Greg Finak

List of Publications by Year
in descending order

51 papers	7,360 citations	28 h-index	51 g-index
		186265	182427
60 all docs	60 docs citations	60 times ranked	15011 citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional correlates of malaria in RTS,S/AS01-vaccinated African children: a matched case–control study. ELife, 2022, 11, .	6.0	4
2	Redistribution of <scp>CD8</scp>+ T cell subsets in metastatic renal cell carcinoma patients treated with <scp>anti–PD</scp>–1 therapy. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2022, 101, 597-605.	1.5	2
3	Cytomegalovirus-specific T-cell reconstitution following letermovir prophylaxis after hematopoietic cell transplantation. Blood, 2021, 138, 34-43.	1.4	71
4	New interpretable machine-learning method for single-cell data reveals correlates of clinical response to cancer immunotherapy. Patterns, 2021, 2, 100372.	5.9	22
5	Multidimensional analyses reveal modulation of adaptive and innate immune subsets by tuberculosis vaccines. Communications Biology, 2020, 3, 563.	4.4	14
6	Special Issue on Machine Learning for Single Cell Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 217-218.	1.5	0
7	HIV Skews a Balanced Mtb-Specific Th17 Response in Latent Tuberculosis Subjects to a Pro-inflammatory Profile Independent of Viral Load. Cell Reports, 2020, 33, 108451.	6.4	5
8	BCG revaccination boosts adaptive polyfunctional Th1/Th17 and innate effectors in IGRA+ and IGRA– Indian adults. JCI Insight, 2019, 4, .	5.0	48
9	The Computational article format: Software as a research output. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 1187-1188.	1.5	3
10	<i>CytoML</i> for cross–platform cytometry data sharing. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 1189-1196.	1.5	29
11	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. Gates Open Research, 2018, 2, 31.	1.1	6
12	ggCyto: next generation open-source visualization software for cytometry. Bioinformatics, 2018, 34, 3951-3953.	4.1	64
13	Higher T-Cell Responses Induced by DNA/rAd5 HIV-1 Preventive Vaccine Are Associated With Lower HIV-1 Infection Risk in an Efficacy Trial. Journal of Infectious Diseases, 2017, 215, 1376-1385.	4.0	59
14	DNA Priming Increases Frequency of T-Cell Responses to a Vesicular Stomatitis Virus HIV Vaccine with Specific Enhancement of CD8 ⁺ T-Cell Responses by Interleukin-12 Plasmid DNA. Vaccine Journal, 2017, 24, .	3.1	33
15	Circulating Mycobacterium tuberculosis DosR latency antigen-specific, polyfunctional, regulatory IL10+ Th17 CD4 T-cells differentiate latent from active tuberculosis. Scientific Reports, 2017, 7, 11948.	3.3	37
16	Safety and immunogenicity of a mRNA rabies vaccine in healthy adults: an open-label, non-randomised, prospective, first-in-human phase 1 clinical trial. Lancet, The, 2017, 390, 1511-1520.	13.7	350
17	Combined single-cell quantitation of host and SIV genes and proteins ex vivo reveals host-pathogen interactions in individual cells. PLoS Pathogens, 2017, 13, e1006445.	4.7	25
18	Promises and Pitfalls of High-Throughput Biological Assays. Methods in Molecular Biology, 2016, 1415, 225-243.	0.9	10

#	Article	IF	Citations
19	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 16-21.	1.5	65
20	Automated analysis of flow cytometry data comes of age. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 13-15.	1.5	23
21	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human ImmunoPhenotyping Consortium. Scientific Reports, 2016, 6, 20686.	3.3	240
22	The contribution of cell cycle to heterogeneity in single-cell RNA-seq data. Nature Biotechnology, 2016, 34, 591-593.	17.5	58
23	Reply to The contribution of cell cycle to heterogeneity in single-cell RNA-seq data. Nature Biotechnology, 2016, 34, 593-595.	17.5	2
24	Distinct activation thresholds of human conventional and innate-like memory T cells. JCI Insight, 2016, 1, .	5.0	116
25	Pooled-Peptide Epitope Mapping Strategies Are Efficient and Highly Sensitive: An Evaluation of Methods for Identifying Human T Cell Epitope Specificities in Large-Scale HIV Vaccine Efficacy Trials. PLoS ONE, 2016, 11, e0147812.	2.5	42
26	MAST: a flexible statistical framework for assessing transcriptional changes and characterizing heterogeneity in single-cell RNA sequencing data. Genome Biology, 2015, 16, 278.	8.8	2,047
27	Identification and visualization of multidimensional antigenâ€specific Tâ€cell populations in polychromatic cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 675-682.	1.5	25
28	Stateâ€ofâ€theâ€Art in the Computational Analysis of Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 591-593.	1.5	13
29	COMPASS identifies T-cell subsets correlated with clinical outcomes. Nature Biotechnology, 2015, 33, 610-616.	17.5	232
30	flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. Bioinformatics, 2015, 31, 606-607.	4.1	105
31	Thinking Outside the Gate: Single-Cell Assessments in Multiple Dimensions. Immunity, 2015, 42, 591-592.	14.3	67
32	T Cell Responses against Mycobacterial Lipids and Proteins Are Poorly Correlated in South African Adolescents. Journal of Immunology, 2015, 195, 4595-4603.	0.8	27
33	Abstract P4-04-01: A new breast cancer classification scheme based on novel classes of tumor stroma. , 2015, , .		0
34	OpenCyto: An Open Source Infrastructure for Scalable, Robust, Reproducible, and Automated, End-to-End Flow Cytometry Data Analysis. PLoS Computational Biology, 2014, 10, e1003806.	3.2	185
35	Modeling Bi-modality Improves Characterization of Cell Cycle on Gene Expression in Single Cells. PLoS Computational Biology, 2014, 10, e1003696.	3.2	70
36	Highâ€throughput flow cytometry data normalization for clinical trials. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2014, 85, 277-286.	1.5	40

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37	Mixture models for single-cell assays with applications to vaccine studies. Biostatistics, 2014, 15, 87-101.	1.5	68
38	Critical assessment of automated flow cytometry data analysis techniques. Nature Methods, 2013, 10, 228-238.	19.0	509
39	Highly multiplexed quantitation of gene expression on single cells. Journal of Immunological Methods, 2013, 391, 133-145.	1.4	72
40	Data exploration, quality control and testing in single-cell qPCR-based gene expression experiments. Bioinformatics, 2013, 29, 461-467.	4.1	372
41	Hypoxia promotes ligand-independent EGF receptor signaling via hypoxia-inducible factor–mediated upregulation of caveolin-1. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4892-4897.	7.1	120
42	Gene-expression profiling of microdissected breast cancer microvasculature identifies distinct tumor vascular subtypes. Breast Cancer Research, 2012, 14, R120.	5.0	30
43	QUAliFiER: An automated pipeline for quality assessment of gated flow cytometry data. BMC Bioinformatics, 2012, 13, 252.	2.6	20
44	Optimizing transformations for automated, high throughput analysis of flow cytometry data. BMC Bioinformatics, 2010, 11, 546.	2.6	75
45	In Silico Ascription of Gene Expression Differences to Tumor and Stromal Cells in a Model to Study Impact on Breast Cancer Outcome. PLoS ONE, 2010, 5, e14002.	2.5	23
46	Merging Mixture Components for Cell Population Identification in Flow Cytometry. Advances in Bioinformatics, 2009, 2009, 1-12.	5.7	92
47	Regulation of endocytosis via the oxygen-sensing pathway. Nature Medicine, 2009, 15, 319-324.	30.7	178
48	Stromal signature identifies basal breast cancers. Nature Medicine, 2009, 15, 238-238.	30.7	1
49	Stromal gene expression predicts clinical outcome in breast cancer. Nature Medicine, 2008, 14, 518-527.	30.7	1,497
50	Gene expression signatures of morphologically normal breast tissue identify basal-like tumors. Breast Cancer Research, 2006, 8, R58.	5.0	122
51	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. Gates Open Research, 0, 2, 31.	1.1	4