

Resource Summary Report

Generated by [kravitz2](#) on Aug 10, 2026

VORTEX

RRID:SCR_017047

Type: Tool

Proper Citation

VORTEX (RRID:SCR_017047)

Resource Information

URL: <https://github.com/nolanlab/VORTEX>

Proper Citation: VORTEX (RRID:SCR_017047)

Description: Software Java graphical tool for single cell analysis, clustering and visualization. Provides multithreaded implementations of clustering algorithms, including nonparametric density based X shift, Hierarchical clustering, Mean shift and K medoids.

Synonyms: Vortex Clustering Environment

Resource Type: data analysis software, software resource, software application, data processing software

Defining Citation: [PMID:27183440](#)

Keywords: single, cell, analysis, clustering, visualization, nonparametric, density, based, X shift

Availability: Free, Available for download, Freely available

Resource Name: VORTEX

Resource ID: SCR_017047

Alternate URLs: <http://web.stanford.edu/~samusik/vortex/>

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260810T040710+0000

Ratings and Alerts

No rating or validation information has been found for VORTEX.

No alerts have been found for VORTEX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kong XX, et al. (2024) Circulation immune cell landscape in canonical pathogenesis of colorectal adenocarcinoma by CyTOF analysis. *iScience*, 27(3), 109229.

Sankowski R, et al. (2024) Multiomic spatial landscape of innate immune cells at human central nervous system borders. *Nature medicine*, 30(1), 186.

Hickey JW, et al. (2023) Organization of the human intestine at single-cell resolution. *Nature*, 619(7970), 572.

Guldborg SM, et al. (2023) Computational Methods for Single-Cell Proteomics. *Annual review of biomedical data science*, 6, 47.

Goossens P, et al. (2022) Integrating multiplex immunofluorescent and mass spectrometry imaging to map myeloid heterogeneity in its metabolic and cellular context. *Cell metabolism*, 34(8), 1214.

Govek KW, et al. (2021) Single-cell transcriptomic analysis of mIHC images via antigen mapping. *Science advances*, 7(10).

Gonzalez VD, et al. (2021) High-grade serous ovarian tumor cells modulate NK cell function to create an immune-tolerant microenvironment. *Cell reports*, 36(9), 109632.

Kennedy-Darling J, et al. (2021) Highly multiplexed tissue imaging using repeated oligonucleotide exchange reaction. *European journal of immunology*, 51(5), 1262.

Hickey JW, et al. (2021) Strategies for Accurate Cell Type Identification in CODEX Multiplexed Imaging Data. *Frontiers in immunology*, 12, 727626.

Martos SN, et al. (2020) Single-cell analyses identify dysfunctional CD16⁺ CD8 T cells in smokers. *Cell reports. Medicine*, 1(4).

Fernández-Zapata C, et al. (2020) The use and limitations of single-cell mass cytometry for studying human microglia function. *Brain pathology (Zurich, Switzerland)*, 30(6), 1178.

Schürch CM, et al. (2020) Coordinated Cellular Neighborhoods Orchestrate Antitumoral Immunity at the Colorectal Cancer Invasive Front. *Cell*, 182(5), 1341.

Hartmann FJ, et al. (2019) Comprehensive Immune Monitoring of Clinical Trials to Advance Human Immunotherapy. *Cell reports*, 28(3), 819.

Giordani L, et al. (2019) High-Dimensional Single-Cell Cartography Reveals Novel Skeletal Muscle-Resident Cell Populations. *Molecular cell*, 74(3), 609.

Good Z, et al. (2019) Proliferation tracing with single-cell mass cytometry optimizes generation of stem cell memory-like T cells. *Nature biotechnology*, 37(3), 259.

Guan Y, et al. (2018) A robust and tunable mitotic oscillator in artificial cells. *eLife*, 7.

Ehaideb SN, et al. (2016) Mutation of orthologous prickle genes causes a similar epilepsy syndrome in flies and humans. *Annals of clinical and translational neurology*, 3(9), 695.

Paemka L, et al. (2015) Seizures are regulated by ubiquitin-specific peptidase 9 X-linked (USP9X), a de-ubiquitinase. *PLoS genetics*, 11(3), e1005022.

Paemka L, et al. (2013) PRICKLE1 interaction with SYNAPSIN I reveals a role in autism spectrum disorders. *PloS one*, 8(12), e80737.