

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 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: 20260808T185905+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](#) .

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

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

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-glia 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 α 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.