

Resource Summary Report

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Pythia

RRID:SCR_004952

Type: Tool

Proper Citation

Pythia (RRID:SCR_004952)

Resource Information

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

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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: 20260829T182213+0000

Ratings and Alerts

No rating or validation information has been found for Pythia.

No alerts have been found for Pythia.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Capraro F, et al. (2026) An intrinsically disordered region mediates RNA-binding selectivity and cellular activities of LARP6. *Nature communications*, 17(1).

Bellemare-Pepin A, et al. (2026) Divergent creativity in humans and large language models. *Scientific reports*, 16(1), 1279.

, et al. (2026) Transforming jet flavour tagging at ATLAS. *Nature communications*, 17(1), 541.

, et al. (2026) Measuring spin correlation between quarks during QCD confinement. *Nature*, 650(8100), 65.

Naert T, et al. (2026) Precise, predictable genome integrations by deep-learning-assisted design of microhomology-based templates. *Nature biotechnology*, 44(6), 1023.

Rizvi SA, et al. (2026) Scaling Large Language Models for Next-Generation Single-Cell Analysis. *bioRxiv : the preprint server for biology*.

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

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

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.

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.

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.

Korbeld KT, et al. (2025) Enriching stabilizing mutations through automated analysis of molecular dynamics simulations using BoostMut. *Protein science : a publication of the*

Protein Society, 34(11), e70334.

, et al. (2025) Temperature measurement of Quark-Gluon plasma at different stages. Nature communications, 16(1), 9098.

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.

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).

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