Pandas

RRID:SCR_018214
Type: Tool

Proper Citation

Pandas (RRID:SCR_018214)

Resource Information

URL: https://pandas.pydata.org

Proper Citation: Pandas (RRID:SCR_018214)

Description: Software Python package for data analysis providing labeled data structures similar to R data. Provides data structures designed to make working with relational or labeled data. Software as building block for doing practical, real world open source data analysis and manipulation tool.

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

Keywords: Data analysis, labeled data, relational data, data structure

Funding: NumFOCUS

Availability: Free, Available for download, Freely available

Resource Name: Pandas

Resource ID: SCR_018214

Alternate URLs: https://github.com/pandas-dev/pandas

License: BSD 3-Clause License

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250412T060227+0000

Ratings and Alerts

No rating or validation information has been found for Pandas.

No alerts have been found for Pandas.

Data and Source Information

Usage and Citation Metrics

We found 425 mentions in open access literature.

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

Litsios A, et al. (2025) Protocol for cell image-based spatiotemporal proteomics in budding yeast. STAR protocols, 6(1), 103577.

Jiang M, et al. (2025) LIN28-Targeting Chromenopyrazoles and Tetrahydroquinolines Induced Cellular Morphological Changes and Showed High Biosimilarity with BRD PROTACs. ChemMedChem, 20(1), e202400547.

Gul L, et al. (2025) Protocol for predicting host-microbe interactions and their downstream effect on host cells using MicrobioLink. STAR protocols, 6(1), 103570.

Wang F, et al. (2024) SPDB: a comprehensive resource and knowledgebase for proteomic data at the single-cell resolution. Nucleic acids research, 52(D1), D562.

Jiang M, et al. (2024) VitTCR: A deep learning method for peptide recognition prediction. iScience, 27(5), 109770.

Strazza V, et al. (2024) Rapid generation of human recombinant monoclonal antibodies from antibody-secreting cells using ferrofluid-based technology. Frontiers in immunology, 15, 1341389.

Malatesta M, et al. (2024) One substrate many enzymes virtual screening uncovers missing genes of carnitine biosynthesis in human and mouse. Nature communications, 15(1), 3199.

Arnedo-Pac C, et al. (2024) Hotspot propensity across mutational processes. Molecular systems biology, 20(1), 6.

Steemans B, et al. (2024) Protocol to train a support vector machine for the automatic curation of bacterial cell detections in microscopy images. STAR protocols, 5(1), 102868.

Mehmood F, et al. (2024) ADH-Enhancer: an attention-based deep hybrid framework for enhancer identification and strength prediction. Briefings in bioinformatics, 25(2).

Noguchi Y, et al. (2024) In vivo CRISPR screening directly targeting testicular cells. Cell genomics, 4(3), 100510.

Wang QS, et al. (2024) Statistically and functionally fine-mapped blood eQTLs and pQTLs from 1,405 humans reveal distinct regulation patterns and disease relevance. Nature genetics, 56(10), 2054.

Sha Y, et al. (2024) CerviFusionNet: A multi-modal, hybrid CNN-transformer-GRU model for enhanced cervical lesion multi-classification. iScience, 27(12), 111313.

Massy R, et al. (2024) Enhanced flight performance in hoverfly migrants. iScience, 27(12), 111345.

Jia J, et al. (2024) Predictive model for totally implanted venous access ports?related long?term complications in patients with lung cancer. Oncology letters, 28(1), 326.

Zhang S, et al. (2024) Machine learning on longitudinal multi-modal data enables the understanding and prognosis of Alzheimer's disease progression. iScience, 27(7), 110263.

Varambally S, et al. (2024) MammOnc-DB, an integrative breast cancer data analysis platform for target discovery. Research square.

Ramos H, et al. (2024) Exposure Scenarios for Estimating Contaminant Levels in Healthy Sustainable Dietary Models: Omnivorous vs. Vegetarian. Foods (Basel, Switzerland), 13(22).

Qin X, et al. (2024) Medioresinol from Eucommiae cortex improves myocardial infarction-induced heart failure through activation of the PI3K/AKT/mTOR pathway: A network analysis and experimental study. PloS one, 19(9), e0311143.

Novielli P, et al. (2024) Personalized identification of autism-related bacteria in the gut microbiome using explainable artificial intelligence. iScience, 27(9), 110709.