Susan P Holmes

List of Publications by Citations

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	DADA2: High-resolution sample inference from Illumina amplicon data. *Nature Methods*, **2016**, 13, 581-3	21.6	7612
178	phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS ONE*, **2013**, 8, e61217	3.7	6869
177	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
176	Waste not, want not: why rarefying microbiome data is inadmissible. *PLoS Computational Biology*, **2014**, 10, e1003531	5	1536
175	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. *ISME Journal*, **2017**, 11, 2639-2643	11.9	1228
174	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. *Microbiome*, **2018**, 6, 226	16.6	680
173	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, 11060-5	11.5	581
172	Advancing our understanding of the human microbiome using QIIME. *Methods in Enzymology*, **2013**, 531, 371-444	1.7	373
171	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. *F1000Research*, **2016**, 5, 1492	3.6	316
170	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. *F1000Research*, **2016**, 5, 1492	3.6	303
169	Geometry of the Space of Phylogenetic Trees. *Advances in Applied Mathematics*, **2001**, 27, 733-767	0.8	293
168	Variability in the analysis of a single neuroimaging dataset by many teams. *Nature*, **2020**, 582, 84-88	50.4	281
167	Colonic contribution to uremic solutes. *Journal of the American Society of Nephrology: JASN*, **2011**, 22, 1769-76	12.7	260
166	Nasal microenvironments and interspecific interactions influence nasal microbiota complexity and S. aureus carriage. *Cell Host and Microbe*, **2013**, 14, 631-40	23.4	221
165	The molecular architecture of the eukaryotic chaperonin TRiC/CCT. *Structure*, **2012**, 20, 814-25	5.2	216
164	Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle. *Microbiome*, **2016**, 4, 15	16.6	210
163	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	11.5	182

162	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, 17059-64	11.5	180
161	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, 1275-85	7	178
160	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, 9010-5	11.5	173
159	Profile of immune cells in axillary lymph nodes predicts disease-free survival in breast cancer. *PLoS Medicine*, **2005**, 2, e284	11.6	161
158	Sequential Monte Carlo Methods for Statistical Analysis of Tables. *Journal of the American Statistical Association*, **2005**, 100, 109-120	2.8	152
157	structSSI: Simultaneous and Selective Inference for Grouped or Hierarchically Structured Data. *Journal of Statistical Software*, **2014**, 59, 1-21	7.3	146
156	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
155	Localized plasticity in the streamlined genomes of vinyl chloride respiring Dehalococcoides. *PLoS Genetics*, **2009**, 5, e1000714	6	135
154	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. *Nature Communications*, **2016**, 7, 10516	17.4	129
153	Human NK cell repertoire diversity reflects immune experience and correlates with viral susceptibility. *Science Translational Medicine*, **2015**, 7, 297ra115	17.5	120
152	Analysis of a nonreversible Markov chain sampler. *Annals of Applied Probability*, **2000**, 10, 726	2	119
151	The effect of individual variation on the structure and function of interaction networks in harvester ants. *Journal of the Royal Society Interface*, **2011**, 8, 1562-73	4.1	116
150	Gene expression network analysis and applications to immunology. *Bioinformatics*, **2007**, 23, 850-8	7.2	116
149	Down-regulation of the interferon signaling pathway in T lymphocytes from patients with metastatic melanoma. *PLoS Medicine*, **2007**, 4, e176	11.6	107
148	Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis. *JCI Insight*, **2020**, 5,	9.9	106
147	Natural variation of HIV-1 group M integrase: implications for a new class of antiretroviral inhibitors. *Retrovirology*, **2008**, 5, 74	3.6	92
146	Ten quick tips for effective dimensionality reduction. *PLoS Computational Biology*, **2019**, 15, e1006907	5	89
145	Dynamical Bias in the Coin Toss. *SIAM Review*, **2007**, 49, 211-235	7.4	89

144	Shiny-phyloseq: Web application for interactive microbiome analysis with provenance tracking. *Bioinformatics*, **2015**, 31, 282-3	7.2	84
143	Bootstrapping Phylogenetic Trees: Theory and Methods. *Statistical Science*, **2003**, 18, 241	2.4	83
142	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science **2018**,		78
141	Diversity and recognition efficiency of T cell responses to cancer. *PLoS Medicine*, **2004**, 1, e28	11.6	76
140	HIV-1 subtype B protease and reverse transcriptase amino acid covariation. *PLoS Computational Biology*, **2007**, 3, e87	5	75
139	Harvester ants use interactions to regulate forager activation and availability. *Animal Behaviour*, **2013**, 86, 197-207	2.8	74
138	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. *Genome Research*, **2018**, 28, 1467-1480	9.7	73
137	Gut microbiome transition across a lifestyle gradient in Himalaya. *PLoS Biology*, **2018**, 16, e2005396	9.7	71
136	Gene expression diversity among Mycobacterium tuberculosis clinical isolates. *Microbiology (United Kingdom)*, **2005**, 151, 5-14	2.9	67
135	Addressing geographical data errors in a classification tree for soil unit prediction. *International Journal of Geographical Information Science*, **1997**, 11, 183-198	4.1	65
134	Minority human immunodeficiency virus type 1 variants in antiretroviral-naive persons with reverse transcriptase codon 215 revertant mutations. *Journal of Virology*, **2008**, 82, 10747-55	6.6	65
133	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. *Nature Communications*, **2018**, 9, 681	17.4	64
132	Detection of cytomegalovirus drug resistance mutations by next-generation sequencing. *Journal of Clinical Microbiology*, **2013**, 51, 3700-10	9.7	63
131	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	1.3	63
130	Error distribution for gene expression data. *Statistical Applications in Genetics and Molecular Biology*, **2005**, 4, Article16	1.2	61
129	Horseshoes in multidimensional scaling and local kernel methods. *Annals of Applied Statistics*, **2008**, 2,	2.1	60
128	Denoising PCR-amplified metagenome data. *BMC Bioinformatics*, **2012**, 13, 283	3.6	58
127	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, 5519-23	11.5	56

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126	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, 14506-11	11.5	55
125	Colony variation in the collective regulation of foraging by harvester ants. *Behavioral Ecology*, **2011**, 22, 429-435	2.3	54
124	Forager activation and food availability in harvester ants. *Animal Behaviour*, **2006**, 71, 815-822	2.8	53
123	Nest site and weather affect the personality of harvester ant colonies. *Behavioral Ecology*, **2012**, 23, 1022-1029	2.3	52
122	HIV-1 Protease, Reverse Transcriptase, and Integrase Variation. *Journal of Virology*, **2016**, 90, 6058-6070	6.6	52
121	More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. *ELife*, **2016**, 5,	8.9	50
120	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. *PLoS ONE*, **2015**, 10, e0142825	3.7	49
119	Site-specific mobilization of vinyl chloride respiration islands by a mechanism common in Dehalococcoides. *BMC Genomics*, **2011**, 12, 287	4.5	49
118	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. *PLoS Computational Biology*, **2017**, 13, e1005706	5	45
117	Genomic interrogation of ancestral Mycobacterium tuberculosis from south India. *Infection, Genetics and Evolution*, **2008**, 8, 474-83	4.5	45
116	Constrained patterns of covariation and clustering of HIV-1 non-nucleoside reverse transcriptase inhibitor resistance mutations. *Journal of Antimicrobial Chemotherapy*, **2010**, 65, 1477-85	5.1	44
115	The short-term regulation of foraging in harvester ants. *Behavioral Ecology*, **2008**, 19, 217-222	2.3	43
114	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	3.7	41
113	Tracking network dynamics: A survey using graph distances. *Annals of Applied Statistics*, **2018**, 12,	2.1	39
112	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	3.7	37
111	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data		37
110	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
109	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19. *Journal of Experimental Medicine*, **2021**, 218,	16.6	34

108	Measuring multivariate association and beyond. *Statistics Surveys*, **2016**, 10, 132-167	1.7	33
107	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. *Microbiome*, **2019**, 7, 131	16.6	32
106	Threshold Graph Limits and Random Threshold Graphs. *Internet Mathematics*, **2008**, 5, 267-320	0	32
105	Statistics for phylogenetic trees. *Theoretical Population Biology*, **2003**, 63, 17-32	1.2	32
104	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. *Periodontology 2000*, **2020**, 82, 26-41	12.9	32
103	Nonpolymorphic human immunodeficiency virus type 1 protease and reverse transcriptase treatment-selected mutations. *Antimicrobial Agents and Chemotherapy*, **2009**, 53, 4869-78	5.9	31
102	Computational Tools for Evaluating Phylogenetic and Hierarchical Clustering Trees. *Journal of Computational and Graphical Statistics*, **2012**, 21, 581-599	1.4	30
101	Use of exchangeable pairs in the analysis of simulations. *Lecture Notes-monograph Series / Institute of Mathematical Statistics*, **2004**, 1-25	0	30
100	Gray codes for randomization procedures. *Statistics and Computing*, **1994**, 4, 287-302	1.8	29
99	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 Suppl 2, S70-7	7	28
98	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	3.5	27
97	Correlations among quality parameters of peach fruit. *Journal of the Science of Food and Agriculture*, **1994**, 66, 241-245	4.3	27
96	Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration. *EBioMedicine*, **2017**, 18, 225-235	8.8	25
95	Differential Induction of IFN-□ and Modulation of CD112 and CD54 Expression Govern the Magnitude of NK Cell IFN-□ Response to Influenza A Viruses. *Journal of Immunology*, **2018**, 201, 2117-2131	5.3	25
94	Unusual codon bias in vinyl chloride reductase genes of Dehalococcoides species. *Applied and Environmental Microbiology*, **2007**, 73, 2744-7	4.8	25
93	Mass Cytometry Analytical Approaches Reveal Cytokine-Induced Changes in Natural Killer Cells. *Cytometry Part B - Clinical Cytometry*, **2017**, 92, 57-67	3.4	24
92	Microarray analysis reveals differences in gene expression of circulating CD8(+) T cells in melanoma patients and healthy donors. *Cancer Research*, **2004**, 64, 3661-7	10.1	24
91	Random Walks on Trees and Matchings. *Electronic Journal of Probability*, **2002**, 7,	1.1	24

90	Pregnancy-Induced Alterations in NK Cell Phenotype and Function. *Frontiers in Immunology*, **2019**, 10, 2469	8.4	23
89	Bayesian Nonparametric Ordination for the Analysis of Microbial Communities. *Journal of the American Statistical Association*, **2017**, 112, 1430-1442	2.8	22
88	Latent variable modeling for the microbiome. *Biostatistics*, **2019**, 20, 599-614	3.7	22
87	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, 343-9	5.9	22
86	PHYLOSEQ: A BIOCONDUCTOR PACKAGE FOR HANDLING AND ANALYSIS OF HIGH-THROUGHPUT PHYLOGENETIC SEQUENCE DATA **2011**,		22
85	Comparisons of distance methods for combining covariates and abundances in microbiome studies. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2012**, 213-24	1.3	22
84	Prototypical Recombinant Multi-Protease-Inhibitor-Resistant Infectious Molecular Clones of Human Immunodeficiency Virus Type 1. *Antimicrobial Agents and Chemotherapy*, **2013**, 57, 4290-4299	5.9	21
83	Sampling from a Manifold. *Institute of Mathematical Statistics Collections*, **2013**, 102-125		20
82	Prevalence of Drug-Resistant Minority Variants in Untreated HIV-1-Infected Individuals With and Those Without Transmitted Drug Resistance Detected by Sanger Sequencing. *Journal of Infectious Diseases*, **2017**, 216, 387-391	7	20
81	Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*, **2021**, 27, 1885-1892	50.5	19
80	An in vitro human cell-based assay to rank the relative immunogenicity of proteins. *Toxicological Sciences*, **2004**, 77, 280-9	4.4	18
79	Phylogenies: An Overview. *The IMA Volumes in Mathematics and Its Applications*, **1999**, 81-118	0.5	18
78	Multivariate data analysis: The French way **2008**, 219-233		17
77	Statistical problems involving permutations with restricted positions. *Lecture Notes-monograph Series / Institute of Mathematical Statistics*, **2001**, 195-222	0	17
76	A classification model for G-to-A hypermutation in hepatitis B virus ultra-deep pyrosequencing reads. *Bioinformatics*, **2010**, 26, 2929-32	7.2	16
75	Human population-based identification of CD4(+) T-cell peptide epitope determinants. *Journal of Immunological Methods*, **2003**, 281, 95-108	2.5	16
74	Rapid assessment of recognition efficiency and functional capacity of antigen-specific T-cell responses. *Journal of Immunotherapy*, **2005**, 28, 297-305	5	15
73	THE DUALITY DIAGRAM IN DATA ANALYSIS: EXAMPLES OF MODERN APPLICATIONS. *Annals of Applied Statistics*, **2011**, 5, 2266-2277	2.1	14

72	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating Dehalococcoides mccartyi Consortium. *Environmental Science & Technology*, **2016**, 50, 12187-12196	10.3	12
71	COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES **2011**,		12
70	A multifaceted analysis of HIV-1 protease multidrug resistance phenotypes. *BMC Bioinformatics*, **2011**, 12, 477	3.6	12
69	Ion channel switch array:A biosensor for detecting multiple pathogens. *Industrial Biotechnology*, **2005**, 1, 26-31	1.3	12
68	Exact sequence variants should replace operational taxonomic units in marker gene data analysis		12
67	Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios. *Journal of Applied Statistics*,1-29	1	12
66	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	12
65	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	4.5	11
64	Multitable Methods for Microbiome Data Integration. *Frontiers in Genetics*, **2019**, 10, 627	4.5	11
63	Gut microbiota plasticity is correlated with sustained weight loss on a low-carb or low-fat dietary intervention. *Scientific Reports*, **2020**, 10, 1405	4.9	11
62	Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19		11
61	Parallel imaging of embryos for quantitative analysis of genetic perturbations of the Ras pathway. *DMM Disease Models and Mechanisms*, **2017**, 10, 923-929	4.1	10
60	Bayesian Unidimensional Scaling for visualizing uncertainty in high dimensional datasets with latent ordering of observations. *BMC Bioinformatics*, **2017**, 18, 394	3.6	10
59	Visualization and statistical comparisons of microbial communities using R packages on Phylochip data. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2011**, 142-53	1.3	10
58	An Interactive Java Statistical Image Segmentation System: GemIdent. *Journal of Statistical Software*, **2009**, 30,	7.3	10
57	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	1.3	10
56	An InteractiveJavaStatistical Image Segmentation System:GemIdent. *Journal of Statistical Software*, **2009**, 30,	7.3	10
55	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. *PLoS ONE*, **2020**, 15, e0225352	3.7	9

54	Interval Graph Limits. *Annals of Combinatorics*, **2013**, 17, 27-52	0.7	9
53	Bioinformatics and Management Science: Some Common Tools and Techniques. *Operations Research*, **2004**, 52, 165-190	2.3	9
52	Template Shape Estimation: Correcting an Asymptotic Bias. *SIAM Journal on Imaging Sciences*, **2017**, 10, 808-844	1.9	8
51	Expanded Spectrum of Antiretroviral-Selected Mutations in Human Immunodeficiency Virus Type 2. *Journal of Infectious Diseases*, **2020**, 221, 1962-1972	7	8
50	Bradley Efron: A Conversation with Good Friends. *Statistical Science*, **2003**, 18,	2.4	8
49	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*, **2020**,	7	8
48	Natural killer cell phenotype is altered in HIV-exposed seronegative women. *PLoS ONE*, **2020**, 15, e0238347	3.7	8
47	Nuclear degradation dynamics in a nonapoptotic programmed cell death. *Cell Death and Differentiation*, **2020**, 27, 711-724	12.7	8
46	Analysis of casino shelf shuffling machines. *Annals of Applied Probability*, **2013**, 23,	2	7
45	CD38 contributes to human natural killer cell responses through a role in immune synapse formation		7
44	Interactive Visualization of Hierarchically Structured Data. *Journal of Computational and Graphical Statistics*, **2018**, 27, 553-563	1.4	6
43	Steins method for the bootstrap. *Lecture Notes-monograph Series / Institute of Mathematical Statistics*, **2004**, 93-132	0	6
42	Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon. *Nature Communications*, **2020**, 11, 3772	17.4	6
41	Characterization of the Impact of Daclizumab Beta on Circulating Natural Killer Cells by Mass Cytometry. *Frontiers in Immunology*, **2020**, 11, 714	8.4	5
40	Statistical proof? The problem of irreproducibility. *Bulletin of the American Mathematical Society*, **2017**, 55, 31-55	1.3	5
39	de Finetti Priors using Markov chain Monte Carlo computations. *Statistics and Computing*, **2015**, 25, 797-808	0.8	5
38	An Interactive Statistical Image Segmentation and Visualization System **2007**,		5
37	Mass Cytometry Analysis of the NK Cell Receptor-Ligand Repertoire Reveals Unique Differences between Dengue-Infected Children and Adults. *ImmunoHorizons*, **2020**, 4, 634-647	2.7	5

36	Treated HIV Infection Alters Phenotype but Not HIV-Specific Function of Peripheral Blood Natural Killer Cells. *Frontiers in Immunology*, **2020**, 11, 829	8.4	4
35	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA **2016**,		4
34	VISUALISING DATA **2006**,		4
33	Connections and Extensions: A Discussion of the Paper by Girolami and Byrne. *Scandinavian Journal of Statistics*, **2014**, 41, 3-7	0.8	3
32	Adaptive importance sampling for network growth models. *Annals of Operations Research*, **2011**, 189, 187-203	3.2	3
31	Unmasking Seasonal Cycles in Human Fertility: How holiday sex and fertility cycles shape birth seasonality		3
30	CytoGLMM: conditional differential analysis for flow and mass cytometry experiments. *BMC Bioinformatics*, **2021**, 22, 137	3.6	3
29	Multivariate Heteroscedasticity Models for Functional Brain Connectivity. *Frontiers in Neuroscience*, **2017**, 11, 696	5.1	2
28	Combined use of metagenomic sequencing and host response profiling for the diagnosis of suspected sepsis		2
27	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. *GigaScience*, **2020**, 9,	7.6	2
26	A Statistical Perspective on the Challenges in Molecular Microbial Biology. *Journal of Agricultural, Biological, and Environmental Statistics*, **2021**, 26, 131-160	1.9	2
25	Community-wide hackathons to identify central themes in single-cell multi-omics. *Genome Biology*, **2021**, 22, 220	18.3	2
24	Statistical Modeling for Practical Pooled Testing During the COVID-19 Pandemic. *Statistical Science*, **2022**, 37,	2.4	2
23	Multi-Table Differential Correlation Analysis of Neuroanatomical and Cognitive Interactions in Turner Syndrome. *Neuroinformatics*, **2018**, 16, 81-93	3.2	1
22	Topologically Constrained Template Estimation via Morse--Smale Complexes Controls Its Statistical Consistency. *SIAM Journal on Applied Algebra and Geometry*, **2018**, 2, 348-375	1.5	1
21	Random Spatial Structure of Geometric Deformations and Bayesian Nonparametrics. *Lecture Notes in Computer Science*, **2013**, 120-127	0.9	1
20	Elements of Large-Sample Theory. *Journal of the American Statistical Association*, **2000**, 95, 328	2.8	1
19	Comment on Ä Model for Studying Display Methods of Statistical Graphics *Journal of Computational and Graphical Statistics*, **1993**, 2, 349-353	1.4	1

18	Comment on "A Model for Studying Display Methods of Statistical Graphics". *Journal of Computational and Graphical Statistics*, **1993**, 2, 349	1.4	1
17	Treated HIV Infection Alters Phenotype But Not HIV-specific Function of Peripheral Blood Natural Killer Cells		1
16	Treatment-Specific Composition of Gut Microbiota Is Associated with Disease Remission in a Pediatric Crohns Disease Cohort		1
15	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome		1
14	Supervised topic modeling for predicting molecular substructure from mass spectrometry. *F1000Research*,10, 403	3.6	1
13	Influenza-Induced Interferon Lambda Response Is Associated With Longer Time to Delivery Among Pregnant Kenyan Women. *Frontiers in Immunology*, **2020**, 11, 452	8.4	1
12	Labeling self-tracked menstrual health records with hidden semi-Markov models		1
11	Labeling self-tracked menstrual health records with hidden semi-Markov models. *IEEE Journal of Biomedical and Health Informatics*, **2021**, PP,	7.2	1
10	Metrics on Compositions and Coincidences among Renewal Sequences. *The IMA Volumes in Mathematics and Its Applications*, **1996**, 81-101	0.5	1
9	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	5.9	0
8	Successful strategies for human microbiome data generation, storage and analyses. *Journal of Biosciences*, **2019**, 44, 1	2.3	
7	Discussion of 50 Years of Data Science. *Journal of Computational and Graphical Statistics*, **2017**, 26, 768-769	1.4	
6	Are there Still Things to Do in Bayesian Statistics? **1997**, 5-18		
5	Elements of Large-Sample Theory **2012**, 1111-1112		
4	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences **2020**, 15, e0225352		
3	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences **2020**, 15, e0225352		
2	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences **2020**, 15, e0225352		
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