Resource Summary Report

Generated by RRID on Aug 4, 2026

Pipeline Pilot

RRID:SCR_014917
Type: Tool

Proper Citation

Pipeline Pilot (RRID:SCR_014917)

Resource Information

URL: http://accelrys.com/products/collaborative-science/biovia-pipeline-pilot/

Proper Citation: Pipeline Pilot (RRID:SCR_014917)

Description: Software used to automate the process of accessing, analyzing and reporting scientific data. This software can be used by a person with little or no software development experience can create scientific protocols that can be executed through a variety of interfaces including: BIOVIA Web Port, other BIOVIA solutions such as BIOVIA Electronic Lab Notebook, Isentris, Chemical Registration and third-party applications such as Microsoft SharePoint. The protocols aggregate and provide immediate access to volumes of research data, they automate the scientific analysis of data and allow researchers to explore, visualize and report results.

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

Keywords: automation, accessing, analysis, analyzing, scientific data, aggregation. aggregate, research, scientific

Availability: Commercial

Resource Name: Pipeline Pilot

Resource ID: SCR_014917

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260804T043556+0000

Ratings and Alerts

No rating or validation information has been found for Pipeline Pilot.

No alerts have been found for Pipeline Pilot.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 352 mentions in open access literature.

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

Svensson E, et al. (2025) Network Analysis of the Organic Chemistry in Patents, Literature, and Pharmaceutical Industry. Molecular informatics, 44(7), e202500011.

Yang Z, et al. (2025) A force-sensitive adhesion GPCR is required for equilibrioception. Cell research, 35(4), 243.

Okabe A, et al. (2025) Discovery of Highly Potent Noncovalent Inhibitors of SARS-CoV-2 Main Protease through Computer-Aided Drug Design. Journal of medicinal chemistry, 68(20), 21330.

Cho NC, et al. (2025) The first South Korean data challenge for drug discovery using human and mouse liver microsomal stability data. Journal of cheminformatics, 17(1), 139.

Wang J, et al. (2025) Decoding the selective chemical modulation of CYP3A4. Nature communications, 16(1), 3423.

Esparza M, et al. (2025) Contrasting interferon-mediated antiviral responses in human lung adenocarcinoma cells. Journal of virology, 99(6), e0046925.

Dvorak NM, et al. (2025) Enhanced motivated behavior mediated by pharmacological targeting of the FGF14/Nav1.6 complex in nucleus accumbens neurons. Nature communications, 16(1), 110.

Scott T, et al. (2025) Drugit: crowd-sourcing molecular design of non-peptidic VHL binders. Nature communications, 16(1), 3548.

Yang CL, et al. (2025) Identification and Biological Evaluation of a Novel CLK4 Inhibitor Targeting Alternative Splicing in Pancreatic Cancer Using Structure-Based Virtual Screening. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(19), e2416323.

Mettu A, et al. (2025) Functionally active modulators targeting the LRRK2 WD40 repeat domain identified by FRASE-bot in CACHE Challenge #1. Chemical science, 16(8), 3430.

McSwiggen DT, et al. (2025) A high-throughput platform for single-molecule tracking identifies drug interaction and cellular mechanisms. eLife, 12.

Hsieh TH, et al. (2025) Hinokiflavone is a novel CK2 inhibitor promoting apoptosis and synergizing with chemotherapeutic agents in cisplatin resistant bladder cancer cells. Scientific reports, 15(1), 20922.

Shan P, et al. (2025) Discovery of a novel potent tubulin inhibitor through virtual screening and target validation for cancer chemotherapy. Cell death discovery, 11(1), 392.

Khalid AQ, et al. (2025) Protocol for predicting ?-tocotrienol and ?-tocotrienol binding to colorectal cancer-related proteins using Schrödinger's Maestro and Glide. STAR protocols, 6(4), 104144.

Akabane T, et al. (2024) THOUSAND-GRAIN WEIGHT 6, which is an IAA-glucose hydrolase, preferentially recognizes the structure of the indole ring. Scientific reports, 14(1), 6778.

Shen L, et al. (2024) Pocket Crafter: a 3D generative modeling based workflow for the rapid generation of hit molecules in drug discovery. Journal of cheminformatics, 16(1), 33.

Robinson SD, et al. (2024) Peptide toxins that target vertebrate voltage-gated sodium channels underly the painful stings of harvester ants. The Journal of biological chemistry, 300(1), 105577.

Tu HJ, et al. (2024) Discovering a novel dual specificity tyrosine-phosphorylation-regulated kinase 1A (DYRK1A) inhibitor and its impact on tau phosphorylation and amyloid-? formation. Journal of enzyme inhibition and medicinal chemistry, 39(1), 2418470.

Powell RT, et al. (2024) Targeting neddylation and sumoylation in chemoresistant triple negative breast cancer. NPJ breast cancer, 10(1), 37.

Meyniel-Schicklin L, et al. (2024) Viruses traverse the human proteome through peptide interfaces that can be biomimetically leveraged for drug discovery. Proceedings of the National Academy of Sciences of the United States of America, 121(5), e2308776121.