

Frederick A Matsen Iv

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

3,215
citations

186265
28
h-index

189892
50
g-index

103
all docs

103
docs citations

103
times ranked

5026
citing authors

#	ARTICLE	IF	CITATIONS
1	ppplacer: linear time maximum-likelihood and Bayesian phylogenetic placement of sequences onto a fixed reference tree. BMC Bioinformatics, 2010, 11, 538.	2.6	901
2	Propionibacterium Persists in the Skin Despite Standard Surgical Preparation. Journal of Bone and Joint Surgery - Series A, 2014, 96, 1447-1450.	3.0	150
3	Consistency of VDJ Rearrangement and Substitution Parameters Enables Accurate B Cell Receptor Sequence Annotation. PLoS Computational Biology, 2016, 12, e1004409.	3.2	130
4	Human T cell receptor occurrence patterns encode immune history, genetic background, and receptor specificity. ELife, 2018, 7, .	6.0	124
5	Bacterial Composition of the Human Upper Gastrointestinal Tract Microbiome Is Dynamic and Associated with Genomic Instability in a Barrett's Esophagus Cohort. PLoS ONE, 2015, 10, e0129055.	2.5	107
6	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. Frontiers in Immunology, 2017, 8, 1418.	4.8	102
7	Likelihood-Based Inference of B Cell Clonal Families. PLoS Computational Biology, 2016, 12, e1005086.	3.2	93
8	What Factors are Predictive of Patient-reported Outcomes? A Prospective Study of 337 Shoulder Arthroplasties. Clinical Orthopaedics and Related Research, 2016, 474, 2496-2510.	1.5	90
9	Quantifying MCMC Exploration of Phylogenetic Tree Space. Systematic Biology, 2015, 64, 472-491.	5.6	71
10	Non-Human Primates Harbor Diverse Mammalian and Avian Astroviruses Including Those Associated with Human Infections. PLoS Pathogens, 2015, 11, e1005225.	4.7	68
11	A Format for Phylogenetic Placements. PLoS ONE, 2012, 7, e31009.	2.5	60
12	Deep generative models for T cell receptor protein sequences. ELife, 2019, 8, .	6.0	60
13	Healing of reamed glenoid bone articulating with a metal humeral hemiarthroplasty: A canine model. Journal of Orthopaedic Research, 2005, 23, 18-26.	2.3	55
14	Using Genotype Abundance to Improve Phylogenetic Inference. Molecular Biology and Evolution, 2018, 35, 1253-1265.	8.9	55
15	Does Postoperative Glenoid Retroversion Affect the 2-Year Clinical and Radiographic Outcomes for Total Shoulder Arthroplasty?. Clinical Orthopaedics and Related Research, 2017, 475, 2726-2739.	1.5	53
16	Per-sample immunoglobulin germline inference from B cell receptor deep sequencing data. PLoS Computational Biology, 2019, 15, e1007133.	3.2	51
17	The mean and variance of phylogenetic diversity under rarefaction. Methods in Ecology and Evolution, 2013, 4, 566-572.	5.2	50
18	Comment on "A Database of Human Immune Receptor Alleles Recovered from Population Sequencing Data". Journal of Immunology, 2017, 198, 3371-3373.	0.8	46

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19	Quantifying evolutionary constraints on B-cell affinity maturation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140244.	4.0	45
20	Epitope profiling reveals binding signatures of SARS-CoV-2 immune response in natural infection and cross-reactivity with endemic human CoVs. <i>Cell Reports</i> , 2021, 35, 109164.	6.4	44
21	HIV-1 Superinfection Occurs Less Frequently Than Initial Infection in a Cohort of High-Risk Kenyan Women. <i>PLoS Pathogens</i> , 2013, 9, e1003593.	4.7	41
22	Dynamics of HIV DNA reservoir seeding in a cohort of superinfected Kenyan women. <i>PLoS Pathogens</i> , 2020, 16, e1008286.	4.7	41
23	Zoonotic simian foamy virus in Bangladesh reflects diverse patterns of transmission and co-infection. <i>Emerging Microbes and Infections</i> , 2013, 2, 1-10.	6.5	39
24	Phylogenetics and the Human Microbiome. <i>Systematic Biology</i> , 2015, 64, e26-e41.	5.6	36
25	High-resolution profiling of pathways of escape for SARS-CoV-2 spike-binding antibodies. <i>Cell</i> , 2021, 184, 2927-2938.e11.	28.9	35
26	The evolution within us. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140235.	4.0	34
27	High-throughput sequencing of B- and T-lymphocyte antigen receptors in hematology. <i>Blood</i> , 2013, 122, 19-22.	1.4	33
28	Kappa chain maturation helps drive rapid development of an infant HIV-1 broadly neutralizing antibody lineage. <i>Nature Communications</i> , 2019, 10, 2190.	12.8	31
29	A Method for Investigating Relative Timing Information on Phylogenetic Trees. <i>Systematic Biology</i> , 2009, 58, 167-183.	5.6	30
30	Preoperative Skin-Surface Cultures Can Help to Predict the Presence of Propionibacterium in Shoulder Arthroplasty Wounds. <i>JBJS Open Access</i> , 2018, 3, e0052.	1.5	30
31	OGRDB: a reference database of inferred immune receptor genes. <i>Nucleic Acids Research</i> , 2020, 48, D964-D970.	14.5	30
32	Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals. <i>Systematic Biology</i> , 2018, 67, 490-502.	5.6	29
33	Benchmarking Tree and Ancestral Sequence Inference for B Cell Receptor Sequences. <i>Frontiers in Immunology</i> , 2018, 9, 2451.	4.8	26
34	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. <i>Virus Evolution</i> , 2019, 5, vez003.	4.9	26
35	Functional Outcomes of the Ream-and-Run Shoulder Arthroplasty. <i>Journal of Bone and Joint Surgery - Series A</i> , 2017, 99, 1999-2003.	3.0	25
36	sumrep: A Summary Statistic Framework for Immune Receptor Repertoire Comparison and Model Validation. <i>Frontiers in Immunology</i> , 2019, 10, 2533.	4.8	22

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37	Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo. <i>Systematic Biology</i> , 2018, 67, 503-517.	5.6	21
38	A Bayesian phylogenetic hidden Markov model for B cell receptor sequence analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1008030.	3.2	20
39	Comprehensive characterization of the antibody responses to SARS-CoV-2 Spike protein finds additional vaccine-induced epitopes beyond those for mild infection. <i>ELife</i> , 2022, 11, .	6.0	19
40	Assessing the Value to the Patient of New Technologies in Anatomic Total Shoulder Arthroplasty. <i>Journal of Bone and Joint Surgery - Series A</i> , 2021, 103, 761-770.	3.0	16
41	SARS-CoV-2 Antibody Binding and Neutralization in Dried Blood Spot Eluates and Paired Plasma. <i>Microbiology Spectrum</i> , 2021, 9, e0129821.	3.0	15
42	The combinatorics of discrete time-trees: theory and open problems. <i>Journal of Mathematical Biology</i> , 2018, 76, 1101-1121.	1.9	14
43	Shoulder Hemiarthroplasty with Nonprosthetic Glenoid Arthroplasty. <i>JBJS Reviews</i> , 2021, 9, .	2.0	13
44	Using B cell receptor lineage structures to predict affinity. <i>PLoS Computational Biology</i> , 2020, 16, e1008391.	3.2	13
45	The Bayesian optimist's guide to adaptive immune receptor repertoire analysis. <i>Immunological Reviews</i> , 2018, 284, 148-166.	6.0	12
46	Estimation of cell lineage trees by maximum-likelihood phylogenetics. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	12
47	Anatomic Total Shoulder Arthroplasty with All-Polyethylene Glenoid Component for Primary Osteoarthritis with Glenoid Deficiencies. <i>JBJS Open Access</i> , 2020, 5, e20.00002-e20.00002.	1.5	12
48	Combining genotypes and T cell receptor distributions to infer genetic loci determining V(D)J recombination probabilities. <i>ELife</i> , 2022, 11, .	6.0	12
49	Minimizing the Average Distance to a Closest Leaf in a Phylogenetic Tree. <i>Systematic Biology</i> , 2013, 62, 824-836.	5.6	11
50	Calculating the Unrooted Subtree Prune-and-Regraft Distance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 898-911.	3.0	11
51	Diversity and Function of Maternal HIV-1-Specific Antibodies at the Time of Vertical Transmission. <i>Journal of Virology</i> , 2020, 94, .	3.4	11
52	Ricciâ€™Ollivier curvature of the rooted phylogenetic subtreeâ€™pruneâ€™regraft graph. <i>Theoretical Computer Science</i> , 2017, 699, 1-20.	0.9	10
53	Predicting B cell receptor substitution profiles using public repertoire data. <i>PLoS Computational Biology</i> , 2018, 14, e1006388.	3.2	8
54	Survival analysis of DNA mutation motifs with penalized proportional hazards. <i>Annals of Applied Statistics</i> , 2019, 13, 1268-1294.	1.1	8

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55	Distinct Antibody Responses to Endemic Coronaviruses Pre- and Post-SARS-CoV-2 Infection in Kenyan Infants and Mothers. <i>Viruses</i> , 2022, 14, 1517.	3.3	8
56	Ubiquity of synonymy: almost all large binary trees are not uniquely identified by their spectra or their immanantal polynomials. <i>Algorithms for Molecular Biology</i> , 2012, 7, 14.	1.2	7
57	nestly—a framework for running software with nested parameter choices and aggregating results. <i>Bioinformatics</i> , 2013, 29, 387-388.	4.1	7
58	On the enumeration of tanglegrams and tangled chains. <i>Journal of Combinatorial Theory - Series A</i> , 2017, 146, 239-263.	0.8	7
59	Tanglegrams: A Reduction Tool for Mathematical Phylogenetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 343-349.	3.0	7
60	Functional development of a V3/glycan-specific broadly neutralizing antibody isolated from a case of HIV superinfection. <i>ELife</i> , 2021, 10, .	6.0	6
61	Detailed analysis of antibody responses to SARS-CoV-2 vaccination and infection in macaques. <i>PLoS Pathogens</i> , 2022, 18, e1010155.	4.7	6
62	Consistency and convergence rate of phylogenetic inference via regularization. <i>Annals of Statistics</i> , 2018, 46, 1481-1512.	2.6	5
63	Joint Maximum Likelihood of Phylogeny and Ancestral States Is Not Consistent. <i>Molecular Biology and Evolution</i> , 2019, 36, 2352-2357.	8.9	5
64	A Surrogate Function for One-Dimensional Phylogenetic Likelihoods. <i>Molecular Biology and Evolution</i> , 2018, 35, 242-246.	8.9	4
65	Oral and IV Antibiotic Administration After Single-Stage Revision Shoulder Arthroplasty. <i>Journal of Bone and Joint Surgery - Series A</i> , 2021, Publish Ahead of Print, .	3.0	4
66	Subluxation in the Arthritic Shoulder. <i>JBJS Reviews</i> , 2021, 9, .	2.0	4
67	Efficacy of Home Prophylactic Benzoyl Peroxide and Chlorhexidine in Shoulder Surgery. <i>JBJS Reviews</i> , 2020, 8, e20.00023.	2.0	3
68	Development of antibody-dependent cell cytotoxicity function in HIV-1 antibodies. <i>ELife</i> , 2021, 10, .	6.0	3
69	Lack of Evidence for a Substantial Rate of Templated Mutagenesis in B Cell Diversification. <i>Journal of Immunology</i> , 2020, 205, 936-944.	0.8	1
70	Nonbifurcating Phylogenetic Tree Inference via the Adaptive LASSO. <i>Journal of the American Statistical Association</i> , 2021, 116, 858-873.	3.1	1
71	constNJ: An Algorithm to Reconstruct Sets of Phylogenetic Trees Satisfying Pairwise Topological Constraints. <i>Journal of Computational Biology</i> , 2010, 17, 799-818.	1.6	0
72	On the convergence of the maximum likelihood estimator for the transition rate under a 2-state symmetric model. <i>Journal of Mathematical Biology</i> , 2020, 80, 1119-1138.	1.9	0

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73	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
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75	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
76	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
77	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
78	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
79	Enabling Inference for Context-Dependent Models of Mutation by Bounding the Propagation of Dependency. Journal of Computational Biology, 2022, 29, 802-824.	1.6	0