

# Greg Finak

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49  
papers

4,977  
citations

26  
h-index

60  
g-index

60  
ext. papers

6,428  
ext. citations

12.1  
avg. IF

5.02  
L-index

#	Paper	IF	Citations
49	New interpretable machine-learning method for single-cell data reveals correlates of clinical response to cancer immunotherapy.. <i>Patterns</i> , <b>2021</b> , 2, 100372	5.1	4
48	Cytomegalovirus-specific T-cell reconstitution following letermovir prophylaxis after hematopoietic cell transplantation. <i>Blood</i> , <b>2021</b> , 138, 34-43	2.2	13
47	HIV Skews a Balanced Mtb-Specific Th17 Response in Latent Tuberculosis Subjects to a Pro-inflammatory Profile Independent of Viral Load. <i>Cell Reports</i> , <b>2020</b> , 33, 108451	10.6	4
46	Multidimensional analyses reveal modulation of adaptive and innate immune subsets by tuberculosis vaccines. <i>Communications Biology</i> , <b>2020</b> , 3, 563	6.7	10
45	BCG revaccination boosts adaptive polyfunctional Th1/Th17 and innate effectors in IGRA+ and IGRA- Indian adults. <i>JCI Insight</i> , <b>2019</b> , 4,	9.9	22
44	ggCyto: next generation open-source visualization software for cytometry. <i>Bioinformatics</i> , <b>2018</b> , 34, 3951-3953	29	29
43	The Computational article format: Software as a research output. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2018</b> , 93, 1187-1188	4.6	1
42	CytoML for cross-platform cytometry data sharing. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2018</b> , 93, 1189-1196	4.6	17
41	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. <i>Gates Open Research</i> , <b>2018</b> , 2, 31	2.4	4
40	Higher T-Cell Responses Induced by DNA/rAd5 HIV-1 Preventive Vaccine Are Associated With Lower HIV-1 Infection Risk in an Efficacy Trial. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 215, 1376-1385	7	43
39	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. <i>Vaccine Journal</i> , <b>2017</b> , 24,		24
38	Combined single-cell quantitation of host and SIV genes and proteins ex vivo reveals host-pathogen interactions in individual cells. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006445	7.6	20
37	Circulating Mycobacterium tuberculosis DosR latency antigen-specific, polyfunctional, regulatory IL10 Th17 CD4 T-cells differentiate latent from active tuberculosis. <i>Scientific Reports</i> , <b>2017</b> , 7, 11948	4.9	23
36	Safety and immunogenicity of a mRNA rabies vaccine in healthy adults: an open-label, non-randomised, prospective, first-in-human phase 1 clinical trial. <i>Lancet, The</i> , <b>2017</b> , 390, 1511-1520	40	221
35	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human Immunophenotyping Consortium. <i>Scientific Reports</i> , <b>2016</b> , 6, 20686	4.9	168
34	The contribution of cell cycle to heterogeneity in single-cell RNA-seq data. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 591-3	44.5	43
33	Reply to The contribution of cell cycle to heterogeneity in single-cell RNA-seq data. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 593-5	44.5	

32	Distinct activation thresholds of human conventional and innate-like memory T cells. <i>JCI Insight</i> , <b>2016</b> , 1,	9.9	88
31	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. <i>PLoS ONE</i> , <b>2016</b> , 11, e0147812	3.7	30
30	Promises and Pitfalls of High-Throughput Biological Assays. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1415, 225-43	1.4	7
29	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2016</b> , 89, 16-21	4.6	51
28	Thinking outside the gate: single-cell assessments in multiple dimensions. <i>Immunity</i> , <b>2015</b> , 42, 591-2	32.3	51
27	T Cell Responses against Mycobacterial Lipids and Proteins Are Poorly Correlated in South African Adolescents. <i>Journal of Immunology</i> , <b>2015</b> , 195, 4595-603	5.3	17
26	MAST: a flexible statistical framework for assessing transcriptional changes and characterizing heterogeneity in single-cell RNA sequencing data. <i>Genome Biology</i> , <b>2015</b> , 16, 278	18.3	970
25	Identification and visualization of multidimensional antigen-specific T-cell populations in polychromatic cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2015</b> , 87, 675-82	4.6	22
24	COMPASS identifies T-cell subsets correlated with clinical outcomes. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 610-6	44.5	165
23	flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. <i>Bioinformatics</i> , <b>2015</b> , 31, 606-7	7.2	73
22	Mixture models for single-cell assays with applications to vaccine studies. <i>Biostatistics</i> , <b>2014</b> , 15, 87-101	3.7	52
21	OpenCyto: an open source infrastructure for scalable, robust, reproducible, and automated, end-to-end flow cytometry data analysis. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003806	5	126
20	Modeling bi-modality improves characterization of cell cycle on gene expression in single cells. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003696	5	44
19	High-throughput flow cytometry data normalization for clinical trials. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2014</b> , 85, 277-86	4.6	30
18	Critical assessment of automated flow cytometry data analysis techniques. <i>Nature Methods</i> , <b>2013</b> , 10, 228-38	21.6	392
17	Highly multiplexed quantitation of gene expression on single cells. <i>Journal of Immunological Methods</i> , <b>2013</b> , 391, 133-45	2.5	58
16	Data exploration, quality control and testing in single-cell qPCR-based gene expression experiments. <i>Bioinformatics</i> , <b>2013</b> , 29, 461-7	7.2	241
15	Gene-expression profiling of microdissected breast cancer microvasculature identifies distinct tumor vascular subtypes. <i>Breast Cancer Research</i> , <b>2012</b> , 14, R120	8.3	29

14	QUALiFiER: an automated pipeline for quality assessment of gated flow cytometry data. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 252	3.6	14
13	Hypoxia promotes ligand-independent EGF receptor signaling via hypoxia-inducible factor-mediated upregulation of caveolin-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 4892-7	11.5	101
12	In silico ascription of gene expression differences to tumor and stromal cells in a model to study impact on breast cancer outcome. <i>PLoS ONE</i> , <b>2010</b> , 5, e14002	3.7	20
11	Optimizing transformations for automated, high throughput analysis of flow cytometry data. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 546	3.6	60
10	Regulation of endocytosis via the oxygen-sensing pathway. <i>Nature Medicine</i> , <b>2009</b> , 15, 319-24	50.5	158
9	Stromal signature identifies basal breast cancers. <i>Nature Medicine</i> , <b>2009</b> , 15, 238-238	50.5	1
8	Merging mixture components for cell population identification in flow cytometry. <i>Advances in Bioinformatics</i> , <b>2009</b> , 247646	5.5	72
7	Stromal gene expression predicts clinical outcome in breast cancer. <i>Nature Medicine</i> , <b>2008</b> , 14, 518-27	50.5	1297
6	Gene expression signatures of morphologically normal breast tissue identify basal-like tumors. <i>Breast Cancer Research</i> , <b>2006</b> , 8, R58	8.3	107
5	Bioinformatics Tools for Gene-expression Studies415-432		
4	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. <i>Gates Open Research</i> , <b>2</b> , 31	2.4	3
3	New interpretable machine learning method for single-cell data reveals correlates of clinical response to cancer immunotherapy		6
2	MAST: A flexible statistical framework for assessing transcriptional changes and characterizing heterogeneity in single-cell RNA-seq data.		4
1	A baseline transcriptional signature associates with clinical malaria risk in RTS,S/AS01-vaccinated African children		1