

Susan P Holmes

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.

179
papers

30,985
citations

55
h-index

176
g-index

212
ext. papers

50,163
ext. citations

6.5
avg, IF

7.89
L-index

#	Paper	IF	Citations
179	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	5.9	0
178	Statistical Modeling for Practical Pooled Testing During the COVID-19 Pandemic. <i>Statistical Science</i> , 2022 , 37,	2.4	2
177	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
176	CytoGLMM: conditional differential analysis for flow and mass cytometry experiments. <i>BMC Bioinformatics</i> , 2021 , 22, 137	3.6	3
175	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	34
174	A Statistical Perspective on the Challenges in Molecular Microbial Biology. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2021 , 26, 131-160	1.9	2
173	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021 , 22, 220	18.3	2
172	Labeling self-tracked menstrual health records with hidden semi-Markov models. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , PP,	7.2	1
171	Variability in the analysis of a single neuroimaging dataset by many teams. <i>Nature</i> , 2020 , 582, 84-88	50.4	281
170	Treated HIV Infection Alters Phenotype but Not HIV-Specific Function of Peripheral Blood Natural Killer Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 829	8.4	4
169	TIGIT is upregulated by HIV-1 infection and marks a highly functional adaptive and mature subset of natural killer cells. <i>Aids</i> , 2020 , 34, 801-813	3.5	27
168	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. <i>PLoS ONE</i> , 2020 , 15, e0225352	3.7	9
167	Expanded Spectrum of Antiretroviral-Selected Mutations in Human Immunodeficiency Virus Type 2. <i>Journal of Infectious Diseases</i> , 2020 , 221, 1962-1972	7	8
166	Characterization of the Impact of Daclizumab Beta on Circulating Natural Killer Cells by Mass Cytometry. <i>Frontiers in Immunology</i> , 2020 , 11, 714	8.4	5
165	Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis. <i>JCI Insight</i> , 2020 , 5,	9.9	106
164	Mass Cytometry Analysis of the NK Cell Receptor-Ligand Repertoire Reveals Unique Differences between Dengue-Infected Children and Adults. <i>ImmunoHorizons</i> , 2020 , 4, 634-647	2.7	5
163	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	4.9	11

162	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020 , 82, 26-41	12.9	32
161	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020 , 9,	7.6	2
160	Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon. <i>Nature Communications</i> , 2020 , 11, 3772	17.4	6
159	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> , 2020 ,	7	8
158	Natural killer cell phenotype is altered in HIV-exposed seronegative women. <i>PLoS ONE</i> , 2020 , 15, e0238347	3.7	8
157	Nuclear degradation dynamics in a nonapoptotic programmed cell death. <i>Cell Death and Differentiation</i> , 2020 , 27, 711-724	12.7	8
156	Influenza-Induced Interferon Lambda Response Is Associated With Longer Time to Delivery Among Pregnant Kenyan Women. <i>Frontiers in Immunology</i> , 2020 , 11, 452	8.4	1
155	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences 2020 , 15, e0225352		
154	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences 2020 , 15, e0225352		
153	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences 2020 , 15, e0225352		
152	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences 2020 , 15, e0225352		
151	Successful strategies for human microbiome data generation, storage and analyses. <i>Journal of Biosciences</i> , 2019 , 44, 1	2.3	
150	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. <i>Microbiome</i> , 2019 , 7, 131	16.6	32
149	Ten quick tips for effective dimensionality reduction. <i>PLoS Computational Biology</i> , 2019 , 15, e1006907	5	89
148	Latent variable modeling for the microbiome. <i>Biostatistics</i> , 2019 , 20, 599-614	3.7	22
147	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	4.5	11
146	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
145	Multitable Methods for Microbiome Data Integration. <i>Frontiers in Genetics</i> , 2019 , 10, 627	4.5	11

144	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. <i>Frontiers in Immunology</i> , 2019 , 10, 2469	8.4	23
143	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. <i>Nature Communications</i> , 2018 , 9, 681	17.4	64
142	Multi-Table Differential Correlation Analysis of Neuroanatomical and Cognitive Interactions in Turner Syndrome. <i>Neuroinformatics</i> , 2018 , 16, 81-93	3.2	1
141	Interactive Visualization of Hierarchically Structured Data. <i>Journal of Computational and Graphical Statistics</i> , 2018 , 27, 553-563	1.4	6
140	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	1.5	1
139	Tracking network dynamics: A survey using graph distances. <i>Annals of Applied Statistics</i> , 2018 , 12,	2.1	39
138	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. <i>Journal of Immunology</i> , 2018 , 201, 2117-2131	5.3	25
137	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
136	Gut microbiome transition across a lifestyle gradient in Himalaya. <i>PLoS Biology</i> , 2018 , 16, e2005396	9.7	71
135	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. <i>Microbiome</i> , 2018 , 6, 226	16.6	680
134	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018 , 28, 1467-1480	9.7	73
133	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. <i>Journal of the American Statistical Association</i> , 2017 , 112, 1430-1442	2.8	22
132	Parallel imaging of embryos for quantitative analysis of genetic perturbations of the Ras pathway. <i>DMM Disease Models and Mechanisms</i> , 2017 , 10, 923-929	4.1	10
131	Template Shape Estimation: Correcting an Asymptotic Bias. <i>SIAM Journal on Imaging Sciences</i> , 2017 , 10, 808-844	1.9	8
130	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	8.8	25
129	Mass Cytometry Analytical Approaches Reveal Cytokine-Induced Changes in Natural Killer Cells. <i>Cytometry Part B - Clinical Cytometry</i> , 2017 , 92, 57-67	3.4	24
128	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. <i>PLoS Computational Biology</i> , 2017 , 13, e1005706	5	45
127	Bayesian Unidimensional Scaling for visualizing uncertainty in high dimensional datasets with latent ordering of observations. <i>BMC Bioinformatics</i> , 2017 , 18, 394	3.6	10

126	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	11.5	182
125	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. <i>ISME Journal</i> , 2017 , 11, 2639-2643	11.9	1228
124	Prevalence of Drug-Resistant Minority Variants in Untreated HIV-1-Infected Individuals With and Those Without Transmitted Drug Resistance Detected by Sanger Sequencing. <i>Journal of Infectious Diseases</i> , 2017 , 216, 387-391	7	20
123	Discussion of 50 Years of Data Science. <i>Journal of Computational and Graphical Statistics</i> , 2017 , 26, 768-769	1.4	
122	Statistical proof? The problem of irreproducibility. <i>Bulletin of the American Mathematical Society</i> , 2017 , 55, 31-55	1.3	5
121	Multivariate Heteroscedasticity Models for Functional Brain Connectivity. <i>Frontiers in Neuroscience</i> , 2017 , 11, 696	5.1	2
120	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating Dehalococcoides mccartyi Consortium. <i>Environmental Science & Technology</i> , 2016 , 50, 12187-12196	10.3	12
119	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA 2016 ,		4
118	Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle. <i>Microbiome</i> , 2016 , 4, 15	16.6	210
117	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. <i>Nature Communications</i> , 2016 , 7, 10516	17.4	129
116	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. <i>F1000Research</i> , 2016 , 5, 1492	3.6	316
115	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016 , 21, 183-94	1.3	10
114	More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. <i>ELife</i> , 2016 , 5,	8.9	50
113	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. <i>F1000Research</i> , 2016 , 5, 1492	3.6	303
112	HIV-1 Protease, Reverse Transcriptase, and Integrase Variation. <i>Journal of Virology</i> , 2016 , 90, 6058-6070	6.6	52
111	Measuring multivariate association and beyond. <i>Statistics Surveys</i> , 2016 , 10, 132-167	1.7	33
110	DADA2: High-resolution sample inference from Illumina amplicon data. <i>Nature Methods</i> , 2016 , 13, 581-3	21.6	7612
109	Shiny-phyloseq: Web application for interactive microbiome analysis with provenance tracking. <i>Bioinformatics</i> , 2015 , 31, 282-3	7.2	84

108	Human NK cell repertoire diversity reflects immune experience and correlates with viral susceptibility. <i>Science Translational Medicine</i> , 2015 , 7, 297ra115	17.5	120
107	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, 11060-5	11.5	581
106	de Finetti Priors using Markov chain Monte Carlo computations. <i>Statistics and Computing</i> , 2015 , 25, 797-808		5
105	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. <i>PLoS ONE</i> , 2015 , 10, e0142825	3.7	49
104	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, 14506-11	11.5	55
103	Waste not, want not: why rarefying microbiome data is inadmissible. <i>PLoS Computational Biology</i> , 2014 , 10, e1003531	5	1536
102	Connections and Extensions: A Discussion of the Paper by Girolami and Byrne. <i>Scandinavian Journal of Statistics</i> , 2014 , 41, 3-7	0.8	3
101	structSSI: Simultaneous and Selective Inference for Grouped or Hierarchically Structured Data. <i>Journal of Statistical Software</i> , 2014 , 59, 1-21	7.3	146
100	Harvester ants use interactions to regulate forager activation and availability. <i>Animal Behaviour</i> , 2013 , 86, 197-207	2.8	74
99	Interval Graph Limits. <i>Annals of Combinatorics</i> , 2013 , 17, 27-52	0.7	9
98	Sampling from a Manifold. <i>Institute of Mathematical Statistics Collections</i> , 2013 , 102-125		20
97	Random Spatial Structure of Geometric Deformations and Bayesian Nonparametrics. <i>Lecture Notes in Computer Science</i> , 2013 , 120-127	0.9	1
96	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, 17059-64	11.5	180
95	Nasal microenvironments and interspecific interactions influence nasal microbiota complexity and <i>S. aureus</i> carriage. <i>Cell Host and Microbe</i> , 2013 , 14, 631-40	23.4	221
94	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.7	373
93	Analysis of casino shelf shuffling machines. <i>Annals of Applied Probability</i> , 2013 , 23,	2	7
92	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	5.9	21
91	Nucleoside reverse transcriptase inhibitor resistance mutations associated with first-line stavudine-containing antiretroviral therapy: programmatic implications for countries phasing out stavudine. <i>Journal of Infectious Diseases</i> , 2013 , 207 Suppl 2, S70-7	7	28

90	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, 343-9	5.9	22
89	Detection of cytomegalovirus drug resistance mutations by next-generation sequencing. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 3700-10	9.7	63
88	phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. <i>PLoS ONE</i> , 2013 , 8, e61217	3.7	6869
87	The molecular architecture of the eukaryotic chaperonin TRiC/CCT. <i>Structure</i> , 2012 , 20, 814-25	5.2	216
86	Computational Tools for Evaluating Phylogenetic and Hierarchical Clustering Trees. <i>Journal of Computational and Graphical Statistics</i> , 2012 , 21, 581-599	1.4	30
85	Denosing PCR-amplified metagenome data. <i>BMC Bioinformatics</i> , 2012 , 13, 283	3.6	58
84	PRC2/EED-EZH2 complex is up-regulated in breast cancer lymph node metastasis compared to primary tumor and correlates with tumor proliferation in situ. <i>PLoS ONE</i> , 2012 , 7, e51239	3.7	41
83	Nest site and weather affect the personality of harvester ant colonies. <i>Behavioral Ecology</i> , 2012 , 23, 1022-1029	3.52	
82	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	1.3	63
81	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	1.3	22
80	Elements of Large-Sample Theory 2012 , 1111-1112		
79	PHYLOSEQ: A BIOCONDUCTOR PACKAGE FOR HANDLING AND ANALYSIS OF HIGH-THROUGHPUT PHYLOGENETIC SEQUENCE DATA 2011 ,		22
78	Colony variation in the collective regulation of foraging by harvester ants. <i>Behavioral Ecology</i> , 2011 , 22, 429-435	2.3	54
77	COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES 2011 ,		12
76	THE DUALITY DIAGRAM IN DATA ANALYSIS: EXAMPLES OF MODERN APPLICATIONS. <i>Annals of Applied Statistics</i> , 2011 , 5, 2266-2277	2.1	14
75	A multifaceted analysis of HIV-1 protease multidrug resistance phenotypes. <i>BMC Bioinformatics</i> , 2011 , 12, 477	3.6	12
74	Adaptive importance sampling for network growth models. <i>Annals of Operations Research</i> , 2011 , 189, 187-203	3.2	3
73	Site-specific mobilization of vinyl chloride respiration islands by a mechanism common in <i>Dehalococcoides</i> . <i>BMC Genomics</i> , 2011 , 12, 287	4.5	49

72	Visualization and statistical comparisons of microbial communities using R packages on Phylochip data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2011 , 142-53	1.3	10
71	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, 1562-73	4.1	116
70	Colonic contribution to uremic solutes. <i>Journal of the American Society of Nephrology: JASN</i> , 2011 , 22, 1769-76	12.7	260
69	Constrained patterns of covariation and clustering of HIV-1 non-nucleoside reverse transcriptase inhibitor resistance mutations. <i>Journal of Antimicrobial Chemotherapy</i> , 2010 , 65, 1477-85	5.1	44
68	A classification model for G-to-A hypermutation in hepatitis B virus ultra-deep pyrosequencing reads. <i>Bioinformatics</i> , 2010 , 26, 2929-32	7.2	16
67	Quantitative, architectural analysis of immune cell subsets in tumor-draining lymph nodes from breast cancer patients and healthy lymph nodes. <i>PLoS ONE</i> , 2010 , 5, e12420	3.7	37
66	Nonpolymorphic human immunodeficiency virus type 1 protease and reverse transcriptase treatment-selected mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2009 , 53, 4869-78	5.9	31
65	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, 9010-5	11.5	173
64	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, 1275-85	7	178
63	Localized plasticity in the streamlined genomes of vinyl chloride respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000714	6	135
62	An Interactive Java Statistical Image Segmentation System: GemIdent. <i>Journal of Statistical Software</i> , 2009 , 30,	7.3	10
61	An InteractiveJavaStatistical Image Segmentation System:GemIdent. <i>Journal of Statistical Software</i> , 2009 , 30,	7.3	10
60	Natural variation of HIV-1 group M integrase: implications for a new class of antiretroviral inhibitors. <i>Retrovirology</i> , 2008 , 5, 74	3.6	92
59	Threshold Graph Limits and Random Threshold Graphs. <i>Internet Mathematics</i> , 2008 , 5, 267-320	0	32
58	The short-term regulation of foraging in harvester ants. <i>Behavioral Ecology</i> , 2008 , 19, 217-222	2.3	43
57	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, 10747-55	6.6	65
56	Horseshoes in multidimensional scaling and local kernel methods. <i>Annals of Applied Statistics</i> , 2008 , 2,	2.1	60
55	Multivariate data analysis: The French way 2008 , 219-233		17

54	Genomic interrogation of ancestral Mycobacterium tuberculosis from south India. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 474-83	4.5	45
53	An Interactive Statistical Image Segmentation and Visualization System 2007 ,		5
52	HIV-1 subtype B protease and reverse transcriptase amino acid covariation. <i>PLoS Computational Biology</i> , 2007 , 3, e87	5	75
51	Down-regulation of the interferon signaling pathway in T lymphocytes from patients with metastatic melanoma. <i>PLoS Medicine</i> , 2007 , 4, e176	11.6	107
50	Dynamical Bias in the Coin Toss. <i>SIAM Review</i> , 2007 , 49, 211-235	7.4	89
49	Gene expression network analysis and applications to immunology. <i>Bioinformatics</i> , 2007 , 23, 850-8	7.2	116
48	Unusual codon bias in vinyl chloride reductase genes of Dehalococcoides species. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 2744-7	4.8	25
47	Forager activation and food availability in harvester ants. <i>Animal Behaviour</i> , 2006 , 71, 815-822	2.8	53
46	VISUALISING DATA 2006 ,		4
45	Sequential Monte Carlo Methods for Statistical Analysis of Tables. <i>Journal of the American Statistical Association</i> , 2005 , 100, 109-120	2.8	152
44	Gene expression diversity among Mycobacterium tuberculosis clinical isolates. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 5-14	2.9	67
43	Profile of immune cells in axillary lymph nodes predicts disease-free survival in breast cancer. <i>PLoS Medicine</i> , 2005 , 2, e284	11.6	161
42	Rapid assessment of recognition efficiency and functional capacity of antigen-specific T-cell responses. <i>Journal of Immunotherapy</i> , 2005 , 28, 297-305	5	15
41	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, 5519-23	11.5	56
40	Error distribution for gene expression data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005 , 4, Article16	1.2	61
39	Ion channel switch array:A biosensor for detecting multiple pathogens. <i>Industrial Biotechnology</i> , 2005 , 1, 26-31	1.3	12
38	An in vitro human cell-based assay to rank the relative immunogenicity of proteins. <i>Toxicological Sciences</i> , 2004 , 77, 280-9	4.4	18
37	Microarray analysis reveals differences in gene expression of circulating CD8(+) T cells in melanoma patients and healthy donors. <i>Cancer Research</i> , 2004 , 64, 3661-7	10.1	24

36	Diversity and recognition efficiency of T cell responses to cancer. <i>PLoS Medicine</i> , 2004 , 1, e28	11.6	76
35	Bioinformatics and Management Science: Some Common Tools and Techniques. <i>Operations Research</i> , 2004 , 52, 165-190	2.3	9
34	Use of exchangeable pairs in the analysis of simulations. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 2004 , 1-25	0	30
33	Stein's method for the bootstrap. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 2004 , 93-132	0	6
32	Bootstrapping Phylogenetic Trees: Theory and Methods. <i>Statistical Science</i> , 2003 , 18, 241	2.4	83
31	Statistics for phylogenetic trees. <i>Theoretical Population Biology</i> , 2003 , 63, 17-32	1.2	32
30	Human population-based identification of CD4(+) T-cell peptide epitope determinants. <i>Journal of Immunological Methods</i> , 2003 , 281, 95-108	2.5	16
29	Bradley Efron: A Conversation with Good Friends. <i>Statistical Science</i> , 2003 , 18,	2.4	8
28	Random Walks on Trees and Matchings. <i>Electronic Journal of Probability</i> , 2002 , 7,	1.1	24
27	Geometry of the Space of Phylogenetic Trees. <i>Advances in Applied Mathematics</i> , 2001 , 27, 733-767	0.8	293
26	Statistical problems involving permutations with restricted positions. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 2001 , 195-222	0	17
25	Analysis of a nonreversible Markov chain sampler. <i>Annals of Applied Probability</i> , 2000 , 10, 726	2	119
24	Elements of Large-Sample Theory. <i>Journal of the American Statistical Association</i> , 2000 , 95, 328	2.8	1
23	Phylogenies: An Overview. <i>The IMA Volumes in Mathematics and Its Applications</i> , 1999 , 81-118	0.5	18
22	Addressing geographical data errors in a classification tree for soil unit prediction. <i>International Journal of Geographical Information Science</i> , 1997 , 11, 183-198	4.1	65
21	Are there Still Things to Do in Bayesian Statistics? 1997 , 5-18		
20	Metrics on Compositions and Coincidences among Renewal Sequences. <i>The IMA Volumes in Mathematics and Its Applications</i> , 1996 , 81-101	0.5	1
19	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	12

18	Gray codes for randomization procedures. <i>Statistics and Computing</i> , 1994 , 4, 287-302	1.8	29
17	Correlations among quality parameters of peach fruit. <i>Journal of the Science of Food and Agriculture</i> , 1994 , 66, 241-245	4.3	27
16	Comment on "A Model for Studying Display Methods of Statistical Graphics" <i>Journal of Computational and Graphical Statistics</i> , 1993 , 2, 349-353	1.4	1
15	Comment on "A Model for Studying Display Methods of Statistical Graphics". <i>Journal of Computational and Graphical Statistics</i> , 1993 , 2, 349	1.4	1
14	Treated HIV Infection Alters Phenotype But Not HIV-specific Function of Peripheral Blood Natural Killer Cells		1
13	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
12	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
11	Treatment-Specific Composition of Gut Microbiota Is Associated with Disease Remission in a Pediatric Crohn's Disease Cohort		1
10	Exact sequence variants should replace operational taxonomic units in marker gene data analysis		12
9	Unmasking Seasonal Cycles in Human Fertility: How holiday sex and fertility cycles shape birth seasonality		3
8	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19		11
7	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data		37
6	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome		1
5	CD38 contributes to human natural killer cell responses through a role in immune synapse formation		7
4	Combined use of metagenomic sequencing and host response profiling for the diagnosis of suspected sepsis		2
3	Supervised topic modeling for predicting molecular substructure from mass spectrometry. <i>F1000Research</i> , 10, 403	3.6	1
2	Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios. <i>Journal of Applied Statistics</i> , 1-29	1	12
1	Labeling self-tracked menstrual health records with hidden semi-Markov models		1

