Susan P Holmes

List of Publications by Year
in descending order

176 papers	64,668 citations	22153 59 h-index	6131 159 g-index
212 all docs	212 docs citations	212 times ranked	56343 citing authors

#	Article	IF	Citations
1	Effect of Water, Sanitation, Handwashing, and Nutrition Interventions on Enteropathogens in Children 14 Months Old: A Cluster-Randomized Controlled Trial in Rural Bangladesh. Journal of Infectious Diseases, 2023, 227, 434-447.	4.0	23
2	Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios. Journal of Applied Statistics, 2023, 50, 2518-2546.	1.3	22
3	Labeling Self-Tracked Menstrual Health Records With Hidden Semi-Markov Models. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 1297-1308.	6.3	2
4	Stereotypic Expansion of T Regulatory and Th17 Cells during Infancy Is Disrupted by HIV Exposure and Gut Epithelial Damage. Journal of Immunology, 2022, 208, 27-37.	0.8	6
5	Natural Killer Cell Receptors and Ligands Are Associated With Markers of HIV-1 Persistence in Chronically Infected ART Suppressed Patients. Frontiers in Cellular and Infection Microbiology, 2022, 12, 757846.	3.9	5
6	Statistical Modeling for Practical Pooled Testing During the COVID-19 Pandemic. Statistical Science, 2022, 37, .	2.8	6
7	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. Science, 2022, 376, 1220-1223.	12.6	63
8	A Statistical Perspective on the Challenges in Molecular Microbial Biology. Journal of Agricultural, Biological, and Environmental Statistics, 2021, 26, 131-160.	1.4	10
9	CytoGLMM: conditional differential analysis for flow and mass cytometry experiments. BMC Bioinformatics, 2021, 22, 137.	2.6	14
10	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. Journal of Experimental Medicine, 2021, 218, .	8.5	139
11	Community-wide hackathons to identify central themes in single-cell multi-omics. Genome Biology, 2021, 22, 220.	8.8	9
12	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
13	Nuclear degradation dynamics in a nonapoptotic programmed cell death. Cell Death and Differentiation, 2020, 27, 711-724.	11.2	11
14	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. Periodontology 2000, 2020, 82, 26-41.	13.4	50
15	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. GigaScience, 2020, 9, .	6.4	6
16	Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon. Nature Communications, 2020, 11, 3772.	12.8	29
17	Natural killer cell phenotype is altered in HIV-exposed seronegative women. PLoS ONE, 2020, 15, e0238347.	2.5	18
18	Variability in the analysis of a single neuroimaging dataset by many teams. Nature, 2020, 582, 84-88.	27.8	634

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19	Treated HIV Infection Alters Phenotype but Not HIV-Specific Function of Peripheral Blood Natural Killer Cells. Frontiers in Immunology, 2020, 11, 829.	4.8	10
20	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.	2.2	40
21	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. PLoS ONE, 2020, 15, e0225352.	2.5	20
22	Expanded Spectrum of Antiretroviral-Selected Mutations in Human Immunodeficiency Virus Type 2. Journal of Infectious Diseases, 2020, 221, 1962-1972.	4.0	14
23	Characterization of the Impact of Daclizumab Beta on Circulating Natural Killer Cells by Mass Cytometry. Frontiers in Immunology, 2020, 11, 714.	4.8	10
24	Influenza-Induced Interferon Lambda Response Is Associated With Longer Time to Delivery Among Pregnant Kenyan Women. Frontiers in Immunology, 2020, 11, 452.	4.8	1
25	Gut microbiota plasticity is correlated with sustained weight loss on a low-carb or low-fat dietary intervention. Scientific Reports, 2020, 10, 1405.	3.3	22
26	Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis. JCI Insight, 2020, 5, .	5.0	196
27	Mass Cytometry Analysis of the NK Cell Receptor–Ligand Repertoire Reveals Unique Differences between Dengue-Infected Children and Adults. ImmunoHorizons, 2020, 4, 634-647.	1.8	7
28	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
29	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
30	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
31	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
32	Latent variable modeling for the microbiome. Biostatistics, 2019, 20, 599-614.	1.5	51
33	Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort. Inflammatory Bowel Diseases, 2019, 25, 1927-1938.	1.9	20
34	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
35	Multitable Methods for Microbiome Data Integration. Frontiers in Genetics, 2019, 10, 627.	2.3	21
36	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. Frontiers in Immunology, 2019, 10, 2469.	4.8	36

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37	Successful strategies for human microbiome data generation, storage and analyses. Journal of Biosciences, 2019, 44, 1.	1.1	1
38	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. Microbiome, 2019, 7, 131.	11.1	65
39	Ten quick tips for effective dimensionality reduction. PLoS Computational Biology, 2019, 15, e1006907.	3.2	174
40	Convex Hierarchical Clustering for Graph-Structured Data. , 2019, , .		0
41	Successful strategies for human microbiome data generation, storage and analyses. Journal of Biosciences, 2019, 44, .	1.1	0
42	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. Nature Communications, 2018, 9, 681.	12.8	87
43	Multi-Table Differential Correlation Analysis of Neuroanatomical and Cognitive Interactions in Turner Syndrome. Neuroinformatics, 2018, 16, 81-93.	2.8	1
44	Interactive Visualization of Hierarchically Structured Data. Journal of Computational and Graphical Statistics, 2018, 27, 553-563.	1.7	11
45	Gut microbiome transition across a lifestyle gradient in Himalaya. PLoS Biology, 2018, 16, e2005396.	5.6	128
46	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. Microbiome, 2018, 6, 226.	11.1	1,729
47	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. Genome Research, 2018, 28, 1467-1480.	5.5	117
48	Topologically Constrained Template Estimation via Morse--Smale Complexes Controls Its Statistical Consistency. SIAM Journal on Applied Algebra and Geometry, 2018, 2, 348-375.	1.4	1
49	Tracking network dynamics: A survey using graph distances. Annals of Applied Statistics, 2018, 12, .	1.1	70
50	Differential Induction of IFN-α 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.	0.8	42
51	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. Journal of the American Statistical Association, 2017, 112, 1430-1442.	3.1	30
52	Parallel imaging of Drosophila embryos for quantitative analysis of genetic perturbations of the Ras pathway. DMM Disease Models and Mechanisms, 2017, 10, 923-929.	2.4	12
53	Template Shape Estimation: Correcting an Asymptotic Bias. SIAM Journal on Imaging Sciences, 2017, 10, 808-844.	2.2	9
54	Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration. EBioMedicine, 2017, 18, 225-235.	6.1	28

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55	Mass Cytometry Analytical Approaches Reveal Cytokineâ€‐Induced Changes in Natural Killer Cells. Cytometry Part B - Clinical Cytometry, 2017, 92, 57-67.	1.5	40
56	Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9966-9971.	7.1	297
57	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. ISME Journal, 2017, 11, 2639-2643.	9.8	2,357
58	Prevalence of Drug-Resistant Minority Variants in Untreated HIV-1â€"Infected Individuals With and Those Without Transmitted Drug Resistance Detected by Sanger Sequencing. Journal of Infectious Diseases, 2017, 216, 387-391.	4.0	28
59	Discussion of â€œ50 Years of Data Scienceâ€• Journal of Computational and Graphical Statistics, 2017, 26, 768-769.	1.7	0
60	Statistical proof? The problem of irreproducibility. Bulletin of the American Mathematical Society, 2017, 55, 31-55.	1.5	6
61	Multivariate Heteroscedasticity Models for Functional Brain Connectivity. Frontiers in Neuroscience, 2017, 11, 696.	2.8	9
62	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. PLoS Computational Biology, 2017, 13, e1005706.	3.2	64
63	Bayesian Unidimensional Scaling for visualizing uncertainty in high dimensional datasets with latent ordering of observations. BMC Bioinformatics, 2017, 18, 394.	2.6	11
64	Bioconductor Workflow for Microbiome Data Analysis: from raw reads to community analyses. F1000Research, 2016, 5, 1492.	1.6	664
65	HIV-1 Protease, Reverse Transcriptase, and Integrase Variation. Journal of Virology, 2016, 90, 6058-6070.	3.4	72
66	Measuring multivariate association and beyond. Statistics Surveys, 2016, 10, 132-167.	11.3	52
67	DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 2016, 13, 581-583.	19.0	18,691
68	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating <i>Dehalococcoides mccartyi</i> Consortium. Environmental Science & Technology, 2016, 50, 12187-12196.	10.0	16
69	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. , 2016, , .		16
70	Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle. Microbiome, 2016, 4, 15.	11.1	348
71	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. Nature Communications, 2016, 7, 10516.	12.8	196
72	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. F1000Research, 2016, 5, 1492.	1.6	466

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73	More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. ELife, 2016, 5, .	6.0	70
74	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
75	de Finetti Priors using Markov chain Monte Carlo computations. Statistics and Computing, 2015, 25, 797-808.	1.5	8
76	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. PLoS ONE, 2015, 10, e0142825.	2.5	84
77	Shiny-phyloseq: Web application for interactive microbiome analysis with provenance tracking. Bioinformatics, 2015, 31, 282-283.	4.1	131
78	Human NK cell repertoire diversity reflects immune experience and correlates with viral susceptibility. Science Translational Medicine, 2015, 7, 297ra115.	12.4	177
79	Temporal and spatial variation of the human microbiota during pregnancy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11060-11065.	7.1	876
80	Waste Not, Want Not: Why Rarefying Microbiome Data Is Inadmissible. PLoS Computational Biology, 2014, 10, e1003531.	3.2	2,343
81	HIV-1 Transmission Networks in a Small World. Journal of Infectious Diseases, 2014, 209, 180-182.	4.0	5
82	Connections and Extensions: A Discussion of the Paper by Girolami and Byrne. Scandinavian Journal of Statistics, 2014, 41, 3-7.	1.4	4
83	Enhanced natural killer-cell and T-cell responses to influenza A virus during pregnancy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14506-14511.	7.1	95
84	structSSI: Simultaneous and Selective Inference for Grouped or Hierarchically Structured Data. Journal of Statistical Software, 2014, 59, 1-21.	3.7	488
85	Harvester ants use interactions to regulate forager activation and availability. Animal Behaviour, 2013, 86, 197-207.	1.9	105
86	Interval Graph Limits. Annals of Combinatorics, 2013, 17, 27-52.	0.6	15
87	Sampling from a Manifold. Institute of Mathematical Statistics Collections, 2013, , 102-125.	0.3	41
88	Random Spatial Structure of Geometric Deformations and Bayesian Nonparametrics. Lecture Notes in Computer Science, 2013, , 120-127.	1.3	1
89	Genetically dictated change in host mucus carbohydrate landscape exerts a diet-dependent effect on the gut microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17059-17064.	7.1	237
90	Nasal Microenvironments and Interspecific Interactions Influence Nasal Microbiota Complexity and S.Âaureus Carriage. Cell Host and Microbe, 2013, 14, 631-640.	11.0	294

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91	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553
92	Analysis of casino shelf shuffling machines. Annals of Applied Probability, 2013, 23, .	1.3	11
93	Prototypical Recombinant Multi-Protease-Inhibitor-Resistant Infectious Molecular Clones of Human Immunodeficiency Virus Type 1. Antimicrobial Agents and Chemotherapy, 2013, 57, 4290-4299.	3.2	23
94	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.	4.0	30
95	Low-Level Persistence of Drug Resistance Mutations in Hepatitis B Virus-Infected Subjects with a Past History of Lamivudine Treatment. Antimicrobial Agents and Chemotherapy, 2013, 57, 343-349.	3.2	24
96	Detection of Cytomegalovirus Drug Resistance Mutations by Next-Generation Sequencing. Journal of Clinical Microbiology, 2013, 51, 3700-3710.	3.9	91
97	phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. PLoS ONE, 2013, 8, e61217.	2.5	13,960
98	Nest site and weather affect the personality of harvester ant colonies. Behavioral Ecology, 2012, 23, 1022-1029.	2.2	60
99	Computational Tools for Evaluating Phylogenetic and Hierarchical Clustering Trees. Journal of Computational and Graphical Statistics, 2012, 21, 581-599.	1.7	40
100	Denoising PCR-amplified metagenome data. BMC Bioinformatics, 2012, 13, 283.	2.6	85
101	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.	2.5	48
102	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. Structure, 2012, 20, 814-825.	3.3	261
103	Elements of Large-Sample Theory. , 2012, , 1111-1112.		151
104	Phyloseq: a bioconductor package for handling and analysis of high-throughput phylogenetic sequence data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 235-46.	0.7	84
105	Comparisons of distance methods for combining covariates and abundances in microbiome studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 213-24.	0.7	24
106	PHYLOSEQ: A BIOCONDUCTOR PACKAGE FOR HANDLING AND ANALYSIS OF HIGH-THROUGHPUT PHYLOGENETIC SEQUENCE DATA. , 2011, , .		45
107	Colony variation in the collective regulation of foraging by harvester ants. Behavioral Ecology, 2011, 22, 429-435.	2.2	71
108	COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES. , 2011, , .		29

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109	The duality diagram in data analysis: Examples of modern applications. Annals of Applied Statistics, 2011, 5, 2266-2277.	1.1	22
110	A multifaceted analysis of HIV-1 protease multidrug resistance phenotypes. BMC Bioinformatics, 2011, 12, 477.	2.6	15
111	Adaptive importance sampling for network growth models. Annals of Operations Research, 2011, 189, 187-203.	4.1	4
112	Site-Specific Mobilization of Vinyl Chloride Respiration Islands by a Mechanism Common in Dehalococcoides. BMC Genomics, 2011, 12, 287.	2.8	55
113	The effect of individual variation on the structure and function of interaction networks in harvester ants. Journal of the Royal Society Interface, 2011, 8, 1562-1573.	3.4	134
114	Colonic Contribution to Uremic Solutes. Journal of the American Society of Nephrology: JASN, 2011, 22, 1769-1776.	6.1	340
115	Constrained patterns of covariation and clustering of HIV-1 non-nucleoside reverse transcriptase inhibitor resistance mutations. Journal of Antimicrobial Chemotherapy, 2010, 65, 1477-1485.	3.0	52
116	A classification model for G-to-A hypermutation in hepatitis B virus ultra-deep pyrosequencing reads. Bioinformatics, 2010, 26, 2929-2932.	4.1	17
117	VISUALIZATION AND STATISTICAL COMPARISONS OF MICROBIAL COMMUNITIES USING PACKAGES ON PHYLOCHIP DATA. , 2010, , 142-153.		11
118	W1926 Shifts in Luminal and Mucosal Microbial Communities Associated With an Experimental Model of Irritable Bowel Syndrome. Gastroenterology, 2010, 138, S-767.	1.3	0
119	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.	2.5	43
120	Nonpolymorphic Human Immunodeficiency Virus Type 1 Protease and Reverse Transcriptase Treatment-Selected Mutations. Antimicrobial Agents and Chemotherapy, 2009, 53, 4869-4878.	3.2	32
121	Impaired interferon signaling is a common immune defect in human cancer. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9010-9015.	7.1	240
122	Ultra–Deep Pyrosequencing of Hepatitis B Virus Quasispecies from Nucleoside and Nucleotide Reverse–Transcriptase Inhibitor (NRTI)–Treated Patients and NRTI–Naive Patients. Journal of Infectious Diseases, 2009, 199, 1275-1285.	4.0	195
123	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring Dehalococcoides. PLoS Genetics, 2009, 5, e1000714.	3.5	162
124	An InteractiveJavaStatistical Image Segmentation System:GemIdent. Journal of Statistical Software, 2009, 30, .	3.7	13
125	An Interactive Java Statistical Image Segmentation System: GemIdent. Journal of Statistical Software, 2009, 30, .	3.7	11
126	Genomic interrogation of ancestral Mycobacterium tuberculosis from south India. Infection, Genetics and Evolution, 2008, 8, 474-483.	2.3	48

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127	Natural variation of HIV-1 group M integrase: Implications for a new class of antiretroviral inhibitors. Retrovirology, 2008, 5, 74.	2.0	102
128	Threshold Graph Limits and Random Threshold Graphs. Internet Mathematics, 2008, 5, 267-320.	0.7	46
129	The short-term regulation of foraging in harvester ants. Behavioral Ecology, 2008, 19, 217-222.	2.2	53
130	Minority Human Immunodeficiency Virus Type 1 Variants in Antiretroviral-Naive Persons with Reverse Transcriptase Codon 215 Revertant Mutations. Journal of Virology, 2008, 82, 10747-10755.	3.4	72
131	Horseshoes in multidimensional scaling and local kernel methods. Annals of Applied Statistics, 2008, 2, .	1.1	81
132	Multivariate data analysis: The French way. , 2008, , 219-233.		24
133	HIV-1 Subtype B Protease and Reverse Transcriptase Amino Acid Covariation. PLoS Computational Biology, 2007, 3, e87.	3.2	92
134	Down-Regulation of the Interferon Signaling Pathway in T Lymphocytes from Patients with Metastatic Melanoma. PLoS Medicine, 2007, 4, e176.	8.4	124
135	Dynamical Bias in the Coin Toss. SIAM Review, 2007, 49, 211-235.	9.5	137
136	Gene expression network analysis and applications to immunology. Bioinformatics, 2007, 23, 850-858.	4.1	149
137	Unusual Codon Bias in Vinyl Chloride Reductase Genes of Dehalococcoides Species. Applied and Environmental Microbiology, 2007, 73, 2744-2747.	3.1	25
138	An Interactive Statistical Image Segmentation and Visualization System. , 2007, , .		6
139	Forager activation and food availability in harvester ants. Animal Behaviour, 2006, 71, 815-822.	1.9	60
140	VISUALISING DATA. , 2006, , .		6
141	Rapid Assessment of Recognition Efficiency and Functional Capacity of Antigen-Specific T-Cell Responses. Journal of Immunotherapy, 2005, 28, 297-305.	2.4	15
142	Memory T cells have gene expression patterns intermediate between naive and effector. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5519-5523.	7.1	62
143	Error Distribution for Gene Expression Data. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article16.	0.6	80
144	Ion channel switch array:A biosensor for detecting multiple pathogens. Industrial Biotechnology, 2005, 1, 26-31.	0.8	15

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145	Sequential Monte Carlo Methods for Statistical Analysis of Tables. Journal of the American Statistical Association, 2005, 100, 109-120.	3.1	231
146	Gene expression diversity among Mycobacterium tuberculosis clinical isolates. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	78
147	Profile of Immune Cells in Axillary Lymph Nodes Predicts Disease-Free Survival in Breast Cancer. PLoS Medicine, 2005, 2, e284.	8.4	182
148	An In Vitro Human Cell-Based Assay to Rank the Relative Immunogenicity of Proteins. Toxicological Sciences, 2004, 77, 280-289.	3.1	20
149	Microarray Analysis Reveals Differences in Gene Expression of Circulating CD8+ T Cells in Melanoma Patients and Healthy Donors. Cancer Research, 2004, 64, 3661-3667.	0.9	24
150	Diversity and Recognition Efficiency of T Cell Responses to Cancer. PLoS Medicine, 2004, 1, e28.	8.4	82
151	Bioinformatics and Management Science: Some Common Tools and Techniques. Operations Research, 2004, 52, 165-190.	1.9	15
152	Use of exchangeable pairs in the analysis of simulations. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 1-25.	1.0	46
153	Stein's method for the bootstrap. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 93-132.	1.0	6
154	Stein's method for birth and death chains. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 42-65.	1.0	8
155	Statistics for phylogenetic trees. Theoretical Population Biology, 2003, 63, 17-32.	1.1	42
156	Human population-based identification of CD4+ T-cell peptide epitope determinants. Journal of Immunological Methods, 2003, 281, 95-108.	1.4	16
157	Bootstrapping Phylogenetic Trees: Theory and Methods. Statistical Science, 2003, 18, 241.	2.8	143
158	Bradley Efron: A Conversation with Good Friends. Statistical Science, 2003, 18, .	2.8	10
159	Random Walks on Trees and Matchings. Electronic Journal of Probability, 2002, 7, .	1.0	30
160	Geometry of the Space of Phylogenetic Trees. Advances in Applied Mathematics, 2001, 27, 733-767.	0.7	400
161	Statistical problems involving permutations with restricted positions. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2001, , 195-222.	1.0	26
162	Analysis of a nonreversible Markov chain sampler. Annals of Applied Probability, 2000, 10, 726.	1.3	176

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163	Elements of Large-Sample Theory. Journal of the American Statistical Association, 2000, 95, 328.	3.1	1
164	Evolutionary Games and Population Dynamics. Journal of the American Statistical Association, 2000, 95, 688.	3.1	3
165	Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology. Journal of the American Statistical Association, 1999, 94, 989.	3.1	39
166	Statistical Graphics for Visualizing Multivariate Data. Journal of the American Statistical Association, 1999, 94, 981.	3.1	0
167	Phylogenies: An Overview. The IMA Volumes in Mathematics and Its Applications, 1999, , 81-118.	0.5	23
168	Addressing geographical data errors in a classification tree for soil unit prediction. International Journal of Geographical Information Science, 1997, 11, 183-198.	4.8	77
169	Are there Still Things to Do in Bayesian Statistics?. , 1997, , 5-18.		1
170	Metrics on Compositions and Coincidences among Renewal Sequences. The IMA Volumes in Mathematics and Its Applications, 1996, , 81-101.	0.5	3
171	Three Examples of Monte-Carlo Markov Chains: At the Interface Between Statistical Computing, Computer Science, and Statistical Mechanics. The IMA Volumes in Mathematics and Its Applications, 1995, , 43-56.	0.5	14
172	Gray codes for randomization procedures. Statistics and Computing, 1994, 4, 287-302.	1.5	40
173	Correlations among quality parameters of peach fruit. Journal of the Science of Food and Agriculture, 1994, 66, 241-245.	3.5	37
174	Comment on â€œA Model for Studying Display Methods of Statistical Graphicsâ€. Journal of Computational and Graphical Statistics, 1993, 2, 349-353.	1.7	1
175	Comment on "A Model for Studying Display Methods of Statistical Graphics". Journal of Computational and Graphical Statistics, 1993, 2, 349.	1.7	2
176	Supervised topic modeling for predicting molecular substructure from mass spectrometry. F1000Research, 0, 10, 403.	1.6	4