

Susan P Holmes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3452993/publications.pdf>

Version: 2024-02-01

176
papers

64,668
citations

22099

59
h-index

6113

159
g-index

212
all docs

212
docs citations

212
times ranked

56343
citing authors

#	ARTICLE	IF	CITATIONS
1	DADA2: High-resolution sample inference from Illumina amplicon data. <i>Nature Methods</i> , 2016, 13, 581-583.	9.0	18,691
2	phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. <i>PLoS ONE</i> , 2013, 8, e61217.	1.1	13,960
3	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
4	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. <i>ISME Journal</i> , 2017, 11, 2639-2643.	4.4	2,357
5	Waste Not, Want Not: Why Rarefying Microbiome Data Is Inadmissible. <i>PLoS Computational Biology</i> , 2014, 10, e1003531.	1.5	2,343
6	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. <i>Microbiome</i> , 2018, 6, 226.	4.9	1,729
7	Temporal and spatial variation of the human microbiota during pregnancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11060-11065.	3.3	876
8	Bioconductor Workflow for Microbiome Data Analysis: from raw reads to community analyses. <i>F1000Research</i> , 2016, 5, 1492.	0.8	664
9	Variability in the analysis of a single neuroimaging dataset by many teams. <i>Nature</i> , 2020, 582, 84-88.	13.7	634
10	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
11	structSSI : Simultaneous and Selective Inference for Grouped or Hierarchically Structured Data. <i>Journal of Statistical Software</i> , 2014, 59, 1-21.	1.8	488
12	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. <i>F1000Research</i> , 2016, 5, 1492.	0.8	466
13	Geometry of the Space of Phylogenetic Trees. <i>Advances in Applied Mathematics</i> , 2001, 27, 733-767.	0.4	400
14	Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle. <i>Microbiome</i> , 2016, 4, 15.	4.9	348
15	Colonic Contribution to Uremic Solutes. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 1769-1776.	3.0	340
16	Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9966-9971.	3.3	297
17	Nasal Microenvironments and Interspecific Interactions Influence Nasal Microbiota Complexity and <i>S. Aureus</i> Carriage. <i>Cell Host and Microbe</i> , 2013, 14, 631-640.	5.1	294
18	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825.	1.6	261

#	ARTICLE	IF	CITATIONS
19	Impaired interferon signaling is a common immune defect in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9010-9015.	3.3	240
20	Genetically dictated change in host mucus carbohydrate landscape exerts a diet-dependent effect on the gut microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17059-17064.	3.3	237
21	Sequential Monte Carlo Methods for Statistical Analysis of Tables. <i>Journal of the American Statistical Association</i> , 2005, 100, 109-120.	1.8	231
22	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. <i>Nature Communications</i> , 2016, 7, 10516.	5.8	196
23	Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis. <i>JCI Insight</i> , 2020, 5, .	2.3	196
24	Ultra-Deep Pyrosequencing of Hepatitis B Virus Quasispecies from Nucleoside and Nucleotide Reverse-Transcriptase Inhibitor (NRTI)-Treated Patients and NRTI-Naive Patients. <i>Journal of Infectious Diseases</i> , 2009, 199, 1275-1285.	1.9	195
25	Profile of Immune Cells in Axillary Lymph Nodes Predicts Disease-Free Survival in Breast Cancer. <i>PLoS Medicine</i> , 2005, 2, e284.	3.9	182
26	Human NK cell repertoire diversity reflects immune experience and correlates with viral susceptibility. <i>Science Translational Medicine</i> , 2015, 7, 297ra115.	5.8	177
27	Analysis of a nonreversible Markov chain sampler. <i>Annals of Applied Probability</i> , 2000, 10, 726.	0.6	176
28	Ten quick tips for effective dimensionality reduction. <i>PLoS Computational Biology</i> , 2019, 15, e1006907.	1.5	174
29	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
30	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring Dehalococoides. <i>PLoS Genetics</i> , 2009, 5, e1000714.	1.5	162
31	Elements of Large-Sample Theory. , 2012, , 1111-1112.		151
32	Gene expression network analysis and applications to immunology. <i>Bioinformatics</i> , 2007, 23, 850-858.	1.8	149
33	Bootstrapping Phylogenetic Trees: Theory and Methods. <i>Statistical Science</i> , 2003, 18, 241.	1.6	143
34	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	139
35	Dynamical Bias in the Coin Toss. <i>SIAM Review</i> , 2007, 49, 211-235.	4.2	137
36	The effect of individual variation on the structure and function of interaction networks in harvester ants. <i>Journal of the Royal Society Interface</i> , 2011, 8, 1562-1573.	1.5	134

#	ARTICLE	IF	CITATIONS
37	Shiny-phyloseq: Web application for interactive microbiome analysis with provenance tracking. <i>Bioinformatics</i> , 2015, 31, 282-283.	1.8	131
38	Gut microbiome transition across a lifestyle gradient in Himalaya. <i>PLoS Biology</i> , 2018, 16, e2005396.	2.6	128
39	Down-Regulation of the Interferon Signaling Pathway in T Lymphocytes from Patients with Metastatic Melanoma. <i>PLoS Medicine</i> , 2007, 4, e176.	3.9	124
40	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	2.4	117
41	Harvester ants use interactions to regulate forager activation and availability. <i>Animal Behaviour</i> , 2013, 86, 197-207.	0.8	105
42	Natural variation of HIV-1 group M integrase: Implications for a new class of antiretroviral inhibitors. <i>Retrovirology</i> , 2008, 5, 74.	0.9	102
43	Enhanced natural killer-cell and T-cell responses to influenza A virus during pregnancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14506-14511.	3.3	95
44	HIV-1 Subtype B Protease and Reverse Transcriptase Amino Acid Covariation. <i>PLoS Computational Biology</i> , 2007, 3, e87.	1.5	92
45	Detection of Cytomegalovirus Drug Resistance Mutations by Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3700-3710.	1.8	91
46	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. <i>Nature Communications</i> , 2018, 9, 681.	5.8	87
47	Denoising PCR-amplified metagenome data. <i>BMC Bioinformatics</i> , 2012, 13, 283.	1.2	85
48	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. <i>PLoS ONE</i> , 2015, 10, e0142825.	1.1	84
49	Phyloseq: a bioconductor package for handling and analysis of high-throughput phylogenetic sequence data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 235-46.	0.7	84
50	Diversity and Recognition Efficiency of T Cell Responses to Cancer. <i>PLoS Medicine</i> , 2004, 1, e28.	3.9	82
51	Horseshoes in multidimensional scaling and local kernel methods. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	81
52	Error Distribution for Gene Expression Data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article16.	0.2	80
53	Gene expression diversity among Mycobacterium tuberculosis clinical isolates. <i>Microbiology (United Kingdom)</i> 151:1078-1087 (2007)	0.7	78
54	Addressing geographical data errors in a classification tree for soil unit prediction. <i>International Journal of Geographical Information Science</i> , 1997, 11, 183-198.	2.2	77

#	ARTICLE	IF	CITATIONS
55	Minority Human Immunodeficiency Virus Type 1 Variants in Antiretroviral-Naive Persons with Reverse Transcriptase Codon 215 Revertant Mutations. <i>Journal of Virology</i> , 2008, 82, 10747-10755.	1.5	72
56	HIV-1 Protease, Reverse Transcriptase, and Integrase Variation. <i>Journal of Virology</i> , 2016, 90, 6058-6070.	1.5	72
57	Colony variation in the collective regulation of foraging by harvester ants. <i>Behavioral Ecology</i> , 2011, 22, 429-435.	1.0	71
58	Tracking network dynamics: A survey using graph distances. <i>Annals of Applied Statistics</i> , 2018, 12, .	0.5	70
59	More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. <i>ELife</i> , 2016, 5, .	2.8	70
60	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. <i>Microbiome</i> , 2019, 7, 131.	4.9	65
61	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. <i>PLoS Computational Biology</i> , 2017, 13, e1005706.	1.5	64
62	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. <i>Science</i> , 2022, 376, 1220-1223.	6.0	63
63	Memory T cells have gene expression patterns intermediate between naive and effector. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5519-5523.	3.3	62
64	Forager activation and food availability in harvester ants. <i>Animal Behaviour</i> , 2006, 71, 815-822.	0.8	60
65	Nest site and weather affect the personality of harvester ant colonies. <i>Behavioral Ecology</i> , 2012, 23, 1022-1029.	1.0	60
66	Site-Specific Mobilization of Vinyl Chloride Respiration Islands by a Mechanism Common in <i>Dehalococcoides</i> . <i>BMC Genomics</i> , 2011, 12, 287.	1.2	55
67	The short-term regulation of foraging in harvester ants. <i>Behavioral Ecology</i> , 2008, 19, 217-222.	1.0	53
68	Constrained patterns of covariation and clustering of HIV-1 non-nucleoside reverse transcriptase inhibitor resistance mutations. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1477-1485.	1.3	52
69	Measuring multivariate association and beyond. <i>Statistics Surveys</i> , 2016, 10, 132-167.	7.3	52
70	Latent variable modeling for the microbiome. <i>Biostatistics</i> , 2019, 20, 599-614.	0.9	51
71	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020, 82, 26-41.	6.3	50
72	Genomic interrogation of ancestral <i>Mycobacterium tuberculosis</i> from south India. <i>Infection, Genetics and Evolution</i> , 2008, 8, 474-483.	1.0	48

#	ARTICLE	IF	CITATIONS
73	PRC2/EED-EZH2 Complex Is Up-Regulated in Breast Cancer Lymph Node Metastasis Compared to Primary Tumor and Correlates with Tumor Proliferation In Situ. PLoS ONE, 2012, 7, e51239.	1.1	48
74	Threshold Graph Limits and Random Threshold Graphs. Internet Mathematics, 2008, 5, 267-320.	0.7	46
75	Use of exchangeable pairs in the analysis of simulations. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 1-25.	1.0	46
76	PHYLOSEQ: A BIOCONDUCTOR PACKAGE FOR HANDLING AND ANALYSIS OF HIGH-THROUGHPUT PHYLOGENETIC SEQUENCE DATA. , 2011, , .		45
77	Quantitative, Architectural Analysis of Immune Cell Subsets in Tumor-Draining Lymph Nodes from Breast Cancer Patients and Healthy Lymph Nodes. PLoS ONE, 2010, 5, e12420.	1.1	43
78	Statistics for phylogenetic trees. Theoretical Population Biology, 2003, 63, 17-32.	0.5	42
79	Differential Induction of IFN- γ and Modulation of CD112 and CD54 Expression Govern the Magnitude of NK Cell IFN- γ Response to Influenza A Viruses. Journal of Immunology, 2018, 201, 2117-2131.	0.4	42
80	Sampling from a Manifold. Institute of Mathematical Statistics Collections, 2013, , 102-125.	0.3	41
81	Gray codes for randomization procedures. Statistics and Computing, 1994, 4, 287-302.	0.8	40
82	Computational Tools for Evaluating Phylogenetic and Hierarchical Clustering Trees. Journal of Computational and Graphical Statistics, 2012, 21, 581-599.	0.9	40
83	Mass Cytometry Analytical Approaches Reveal Cytokine-Induced Changes in Natural Killer Cells. Cytometry Part B - Clinical Cytometry, 2017, 92, 57-67.	0.7	40
84	TIGIT is upregulated by HIV-1 infection and marks a highly functional adaptive and mature subset of natural killer cells. Aids, 2020, 34, 801-813.	1.0	40
85	Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology. Journal of the American Statistical Association, 1999, 94, 989.	1.8	39
86	Correlations among quality parameters of peach fruit. Journal of the Science of Food and Agriculture, 1994, 66, 241-245.	1.7	37
87	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. Frontiers in Immunology, 2019, 10, 2469.	2.2	36
88	Nonpolymorphic Human Immunodeficiency Virus Type 1 Protease and Reverse Transcriptase Treatment-Selected Mutations. Antimicrobial Agents and Chemotherapy, 2009, 53, 4869-4878.	1.4	32
89	Nucleoside Reverse Transcriptase Inhibitor Resistance Mutations Associated with First-Line Stavudine-Containing Antiretroviral Therapy: Programmatic Implications for Countries Phasing Out Stavudine. Journal of Infectious Diseases, 2013, 207, S70-S77.	1.9	30
90	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. Journal of the American Statistical Association, 2017, 112, 1430-1442.	1.8	30

#	ARTICLE	IF	CITATIONS
91	Random Walks on Trees and Matchings. <i>Electronic Journal of Probability</i> , 2002, 7, .	0.5	30
92	COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES. , 2011, , .		29
93	Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon. <i>Nature Communications</i> , 2020, 11, 3772.	5.8	29
94	Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration. <i>EBioMedicine</i> , 2017, 18, 225-235.	2.7	28
95	Prevalence of Drug-Resistant Minority Variants in Untreated HIV-1â€“Infected Individuals With and Those Without Transmitted Drug Resistance Detected by Sanger Sequencing. <i>Journal of Infectious Diseases</i> , 2017, 216, 387-391.	1.9	28
96	Statistical problems involving permutations with restricted positions. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 2001, , 195-222.	1.0	26
97	Unusual Codon Bias in Vinyl Chloride Reductase Genes of Dehalococcoides Species. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2744-2747.	1.4	25
98	Microarray Analysis Reveals Differences in Gene Expression of Circulating CD8+ T Cells in Melanoma Patients and Healthy Donors. <i>Cancer Research</i> , 2004, 64, 3661-3667.	0.4	24
99	Multivariate data analysis: The French way. , 2008, , 219-233.		24
100	Low-Level Persistence of Drug Resistance Mutations in Hepatitis B Virus-Infected Subjects with a Past History of Lamivudine Treatment. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 343-349.	1.4	24
101	Comparisons of distance methods for combining covariates and abundances in microbiome studies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 213-24.	0.7	24
102	Prototypical Recombinant Multi-Protease-Inhibitor-Resistant Infectious Molecular Clones of Human Immunodeficiency Virus Type 1. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 4290-4299.	1.4	23
103	Effect of Water, Sanitation, Handwashing, and Nutrition Interventions on Enteropathogens in Children 14 Months Old: A Cluster-Randomized Controlled Trial in Rural Bangladesh. <i>Journal of Infectious Diseases</i> , 2023, 227, 434-447.	1.9	23
104	Phylogenies: An Overview. <i>The IMA Volumes in Mathematics and Its Applications</i> , 1999, , 81-118.	0.5	23
105	The duality diagram in data analysis: Examples of modern applications. <i>Annals of Applied Statistics</i> , 2011, 5, 2266-2277.	0.5	22
106	Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios. <i>Journal of Applied Statistics</i> , 2023, 50, 2518-2546.	0.6	22
107	Gut microbiota plasticity is correlated with sustained weight loss on a low-carb or low-fat dietary intervention. <i>Scientific Reports</i> , 2020, 10, 1405.	1.6	22
108	Multitable Methods for Microbiome Data Integration. <i>Frontiers in Genetics</i> , 2019, 10, 627.	1.1	21

#	ARTICLE	IF	CITATIONS
109	An In Vitro Human Cell-Based Assay to Rank the Relative Immunogenicity of Proteins. <i>Toxicological Sciences</i> , 2004, 77, 280-289.	1.4	20
110	Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 1927-1938.	0.9	20
111	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. <i>PLoS ONE</i> , 2020, 15, e0225352.	1.1	20
112	Natural killer cell phenotype is altered in HIV-exposed seronegative women. <i>PLoS ONE</i> , 2020, 15, e0238347.	1.1	18
113	A classification model for G-to-A hypermutation in hepatitis B virus ultra-deep pyrosequencing reads. <i>Bioinformatics</i> , 2010, 26, 2929-2932.	1.8	17
114	Human population-based identification of CD4+ T-cell peptide epitope determinants. <i>Journal of Immunological Methods</i> , 2003, 281, 95-108.	0.6	16
115	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating <i>Dehalococcoides mccartyi</i> Consortium. <i>Environmental Science & Technology</i> , 2016, 50, 12187-12196.	4.6	16
116	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. , 2016, , .		16
117	Bioinformatics and Management Science: Some Common Tools and Techniques. <i>Operations Research</i> , 2004, 52, 165-190.	1.2	15
118	Rapid Assessment of Recognition Efficiency and Functional Capacity of Antigen-Specific T-Cell Responses. <i>Journal of Immunotherapy</i> , 2005, 28, 297-305.	1.2	15
119	Ion channel switch array:A biosensor for detecting multiple pathogens. <i>Industrial Biotechnology</i> , 2005, 1, 26-31.	0.5	15
120	A multifaceted analysis of HIV-1 protease multidrug resistance phenotypes. <i>BMC Bioinformatics</i> , 2011, 12, 477.	1.2	15
121	Interval Graph Limits. <i>Annals of Combinatorics</i> , 2013, 17, 27-52.	0.3	15
122	Expanded Spectrum of Antiretroviral-Selected Mutations in Human Immunodeficiency Virus Type 2. <i>Journal of Infectious Diseases</i> , 2020, 221, 1962-1972.	1.9	14
123	CytoGLMM: conditional differential analysis for flow and mass cytometry experiments. <i>BMC Bioinformatics</i> , 2021, 22, 137.	1.2	14
124	Three Examples of Monte-Carlo Markov Chains: At the Interface Between Statistical Computing, Computer Science, and Statistical Mechanics. <i>The IMA Volumes in Mathematics and Its Applications</i> , 1995, , 43-56.	0.5	14
125	An InteractiveJavaStatistical Image Segmentation System:GemIdent. <i>Journal of Statistical Software</i> , 2009, 30, .	1.8	13
126	Parallel imaging of Drosophila embryos for quantitative analysis of genetic perturbations of the Ras pathway. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 923-929.	1.2	12

#	ARTICLE	IF	CITATIONS
127	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 183-94.	0.7	12
128	VISUALIZATION AND STATISTICAL COMPARISONS OF MICROBIAL COMMUNITIES USING PACKAGES ON PHYLOCHIP DATA. , 2010, , 142-153.		11
129	Analysis of casino shelf shuffling machines. Annals of Applied Probability, 2013, 23, .	0.6	11
130	Bayesian Unidimensional Scaling for visualizing uncertainty in high dimensional datasets with latent ordering of observations. BMC Bioinformatics, 2017, 18, 394.	1.2	11
131	Interactive Visualization of Hierarchically Structured Data. Journal of Computational and Graphical Statistics, 2018, 27, 553-563.	0.9	11
132	Nuclear degradation dynamics in a nonapoptotic programmed cell death. Cell Death and Differentiation, 2020, 27, 711-724.	5.0	11
133	An Interactive Java Statistical Image Segmentation System: GemIdent. Journal of Statistical Software, 2009, 30, .	1.8	11
134	Treated HIV Infection Alters Phenotype but Not HIV-Specific Function of Peripheral Blood Natural Killer Cells. Frontiers in Immunology, 2020, 11, 829.	2.2	10
135	Characterization of the Impact of Daclizumab Beta on Circulating Natural Killer Cells by Mass Cytometry. Frontiers in Immunology, 2020, 11, 714.	2.2	10
136	A Statistical Perspective on the Challenges in Molecular Microbial Biology. Journal of Agricultural, Biological, and Environmental Statistics, 2021, 26, 131-160.	0.7	10
137	Bradley Efron: A Conversation with Good Friends. Statistical Science, 2003, 18, .	1.6	10
138	Template Shape Estimation: Correcting an Asymptotic Bias. SIAM Journal on Imaging Sciences, 2017, 10, 808-844.	1.3	9
139	Multivariate Heteroscedasticity Models for Functional Brain Connectivity. Frontiers in Neuroscience, 2017, 11, 696.	1.4	9
140	Community-wide hackathons to identify central themes in single-cell multi-omics. Genome Biology, 2021, 22, 220.	3.8	9
141	de Finetti Priors using Markov chain Monte Carlo computations. Statistics and Computing, 2015, 25, 797-808.	0.8	8
142	Stein's method for birth and death chains. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 42-65.	1.0	8
143	Mass Cytometry Analysis of the NK Cell Receptor's Ligand Repertoire Reveals Unique Differences between Dengue-Infected Children and Adults. ImmunoHorizons, 2020, 4, 634-647.	0.8	7
144	An Interactive Statistical Image Segmentation and Visualization System. , 2007, , .		6

#	ARTICLE	IF	CITATIONS
145	Statistical proof? The problem of irreproducibility. <i>Bulletin of the American Mathematical Society</i> , 2017, 55, 31-55.	0.8	6
146	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020, 9, .	3.3	6
147	VISUALISING DATA. , 2006, , .		6
148	Stein's method for the bootstrap. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 2004, , 93-132.	1.0	6
149	Stereotypic Expansion of T Regulatory and Th17 Cells during Infancy Is Disrupted by HIV Exposure and Gut Epithelial Damage. <i>Journal of Immunology</i> , 2022, 208, 27-37.	0.4	6
150	Statistical Modeling for Practical Pooled Testing During the COVID-19 Pandemic. <i>Statistical Science</i> , 2022, 37, .	1.6	6
151	HIV-1 Transmission Networks in a Small World. <i>Journal of Infectious Diseases</i> , 2014, 209, 180-182.	1.9	5
152	Natural Killer Cell Receptors and Ligands Are Associated With Markers of HIV-1 Persistence in Chronically Infected ART Suppressed Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 757846.	1.8	5
153	Adaptive importance sampling for network growth models. <i>Annals of Operations Research</i> , 2011, 189, 187-203.	2.6	4
154	Connections and Extensions: A Discussion of the Paper by Girolami and Byrne. <i>Scandinavian Journal of Statistics</i> , 2014, 41, 3-7.	0.9	4
155	Supervised topic modeling for predicting molecular substructure from mass spectrometry. <i>F1000Research</i> , 0, 10, 403.	0.8	4
156	Evolutionary Games and Population Dynamics. <i>Journal of the American Statistical Association</i> , 2000, 95, 688.	1.8	3
157	Metrics on Compositions and Coincidences among Renewal Sequences. <i>The IMA Volumes in Mathematics and Its Applications</i> , 1996, , 81-101.	0.5	3
158	Comment on "A Model for Studying Display Methods of Statistical Graphics". <i>Journal of Computational and Graphical Statistics</i> , 1993, 2, 349.	0.9	2
159	Labeling Self-Tracker Menstrual Health Records With Hidden Semi-Markov Models. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 1297-1308.	3.9	2
160	Comment on "A Model for Studying Display Methods of Statistical Graphics". <i>Journal of Computational and Graphical Statistics</i> , 1993, 2, 349-353.	0.9	1
161	Elements of Large-Sample Theory. <i>Journal of the American Statistical Association</i> , 2000, 95, 328.	1.8	1
162	Random Spatial Structure of Geometric Deformations and Bayesian Nonparametrics. <i>Lecture Notes in Computer Science</i> , 2013, , 120-127.	1.0	1

#	ARTICLE	IF	CITATIONS
163	Multi-Table Differential Correlation Analysis of Neuroanatomical and Cognitive Interactions in Turner Syndrome. <i>Neuroinformatics</i> , 2018, 16, 81-93.	1.5	1
164	Topologically Constrained Template Estimation via Morse-Smale Complexes Controls Its Statistical Consistency. <i>SIAM Journal on Applied Algebra and Geometry</i> , 2018, 2, 348-375.	0.9	1
165	Successful strategies for human microbiome data generation, storage and analyses. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	1
166	Influenza-Induced Interferon Lambda Response Is Associated With Longer Time to Delivery Among Pregnant Kenyan Women. <i>Frontiers in Immunology</i> , 2020, 11, 452.	2.2	1
167	Are there Still Things to Do in Bayesian Statistics?. , 1997, , 5-18.		1
168	Statistical Graphics for Visualizing Multivariate Data. <i>Journal of the American Statistical Association</i> , 1999, 94, 981.	1.8	0
169	W1926 Shifts in Luminal and Mucosal Microbial Communities Associated With an Experimental Model of Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2010, 138, S-767.	0.6	0
170	Discussion of "50 Years of Data Science". <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 768-769.	0.9	0
171	Convex Hierarchical Clustering for Graph-Structured Data. , 2019, , .		0
172	Successful strategies for human microbiome data generation, storage and analyses. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	0
173	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
174	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
175	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
176	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0