*, 134(1), 141.

Bergheim BG, et al. (2025) Molecular dynamics of the matrisome across sea anemone life history. *eLife*, 14.

Antysheva Z, et al. (2025) Machine learning-based single-sample molecular classifier for cancer grading. *Frontiers in oncology*, 15, 1617898.

Azzam N, et al. (2025) Modeling High-Risk Pediatric Cancers in Zebrafish to Inform Precision Therapy. *Cancer research communications*, 5(7), 1215.

Chen X, et al. (2025) A phylogenetic approach uncovers cryptic endogenous retrovirus subfamilies in the primate lineage. *Science advances*, 11(29), eads9164.

Lombardi V, et al. (2025) PatientProfiler: building patient-specific signaling models from proteogenomic data. *Molecular systems biology*, 21(12), 1845.

Hu F, et al. (2025) The systemic wrinkled skin phenotype involves aberrant expression and variation of genes related to the oxidative stress and extracellular matrix in Xiang pigs. *BMC genomics*, 26(1), 1034.

Lingasamy P, et al. (2025) Targeting oncofetal fibronectin and neuropilin-1 in solid tumors with PL2 peptide. *Scientific reports*, 15(1), 29369.

Sawant A, et al. (2025) Immune Checkpoint Blockade Delays Cancer Development and Extends Survival in DNA Polymerase Mutator Syndromes. *Cancer research*, 85(6), 1130.

Mozzarelli AM, et al. (2025) RIT1 Drives Oncogenic Transformation and Is an Actionable Target in Lung Adenocarcinoma. *Cancer research*, 85(17), 3196.

Lin HK, et al. (2025) Integrating large-scale in vitro functional genomic screen and multi-omics data to identify novel breast cancer targets. *Breast cancer research and treatment*.

Mi H, et al. (2025) Spatial Architecture of Single-Cell and Vasculature in Tumor Microenvironment Predicts Clinical Outcomes in Triple-Negative Breast Cancer. *Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc*, 38(2), 100652.

Bayet M, et al. (2025) Modeling the PAX5P80R Mutation Reveals HIF2?? Activation as a Common Feature and Therapeutic Target in B-cell Acute Lymphoblastic Leukemia. *Cancer research*, 85(15), 2820.

Tamura T, et al. (2025) mTOR-mediated p62/SQSTM1 stabilization confers a robust survival mechanism for ovarian cancer. *Cancer letters*, 616, 217565.

Wang L, et al. (2025) Predicting Pancreatic Ductal Adenocarcinoma Occurrence Up to 10 Years in Advance Using Features of the Main Pancreatic Duct in Pre-Diagnostic CT Scans. *Cancers*, 17(11).

Wang T, et al. (2025) TREM2-Mediated Myeloid Cells Protect Against Pathological Choroidal Neovascularization. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(14), e70881.

Tang JP, et al. (2024) Hypophosphatemia Correction Reduces ICANS Incidence and Duration in CAR T-cell Therapy: A Pooled Clinical Trial Analysis. *Cancer research communications*, 4(10), 2589.

Zhu T, et al. (2024) Comprehensive mapping and modelling of the rice regulome landscape unveils the regulatory architecture underlying complex traits. *Nature communications*, 15(1), 6562.

Osmond M, et al. (2024) Estimating dispersal rates and locating genetic ancestors with genome-wide genealogies. *eLife*, 13.

Huey JD, et al. (2024) Bigtools: a high-performance BigWig and BigBed library in Rust. *Bioinformatics (Oxford, England)*, 40(6).