

Raphael Gottardo

List of Publications by Year in descending order

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Version: 2024-02-01

134
papers

22,164
citations

38742

50
h-index

14759

127
g-index

165
all docs

165
docs citations

165
times ranked

32925
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated analysis of plasma and single immune cells uncovers metabolic changes in individuals with COVID-19. <i>Nature Biotechnology</i> , 2022, 40, 110-120.	17.5	81
2	Single-cell immunology of SARS-CoV-2 infection. <i>Nature Biotechnology</i> , 2022, 40, 30-41.	17.5	78
3	Characterization of the cell-mediated immune response to Takeda's live-attenuated tetravalent dengue vaccine in adolescents participating in a phase 2 randomized controlled trial conducted in a dengue-endemic setting. <i>Vaccine</i> , 2022, 40, 1143-1151.	3.8	9
4	Transcriptional correlates of malaria in RTS,S/AS01-vaccinated African children: a matched case-control study. <i>ELife</i> , 2022, 11, .	6.0	4
5	Multiple early factors anticipate post-acute COVID-19 sequelae. <i>Cell</i> , 2022, 185, 881-895.e20.	28.9	605
6	IDEAS: individual level differential expression analysis for single-cell RNA-seq data. <i>Genome Biology</i> , 2022, 23, 33.	8.8	24
7	Targeting an alternate Wilms' tumor antigen 1 peptide bypasses immunoproteasome dependency. <i>Science Translational Medicine</i> , 2022, 14, eabg8070.	12.4	12
8	Global and context-specific transcriptional consequences of oncogenic Fbw7 mutations. <i>ELife</i> , 2022, 11, .	6.0	6
9	Humoral Responses Against Variants of Concern by COVID-19 mRNA Vaccines in Immunocompromised Patients. <i>JAMA Oncology</i> , 2022, 8, e220446.	7.1	48
10	Optimizing clinical dosing of combination broadly neutralizing antibodies for HIV prevention. <i>PLoS Computational Biology</i> , 2022, 18, e1010003.	3.2	8
11	Neoantigen-specific CD4+ T cells in human melanoma have diverse differentiation states and correlate with CD8+ T cell, macrophage, and B cell function. <i>Cancer Cell</i> , 2022, 40, 393-409.e9.	16.8	59
12	Extricating human tumour immune alterations from tissue inflammation. <i>Nature</i> , 2022, 605, 728-735.	27.8	56
13	Monocyte Transcriptional Responses to Mycobacterium tuberculosis Associate with Resistance to Tuberculin Skin Test and Interferon Gamma Release Assay Conversion. <i>MSphere</i> , 2022, 7, .	2.9	8
14	Th2-Biased Transcriptional Profile Predicts HIV Envelope-Specific Polyfunctional CD4+ T Cells That Correlated with Reduced Risk of Infection in RV144 Trial. <i>Journal of Immunology</i> , 2022, 209, 526-534.	0.8	3
15	Development of a clinically relevant ovarian cancer model incorporating surgical cytoreduction to evaluate treatment of micro-metastatic disease. <i>Gynecologic Oncology</i> , 2021, 160, 427-437.	1.4	4
16	Optimal therapeutic targeting by HDAC inhibition in biopsy-derived treatment-naïve diffuse midline glioma models. <i>Neuro-Oncology</i> , 2021, 23, 376-386.	1.2	43
17	Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression. <i>Nature Biotechnology</i> , 2021, 39, 819-824.	17.5	121
18	The human memory T cell compartment changes across tissues of the female reproductive tract. <i>Mucosal Immunology</i> , 2021, 14, 862-872.	6.0	19

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19	CD101 genetic variants modify regulatory and conventional T cell phenotypes and functions. <i>Cell Reports Medicine</i> , 2021, 2, 100322.	6.5	5
20	Integrated analysis of multimodal single-cell data. <i>Cell</i> , 2021, 184, 3573-3587.e29.	28.9	5,912
21	Spatial transcriptomics at subspot resolution with BayesSpace. <i>Nature Biotechnology</i> , 2021, 39, 1375-1384.	17.5	320
22	Comprehensive Data Integration Approach to Assess Immune Responses and Correlates of RTS,S/AS01-Mediated Protection From Malaria Infection in Controlled Human Malaria Infection Trials. <i>Frontiers in Big Data</i> , 2021, 4, 672460.	2.9	8
23	Safety and immunogenicity of an HIV-1 gp120-CD4 chimeric subunit vaccine in a phase 1a randomized controlled trial. <i>Vaccine</i> , 2021, 39, 3879-3891.	3.8	3
24	Monocyte metabolic transcriptional programs associate with resistance to tuberculin skin test/interferon- γ release assay conversion. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	13
25	Spatial UMAP and Image Cytometry for Topographic Immuno-oncology Biomarker Discovery. <i>Cancer Immunology Research</i> , 2021, 9, 1262-1269.	3.4	8
26	Comparative analysis of TCR and CAR signaling informs CAR designs with superior antigen sensitivity and in vivo function. <i>Science Signaling</i> , 2021, 14, .	3.6	67
27	High-throughput single-cell quantification of hundreds of proteins using conventional flow cytometry and machine learning. <i>Science Advances</i> , 2021, 7, eabg0505.	10.3	39
28	New interpretable machine-learning method for single-cell data reveals correlates of clinical response to cancer immunotherapy. <i>Patterns</i> , 2021, 2, 100372.	5.9	22
29	Long-Term Follow-up and Single-Cell Multiomics Characteristics of Infusion Products in Patients with Chronic Lymphocytic Leukemia Treated with CD19 CAR-T Cells. <i>Blood</i> , 2021, 138, 1749-1749.	1.4	1
30	A regulatory T cell signature distinguishes the immune landscape of COVID-19 patients from those with other respiratory infections. <i>Science Advances</i> , 2021, 7, eabj0274.	10.3	28
31	Clonal kinetics and single-cell transcriptional profiling of CAR-T cells in patients undergoing CD19 CAR-T immunotherapy. <i>Nature Communications</i> , 2020, 11, 219.	12.8	167
32	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
33	A Potent Anti-Malarial Human Monoclonal Antibody Targets Circumsporozoite Protein Minor Repeats and Neutralizes Sporozoites in the Liver. <i>Immunity</i> , 2020, 53, 733-744.e8.	14.3	99
34	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. <i>Cell</i> , 2020, 183, 1479-1495.e20.	28.9	449
35	Aggregating transcript-level analyses for single-cell differential gene expression. <i>Nature Methods</i> , 2020, 17, 583-585.	19.0	3
36	3M-052, a synthetic TLR-7/8 agonist, induces durable HIV-1 envelope-specific plasma cells and humoral immunity in nonhuman primates. <i>Science Immunology</i> , 2020, 5, .	11.9	90

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37	Optimal priming of poxvirus vector (NYVAC)-based HIV vaccine regimens for T cell responses requires three DNA injections. Results of the randomized multicentre EV03/ANRS VAC20 Phase I/II Trial. PLoS Pathogens, 2020, 16, e1008522.	4.7	11
38	A Targeted Multi-omic Analysis Approach Measures Protein Expression and Low-Abundance Transcripts on the Single-Cell Level. Cell Reports, 2020, 31, 107499.	6.4	80
39	Graphical models for zero-inflated single cell gene expression. Annals of Applied Statistics, 2019, 13, 848-873.	1.1	19
40	Engineered Adoptive T-cell Therapy Prolongs Survival in a Preclinical Model of Advanced-Stage Ovarian Cancer. Cancer Immunology Research, 2019, 7, 1412-1425.	3.4	26
41	T cell receptor gene therapy targeting WT1 prevents acute myeloid leukemia relapse post-transplant. Nature Medicine, 2019, 25, 1064-1072.	30.7	226
42	Tumor suppression of novel anti-PD-1 antibodies mediated through CD28 costimulatory pathway. Journal of Experimental Medicine, 2019, 216, 1525-1541.	8.5	23
43	Integrated systems approach defines the antiviral pathways conferring protection by the RV144 HIV vaccine. Nature Communications, 2019, 10, 863.	12.8	27
44	Recombinant HIV-1 vaccine candidates based on replication-defective flavivirus vector. Scientific Reports, 2019, 9, 20005.	3.3	10
45	Priming with a Potent HIV-1 DNA Vaccine Frames the Quality of Immune Responses prior to a Poxvirus and Protein Boost. Journal of Virology, 2019, 93, .	3.4	25
46	Replication-Competent NYVAC-KC Yields Improved Immunogenicity to HIV-1 Antigens in Rhesus Macaques Compared to Nonreplicating NYVAC. Journal of Virology, 2019, 93, .	3.4	13
47	A composite immune signature parallels disease progression across T1D subjects. JCI Insight, 2019, 4, .	5.0	15
48	BCG revaccination boosts adaptive polyfunctional Th1/Th17 and innate effectors in IGRA+ and IGRA- Indian adults. JCI Insight, 2019, 4, .	5.0	48
49	Antibody Fc effector functions and IgG3 associate with decreased HIV-1 risk. Journal of Clinical Investigation, 2019, 129, 4838-4849.	8.2	95
50	<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
51	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. Gates Open Research, 2018, 2, 31.	1.1	6
52	Generation and characterization of a bivalent protein boost for future clinical trials: HIV-1 subtypes CR01_AE and B gp120 antigens with a potent adjuvant. PLoS ONE, 2018, 13, e0194266.	2.5	14
53	cytometree: A binary tree algorithm for automatic gating in cytometry analysis. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 1132-1140.	1.5	21
54	Acquired cancer resistance to combination immunotherapy from transcriptional loss of class I HLA. Nature Communications, 2018, 9, 3868.	12.8	211

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55	Whole blood transcriptome changes following controlled human malaria infection in malaria pre-exposed volunteers correlate with parasite prepatent period. <i>PLoS ONE</i> , 2018, 13, e0199392.	2.5	18
56	T Cell-Dependent Affinity Maturation and Innate Immune Pathways Differentially Drive Autoreactive B Cell Responses in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2018, 70, 1732-1744.	5.6	65
57	Effect of Adding Motolimod to Standard Combination Chemotherapy and Cetuximab Treatment of Patients With Squamous Cell Carcinoma of the Head and Neck. <i>JAMA Oncology</i> , 2018, 4, 1583.	7.1	84
58	Phosphoproteomic analysis of chimeric antigen receptor signaling reveals kinetic and quantitative differences that affect cell function. <i>Science Signaling</i> , 2018, 11, .	3.6	323
59	ggCyto: next generation open-source visualization software for cytometry. <i>Bioinformatics</i> , 2018, 34, 3951-3953.	4.1	64
60	Human MAIT cells exit peripheral tissues and recirculate via lymph in steady state conditions. <i>JCI Insight</i> , 2018, 3, .	5.0	72
61	Clonal Kinetics and Single Cell Transcriptional Profiling of Adoptively Transferred CD19 CAR-T Cells. <i>Blood</i> , 2018, 132, 702-702.	1.4	1
62	Superiority in Rhesus Macaques of Targeting HIV-1 Env gp140 to CD40 versus LOX-1 in Combination with Replication-Competent NYVAC-KC for Induction of Env-Specific Antibody and T Cell Responses. <i>Journal of Virology</i> , 2017, 91, .	3.4	29
63	A phase 2, randomized, double-blind, placebo-controlled study of chemo-immunotherapy combination using motolimod with pegylated liposomal doxorubicin in recurrent or persistent ovarian cancer: a Gynecologic Oncology Group partners study. <i>Annals of Oncology</i> , 2017, 28, 996-1004.	1.2	67
64	A Functional Toll-Interacting Protein Variant Is Associated with <i>Bacillus Calmette-Guérin</i> -Specific Immune Responses and Tuberculosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 502-511.	5.6	38
65	Single-Cell RNA Sequencing Reveals Expanded Clones of Islet Antigen-Reactive CD4+ T Cells in Peripheral Blood of Subjects with Type 1 Diabetes. <i>Journal of Immunology</i> , 2017, 199, 323-335.	0.8	62
66	Controlled Human Malaria Infection Leads to Long-Lasting Changes in Innate and Innate-like Lymphocyte Populations. <i>Journal of Immunology</i> , 2017, 199, 107-118.	0.8	45
67	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> , 2017, 215, 1376-1385.	4.0	59
68	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> , 2017, 24, .	3.1	33
69	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology</i> , 2017, 2, .	11.9	122
70	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> , 2017, 390, 1511-1520.	13.7	350
71	Panels of HIV-1 Subtype C Env Reference Strains for Standardized Neutralization Assessments. <i>Journal of Virology</i> , 2017, 91, .	3.4	23
72	Combined single-cell quantitation of host and SIV genes and proteins ex vivo reveals host-pathogen interactions in individual cells. <i>PLoS Pathogens</i> , 2017, 13, e1006445.	4.7	25

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73	Sieve analysis of breakthrough HIV-1 sequences in HVTN 505 identifies vaccine pressure targeting the CD4 binding site of Env-gp120. PLoS ONE, 2017, 12, e0185959.	2.5	27
74	Promises and Pitfalls of High-Throughput Biological Assays. Methods in Molecular Biology, 2016, 1415, 225-243.	0.9	10
75	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
76	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
77	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human ImmunoPhenotyping Consortium. Scientific Reports, 2016, 6, 20686.	3.3	240
78	The contribution of cell cycle to heterogeneity in single-cell RNA-seq data. Nature Biotechnology, 2016, 34, 591-593.	17.5	58
79	Reply to The contribution of cell cycle to heterogeneity in single-cell RNA-seq data. Nature Biotechnology, 2016, 34, 593-595.	17.5	2
80	Bayesian Hierarchical Modeling for Subject-Level Response Classification in Peptide Microarray Immunoassays. Biometrics, 2016, 72, 1206-1215.	1.4	4
81	Potential To Streamline Heterologous DNA Prime and NYVAC/Protein Boost HIV Vaccine Regimens in Rhesus Macaques by Employing Improved Antigens. Journal of Virology, 2016, 90, 4133-4149.	3.4	22
82	Analyzing Peptide Microarray Data with the R pepStat Package. Methods in Molecular Biology, 2016, 1352, 127-142.	0.9	4
83	Distinct activation thresholds of human conventional and innate-like memory T cells. JCI Insight, 2016, 1, .	5.0	116
84	Targeting HIV-1 Env gp140 to LOX-1 Elicits Immune Responses in Rhesus Macaques. PLoS ONE, 2016, 11, e0153484.	2.5	20
85	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
86	Identification and visualization of multidimensional antigen-specific T 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
87	State-of-the-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
88	COMPASS identifies T-cell subsets correlated with clinical outcomes. Nature Biotechnology, 2015, 33, 610-616.	17.5	232
89	Late-Stage Cancer Patients Remain Highly Responsive to Immune Activation by the Selective TLR8 Agonist Motolimod (VTX-2337). Clinical Cancer Research, 2015, 21, 5445-5452.	7.0	33
90	flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. Bioinformatics, 2015, 31, 606-607.	4.1	105

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91	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
92	Notch-mediated expansion of cord blood progenitors: maintenance of transcriptional and epigenetic fidelity. <i>Leukemia</i> , 2015, 29, 1948-1951.	7.2	9
93	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. <i>PLoS Computational Biology</i> , 2015, 11, e1003973.	3.2	51
94	T Cell Responses against Mycobacterial Lipids and Proteins Are Poorly Correlated in South African Adolescents. <i>Journal of Immunology</i> , 2015, 195, 4595-4603.	0.8	27
95	flowCL: ontology-based cell population labelling in flow cytometry. <i>Bioinformatics</i> , 2015, 31, 1337-1339.	4.1	25
96	The Inner Foreskin of Healthy Males at Risk of HIV Infection Harbors Epithelial CD4+ CCR5+ Cells and Has Features of an Inflamed Epidermal Barrier. <i>PLoS ONE</i> , 2014, 9, e108954.	2.5	27
97	OpenCyto: An Open Source Infrastructure for Scalable, Robust, Reproducible, and Automated, End-to-End Flow Cytometry Data Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003806.	3.2	185
98	Modeling Bi-modality Improves Characterization of Cell Cycle on Gene Expression in Single Cells. <i>PLoS Computational Biology</i> , 2014, 10, e1003696.	3.2	70
99	Vaccine-induced Human Antibodies Specific for the Third Variable Region of HIV-1 gp120 Impose Immune Pressure on Infecting Viruses. <i>EBioMedicine</i> , 2014, 1, 37-45.	6.1	55
100	High-throughput flow cytometry data normalization for clinical trials. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 277-286.	1.5	40
101	Computational resources for high-dimensional immune analysis from the Human Immunology Project Consortium. <i>Nature Biotechnology</i> , 2014, 32, 146-148.	17.5	65
102	Immunological and virological mechanisms of vaccine-mediated protection against SIV and HIV. <i>Nature</i> , 2014, 505, 502-508.	27.8	140
103	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A25-A26.	1.1	0
104	Global Panel of HIV-1 Env Reference Strains for Standardized Assessments of Vaccine-Elicited Neutralizing Antibodies. <i>Journal of Virology</i> , 2014, 88, 2489-2507.	3.4	274
105	Analysis of HLA A*02 Association with Vaccine Efficacy in the RV144 HIV-1 Vaccine Trial. <i>Journal of Virology</i> , 2014, 88, 8242-8255.	3.4	55
106	Exosomes in human semen carry a distinctive repertoire of small non-coding RNAs with potential regulatory functions. <i>Nucleic Acids Research</i> , 2014, 42, 7290-7304.	14.5	486
107	Mixture models for single-cell assays with applications to vaccine studies. <i>Biostatistics</i> , 2014, 15, 87-101.	1.5	68
108	FCGR2C polymorphisms associate with HIV-1 vaccine protection in RV144 trial. <i>Journal of Clinical Investigation</i> , 2014, 124, 3879-3890.	8.2	99

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109	Identification and analysis of murine pancreatic islet enhancers. <i>Diabetologia</i> , 2013, 56, 542-552.	6.3	55
110	A computational framework for the analysis of peptide microarray antibody binding data with application to HIV vaccine profiling. <i>Journal of Immunological Methods</i> , 2013, 395, 1-13.	1.4	19
111	Critical assessment of automated flow cytometry data analysis techniques. <i>Nature Methods</i> , 2013, 10, 228-238.	19.0	509
112	Highly multiplexed quantitation of gene expression on single cells. <i>Journal of Immunological Methods</i> , 2013, 391, 133-145.	1.4	72
113	Comparability and reproducibility of biomedical data. <i>Briefings in Bioinformatics</i> , 2013, 14, 391-401.	6.5	40
114	Data exploration, quality control and testing in single-cell qPCR-based gene expression experiments. <i>Bioinformatics</i> , 2013, 29, 461-467.	4.1	372
115	Analysis of V2 Antibody Responses Induced in Vaccinees in the ALVAC/AIDS VAX HIV-1 Vaccine Efficacy Trial. <i>PLoS ONE</i> , 2013, 8, e53629.	2.5	165
116	Plasma IgG to Linear Epitopes in the V2 and V3 Regions of HIV-1 gp120 Correlate with a Reduced Risk of Infection in the RV144 Vaccine Efficacy Trial. <i>PLoS ONE</i> , 2013, 8, e75665.	2.5	214
117	The Thai Phase III HIV Type 1 Vaccine Trial (RV144) Regimen Induces Antibodies That Target Conserved Regions Within the V2 Loop of gp120. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1444-1457.	1.1	191
118	B Cells With High Side Scatter Parameter by Flow Cytometry Correlate With Inferior Survival in Diffuse Large B-Cell Lymphoma. <i>American Journal of Clinical Pathology</i> , 2012, 137, 805-814.	0.7	12
119	Probabilistic Inference for Nucleosome Positioning with MNase-Based or Sonicated Short-Read Data. <i>PLoS ONE</i> , 2012, 7, e32095.	2.5	20
120	On-line changepoint detection and parameter estimation with application to genomic data. <i>Statistics and Computing</i> , 2012, 22, 579-595.	1.5	23
121	PICS: Probabilistic Inference for ChIP-seq. <i>Biometrics</i> , 2011, 67, 151-163.	1.4	62
122	An Integrated Pipeline for the Genome-Wide Analysis of Transcription Factor Binding Sites from ChIP-Seq. <i>PLoS ONE</i> , 2011, 6, e16432.	2.5	39
123	Merging Mixture Components for Cell Population Identification in Flow Cytometry. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-12.	5.7	92
124	Bayesian robust transformation and variable selection: A unified approach. <i>Canadian Journal of Statistics</i> , 2009, 37, 361-380.	0.9	19
125	Automated gating of flow cytometry data via robust model-based clustering. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008, 73A, 321-332.	1.5	224
126	A Flexible and Powerful Bayesian Hierarchical Model for ChIP-Chip Experiments. <i>Biometrics</i> , 2008, 64, 468-478.	1.4	31

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127	Markov Chain Monte Carlo With Mixtures of Mutually Singular Distributions. Journal of Computational and Graphical Statistics, 2008, 17, 949-975.	1.7	23
128	Bayesian Robust Inference for Differential Gene Expression in Microarrays with Multiple Samples. Biometrics, 2006, 62, 10-18.	1.4	83
129	Quality Control and Robust Estimation for cDNA Microarrays With Replicates. Journal of the American Statistical Association, 2006, 101, 30-40.	3.1	9
130	Probabilistic segmentation and intensity estimation for microarray images. Biostatistics, 2006, 7, 85-99.	1.5	24
131	Model-based analysis of tiling-arrays for ChIP-chip. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12457-12462.	7.1	390
132	Evaluation of the host transcriptional response to human cytomegalovirus infection. Physiological Genomics, 2004, 18, 51-62.	2.3	35
133	Statistical analysis of microarray data: a Bayesian approach. Biostatistics, 2003, 4, 597-620.	1.5	58
134	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. Gates Open Research, 0, 2, 31.	1.1	4