Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

NumPy

RRID:SCR_008633
Type: Tool

Proper Citation

NumPy (RRID:SCR_008633)

Resource Information

URL: http://www.numpy.org

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Description: NumPy is the fundamental package needed for scientific computing with Python. It contains among other things: * a powerful N-dimensional array object * sophisticated (broadcasting) functions * tools for integrating C/C and Fortran code * useful linear algebra, Fourier transform, and random number capabilities. Besides its obvious scientific uses, NumPy can also be used as an efficient multi-dimensional container of generic data. Arbitrary data-types can be defined. This allows NumPy to seamlessly and speedily integrate with a wide variety of databases. Sponsored by ENTHOUGHT

Synonyms: NumPy

Resource Type: software resource

Keywords: FASEB list

Resource Name: NumPy

Resource ID: SCR_008633

Alternate IDs: nif-0000-32013

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T195706+0000

Ratings and Alerts

No rating or validation information has been found for NumPy.

No alerts have been found for NumPy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8363 mentions in open access literature.

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

Ayzenberg V, et al. (2026) Functional organization of the human visual system at birth and across late gestation. Neuron.

Borbinha J, et al. (2026) Metabolic reprogramming regulates histone lactylation during zebrafish caudal fin regeneration. iScience, 29(2), 114792.

Zhou X, et al. (2026) Knowledge-enhanced pretraining for vision-language pathology foundation model on cancer diagnosis. Cancer cell, 44(4), 777.

Ghani N, et al. (2026) Active sensing during a visual perceptual decision-making task. iScience, 29(6), 115976.

Chayama Y, et al. (2026) Physiological brain clearance architecture revealed by neuronal protein tracing. Cell, 189(15), 4737.

Fu ZH, et al. (2026) Synthetic rewriting of the IGH locus. Cell genomics, 6(6), 101252.

Perez J MJ, et al. (2026) The mitochondrial unfolded protein response in human microglia disrupts neuronal-glial communication and promotes senescence. Nature neuroscience, 29(8), 1858.

Liang J, et al. (2026) Spatial biomarker discovery via interpretable semantic learning in histopathology. Cancer cell.

Bhattacharya A, et al. (2026) Exosomal misfolded ?1-antitrypsin triggers a cytosolic GRP78-dependent unfolded protein response and pro-survival signaling in pre-metastatic tissues. The Journal of biological chemistry, 302(8), 113282.

Deng M, et al. (2026) Machine learning innovations for reliable gurney energy estimation in energetic materials. iScience, 29(7), 116536.

Shanbhag V, et al. (2026) Tumor CTR1 Expression and Systemic Copper Dynamics Converge on a Copper Axis in High-Grade Triple-Negative Breast Cancer. Cancer research communications, 6(6), 1531.

Peng Y, et al. (2026) Scaffolding human and AI instruction: Neural alignment and learning gains in online education. Neuron.

Feher A, et al. (2026) A kinetic trap mechanism underlies hHv1 inhibition by NZ-58. The Journal of general physiology, 158(4).

Pérez-Verdugo F, et al. (2026) Mechanosensitive feedback organizes cell shape and motion during hindbrain neuropore morphogenesis. Current biology : CB, 36(8), 1903.

Meghdadi B, et al. (2026) Digital twins for in vivo metabolic flux estimations in patients with brain cancer. Cell metabolism, 38(1), 228.

Farsi Z, et al. (2026) Aberrant mRNA splicing and impaired hippocampal neurogenesis in Grin2b mutant mice. iScience, 29(2), 114700.

Huang Q, et al. (2026) Efficient coding in working memory is adapted to the structure of the environment. Cell reports, 45(1), 116861.

Jeong JH, et al. (2026) Population analyses reveal heterogenous encoding in the medial prefrontal cortex during naturalistic foraging. eLife, 13.

Wang P, et al. (2026) Research on features selection of medical diagnostic models based on L-S-ACO algorithm. iScience, 29(3), 115005.

Yasuda K, et al. (2026) RNA-binding protein family diversification correlates with neural complexity across metazoan evolution. iScience, 29(5), 115766.