

# Resource Summary Report

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## Pythia

RRID:SCR\_004952

Type: Tool

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### Proper Citation

Pythia (RRID:SCR\_004952)

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### Resource Information

**URL:** <http://pythia.sourceforge.net/>

**Proper Citation:** Pythia (RRID:SCR\_004952)

**Description:** Pythia is an open source thermodynamically oriented primer design python module. Pythia can be used in two ways. 1. Executable binaries only: under windows with cygwin and python 2.5 (built with mingw, that comes with the cygwin release). These executables allow the user to index DNA files for primer specificity search, design one primer pair per region, and tile regions with PCR amplicons. 2. A python module: under windows with cygwin, python2.5, numpy, swig, and mingw, or under linux with python2.4 or later, numpy, and swig (everything but numpy should be pre-installed on a normal linux system). The module gets you everything that the binaries get you, in a more pythonic framework. This package also includes modules for computing DNA binding and folding energies using the partition function approach with publicly available thermodynamic data. Usage documentation is in the downloads.

**Resource Type:** software resource

**Defining Citation:** [PMID:19528077](#)

**Resource Name:** Pythia

**Resource ID:** SCR\_004952

**Alternate IDs:** nlx\_91969

**Record Creation Time:** 20220129T080227+0000

**Record Last Update:** 20260725T190556+0000

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### Ratings and Alerts

No rating or validation information has been found for Pythia.

No alerts have been found for Pythia.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Ren H, et al. (2025) MixtureFinder: Estimating DNA Mixture Models for Phylogenetic Analyses. *Molecular biology and evolution*, 42(1).

Collienue L, et al. (2025) Phylogenetic Tree Instability After Taxon Addition: Empirical Frequency, Predictability, and Consequences For Online Inference. *Systematic biology*, 74(1), 101.

Brailas A, et al. (2025) Replication Crisis in Psychology, Second-Order Cybernetics, and Transactional Causality: from Experimental Psychology to Applied Psychological Practice. *Integrative psychological & behavioral science*, 59(1), 14.

Song J, et al. (2025) Out-of-distribution generalization via composition: A lens through induction heads in Transformers. *Proceedings of the National Academy of Sciences of the United States of America*, 122(6), e2417182122.

Dai HJ, et al. (2025) Leveraging large language models for the deidentification and temporal normalization of sensitive health information in electronic health records. *NPJ digital medicine*, 8(1), 517.

Hackenburg K, et al. (2025) Scaling language model size yields diminishing returns for single-message political persuasion. *Proceedings of the National Academy of Sciences of the United States of America*, 122(10), e2413443122.

Hu T, et al. (2025) Generative language models exhibit social identity biases. *Nature computational science*, 5(1), 65.

Wiegert J, et al. (2024) Predicting Phylogenetic Bootstrap Values via Machine Learning. *Molecular biology and evolution*, 41(10).

, et al. (2024) Observation of quantum entanglement with top quarks at the ATLAS detector. *Nature*, 633(8030), 542.

Yin DS, et al. (2024) Scaffolding learning: From specific to generic with large language models. *PloS one*, 19(9), e0310409.

Naert T, et al. (2024) Pythia: Non-random DNA repair allows predictable CRISPR/Cas9 integration and gene editing. *bioRxiv : the preprint server for biology*.

Charamis J, et al. (2024) Comparative Genomics Uncovers the Evolutionary Dynamics of Detoxification and Insecticide Target Genes Across 11 Phlebotomine Sand Flies. *Genome biology and evolution*, 16(9).

Kumar S, et al. (2023) Computational Reproducibility of Molecular Phylogenies. *Molecular biology and evolution*, 40(7).

Philip BT, et al. (2023) Fluid sources and overpressures within the central Cascadia Subduction Zone revealed by a warm, high-flux seafloor seep. *Science advances*, 9(4), eadd6688.

Assael Y, et al. (2022) Restoring and attributing ancient texts using deep neural networks. *Nature*, 603(7900), 280.

Haag J, et al. (2022) From Easy to Hopeless-Predicting the Difficulty of Phylogenetic Analyses. *Molecular biology and evolution*, 39(12).

Adam GP, et al. (2022) A novel tool that allows interactive screening of PubMed citations showed promise for the semi-automation of identification of Biomedical Literature. *Journal of clinical epidemiology*, 150, 63.

Otten S, et al. (2021) Event generation and statistical sampling for physics with deep generative models and a density information buffer. *Nature communications*, 12(1), 2985.

Cretin G, et al. (2021) PYTHIA: Deep Learning Approach for Local Protein Conformation Prediction. *International journal of molecular sciences*, 22(16).

Gutierrez-Reyes D, et al. (2021) W-boson production in TMD factorization. *The European physical journal. C, Particles and fields*, 81(5), 418.