

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

Cython C-Extensions for Python

RRID:SCR_008466

Type: Tool

Proper Citation

Cython C-Extensions for Python (RRID:SCR_008466)

Resource Information

URL: <http://cython.org/>

Proper Citation: Cython C-Extensions for Python (RRID:SCR_008466)

Description: Cython is a language that makes writing C extensions for the Python language as easy as Python itself. Cython is based on the well-known Pyrex, but supports more cutting edge functionality and optimizations. The Cython language is very close to the Python language, but Cython additionally supports calling C functions and declaring C types on variables and class attributes. This allows the compiler to generate very efficient C code from Cython code. This makes Cython the ideal language for wrapping external C libraries, and for fast C modules that speed up the execution of Python code. Sponsor. Google and Enthought funded Dag Seljebotn to greatly improve Cython integration with NumPy. Kurt Smith and Danilo Freitas were funded through the Google Summer of Code program to work on improved Fortran and C support respectively.

Synonyms: Cython

Resource Type: software resource

Resource Name: Cython C-Extensions for Python

Resource ID: SCR_008466

Alternate IDs: nif-0000-30401

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260829T182316+0000

Ratings and Alerts

No rating or validation information has been found for Cython C-Extensions for Python.

No alerts have been found for Cython C-Extensions for Python.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 140 mentions in open access literature.

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

Siddiqui YS, et al. (2026) Enhanced anaerobic degradation and modeling of raw and treated municipal solid waste. Scientific reports, 16(1).

Meisner J, et al. (2026) Accurate and scalable genome-wide ancestry estimation using haplotype clusters. HGG advances, 7(2), 100561.

Maurer B, et al. (2026) Inkube: an all-in-one solution for neuron culturing, electrophysiology, and fluidic exchange. Lab on a chip, 26(6), 2074.

Hung LH, et al. (2026) Chromap Suite: an open-source single-binary platform for agentic multiomic RNA + ATAC profiling. bioRxiv : the preprint server for biology.

Flight RM, et al. (2026) Information-Content-Informed Kendall-Tau Correlation Methodology: Interpreting Missing Values in Metabolomics as Potentially Useful Information. Metabolites, 16(4).

Pazzaglia A, et al. (2025) Balancing central control and sensory feedback produces adaptable and robust locomotor patterns in a spiking, neuromechanical model of the salamander spinal cord. PLoS computational biology, 21(1), e1012101.

Potgieter L, et al. (2025) Combining sterile insect releases with refuge areas to delay the evolution of resistance to Bt sugarcane: an agent-based modeling approach. Journal of economic entomology, 118(1), 339.

Jiang R, et al. (2025) scCirclehunter delineates ecDNA-containing cells using single-cell ATAC-seq, with a focus on glioblastoma. Cell discovery, 11(1), 98.

Chen H, et al. (2025) A unified analysis of atlas single-cell data. Genome research, 35(5), 1219.

Ishkhanyan H, et al. (2025) PUCHIK: A Python Package To Analyze Molecular Dynamics Simulations of Aspherical Nanoparticles. Journal of chemical information and modeling, 65(4), 1694.

Munro R, et al. (2025) Enhancing nanopore adaptive sampling for PromethION using readfish at scale. Genome research, 35(4), 877.

Kong Q, et al. (2025) A global high-resolution and bias-corrected dataset of CMIP6 projected heat stress metrics. Scientific data, 12(1), 246.

Bocchi G, et al. (2025) GENEOnet: a breakthrough in protein binding pocket detection using group equivariant non-expansive operators. *Scientific reports*, 15(1), 34597.

Gao S, et al. (2025) Optimization of Decision Support Technology for Offshore Oil Condition Monitoring with Carbon Neutrality as the Goal in the Enterprise Development Process. *PloS one*, 20(3), e0319858.

Meisner J, et al. (2025) Leveraging haplotype information in heritability estimation and polygenic prediction. *Nature communications*, 16(1), 126.

Mohseni A, et al. (2025) MSTmap Online: enhanced usability, visualization, and accessibility. *Nucleic acids research*, 53(W1), W427.

Br??ndl B, et al. (2025) Rapid brain tumor classification from sparse epigenomic data. *Nature medicine*, 31(3), 840.

Guan D, et al. (2024) Low-cost quantum mechanical descriptors for data efficient skin sensitization QSAR models. *Current research in toxicology*, 7, 100183.

Mirabello C, et al. (2024) DockQ v2: improved automatic quality measure for protein multimers, nucleic acids, and small molecules. *Bioinformatics (Oxford, England)*, 40(10).

von Wegner F, et al. (2024) Complexity Measures for EEG Microstate Sequences: Concepts and Algorithms. *Brain topography*, 37(2), 296.