

Resource Summary Report

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Modular Automated Platform for Large Scale Experiments project

RRID:SCR_021557

Type: Tool

Proper Citation

Modular Automated Platform for Large Scale Experiments project (RRID:SCR_021557)

Resource Information

URL: <https://edspace.american.edu/openbehavior/project/maple/>

Proper Citation: Modular Automated Platform for Large Scale Experiments project (RRID:SCR_021557)

Description: Portal related to measurement of fly social networks and behavior. Provides Drosophila handing robot that boasts modular design, allowing platform to both automate diverse phenotyping assays and aid with lab chores (e.g., collecting virgin female flies). MAPLE permits small part manipulator, USB digital camera, and fly manipulator to work simultaneously over platform of flies.

Abbreviations: MAPLE

Synonyms: Modular Automated Platform for Large -Scale Experiments

Resource Type: data or information resource, instrument resource, portal, project portal

Defining Citation: [DOI:10.1101/239459](https://doi.org/10.1101/239459)

Keywords: Instrument, Drosophila handing robot, automate diverse phenotyping assays, collecting virgin female flies, USB digital camera, fly manipulator, flies modular automated platform, large scale experiments, OpenBehavior

Availability: Free, Freely available

Resource Name: Modular Automated Platform for Large Scale Experiments project

Resource ID: SCR_021557

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260919T195454+0000

Ratings and Alerts

No rating or validation information has been found for Modular Automated Platform for Large Scale Experiments project.

No alerts have been found for Modular Automated Platform for Large Scale Experiments project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Zhang Y, et al. (2026) A robust computational framework for methylation age and disease-risk prediction based on pairwise learning. Nature computational science, 6(4), 388.

De Maio N, et al. (2026) Rate variation and recurrent sequence errors in pandemic-scale phylogenetics. Nature methods, 23(3), 565.

Hunt M, et al. (2026) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. Nature methods, 23(3), 653.

Chen H, et al. (2026) Improving Inference in Air Pollution Epidemiology: The Case for Rethinking Multipollutant Adjustment. Epidemiology (Cambridge, Mass.), 37(4), 427.

Lang K, et al. (2026) High-fidelity bidirectional translation between single-cell transcriptomes and DNA methylomes with scBOND. Genome research, 36(4), 769.

Wang X, et al. (2026) MAPLE: a machine-learning force-field-native platform for automated reaction modeling and enzyme design. Chemical science, 17(25), 12394.

Wassel MA, et al. (2026) Tetrodotoxin (TTX) reshapes the functional potential of the gut microbiome in juvenile tiger pufferfish (*Takifugu rubripes*) across salinity gradients. Animal microbiome, 8(1).

Pekar JE, et al. (2025) Transmission dynamics of the 2022 mpox epidemic in New York City. Nature medicine, 31(5), 1464.

Dezordi FZ, et al. (2025) Higher frequency of interstate over international transmission chains of SARS-CoV-2 virus at the Rio Grande do Sul - Brazil state borders. Virus research, 351, 199500.

Dang HM, et al. (2025) Multi-objective optimizing spring placement and stiffness in slider-crank mechanisms for enhanced dynamic parameters. PloS one, 20(9), e0331341.

Sparrow Muñoz I, et al. (2025) A Golden Gate compatible system for continuous directed evolution in *E. coli*. *Synthetic biology* (Oxford, England), 10(1), ysaf014.

Xiong C, et al. (2025) A comprehensive comparison on clustering methods for multi-slice spatially resolved transcriptomics data analysis. *Briefings in bioinformatics*, 26(5).

López Pérez M, et al. (2025) Infants' Knowledge of Individual Words: Investigating Links Between Parent Report and Looking Time. *Infancy : the official journal of the International Society on Infant Studies*, 30(1), e12641.

De Maio N, et al. (2025) Highly Recurrent Multinucleotide Mutations in SARS-CoV-2. *Molecular biology and evolution*, 42(11).

Algolam MS, et al. (2025) Bifurcation analysis, modulation instability and dynamical analysis of soliton solutions for generalized $(3 + 1)$ -dimensional nonlinear wave equation with m -fractional operator. *Scientific reports*, 15(1), 12929.

Constantinescu S, et al. (2024) MAPLE-prepared graphene oxide-based coatings for improved orthopedic screws used in knee interventions. *Romanian journal of morphology and embryology = Revue roumaine de morphologie et embryologie*, 65(3), 433.

Ma B, et al. (2024) Bases-dependent Rapid Phylogenetic Clustering (Bd-RPC) enables precise and efficient phylogenetic estimation in viruses. *Virus evolution*, 10(1), veae005.

Ye Y, et al. (2024) Robust expansion of phylogeny for fast-growing genome sequence data. *PLoS computational biology*, 20(2), e1011871.

Ramezani G, et al. (2024) Advancements in Hybrid Cellulose-Based Films: Innovations and Applications in 2D Nano-Delivery Systems. *Journal of functional biomaterials*, 15(4).

Khurana MP, et al. (2024) High-resolution epidemiological landscape from ~290,000 SARS-CoV-2 genomes from Denmark. *Nature communications*, 15(1), 7123.