

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	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
2	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
3	Detailed analysis of antibody responses to SARS-CoV-2 vaccination and infection in macaques. <i>PLoS Pathogens</i> , 2022, 18, e1010155.	4.7	6
4	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
5	Enabling Inference for Context-Dependent Models of Mutation by Bounding the Propagation of Dependency. <i>Journal of Computational Biology</i> , 2022, 29, 802-824.	1.6	0
6	Nonbifurcating Phylogenetic Tree Inference via the Adaptive LASSO. <i>Journal of the American Statistical Association</i> , 2021, 116, 858-873.	3.1	1
7	Development of antibody-dependent cell cytotoxicity function in HIV-1 antibodies. <i>ELife</i> , 2021, 10, .	6.0	3
8	Estimation of cell lineage trees by maximum-likelihood phylogenetics. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	12
9	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
10	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
11	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
12	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
13	Shoulder Hemiarthroplasty with Nonprosthetic Glenoid Arthroplasty. <i>JBJS Reviews</i> , 2021, 9, .	2.0	13
14	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
15	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
16	Subluxation in the Arthritic Shoulder. <i>JBJS Reviews</i> , 2021, 9, .	2.0	4
17	OGRDB: a reference database of inferred immune receptor genes. <i>Nucleic Acids Research</i> , 2020, 48, D964-D970.	14.5	30
18	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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19	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
20	A Bayesian phylogenetic hidden Markov model for B cell receptor sequence analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1008030.	3.2	20
21	Efficacy of Home Prophylactic Benzoyl Peroxide and Chlorhexidine in Shoulder Surgery. <i>JBJS Reviews</i> , 2020, 8, e20.00023.	2.0	3
22	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
23	Dynamics of HIV DNA reservoir seeding in a cohort of superinfected Kenyan women. <i>PLoS Pathogens</i> , 2020, 16, e1008286.	4.7	41
24	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
25	Using B cell receptor lineage structures to predict affinity. <i>PLoS Computational Biology</i> , 2020, 16, e1008391.	3.2	13
26	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
27	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
28	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
29	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
30	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
31	Using B cell receptor lineage structures to predict affinity. , 2020, 16, e1008391.		0
32	Per-sample immunoglobulin germline inference from B cell receptor deep sequencing data. <i>PLoS Computational Biology</i> , 2019, 15, e1007133.	3.2	51
33	Survival analysis of DNA mutation motifs with penalized proportional hazards. <i>Annals of Applied Statistics</i> , 2019, 13, 1268-1294.	1.1	8
34	Joint Maximum Likelihood of Phylogeny and Ancestral States Is Not Consistent. <i>Molecular Biology and Evolution</i> , 2019, 36, 2352-2357.	8.9	5
35	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
36	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. <i>Virus Evolution</i> , 2019, 5, vez003.	4.9	26

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37	sumrep: A Summary Statistic Framework for Immune Receptor Repertoire Comparison and Model Validation. <i>Frontiers in Immunology</i> , 2019, 10, 2533.	4.8	22
38	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
39	Deep generative models for T cell receptor protein sequences. <i>ELife</i> , 2019, 8, .	6.0	60
40	Using Genotype Abundance to Improve Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2018, 35, 1253-1265.	8.9	55
41	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
42	Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals. <i>Systematic Biology</i> , 2018, 67, 490-502.	5.6	29
43	Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo. <i>Systematic Biology</i> , 2018, 67, 503-517.	5.6	21
44	A Surrogate Function for One-Dimensional Phylogenetic Likelihoods. <i>Molecular Biology and Evolution</i> , 2018, 35, 242-246.	8.9	4
45	Tanglegrams: A Reduction Tool for Mathematical Phylogenetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 343-349.	3.0	7
46	The combinatorics of discrete time-trees: theory and open problems. <i>Journal of Mathematical Biology</i> , 2018, 76, 1101-1121.	1.9	14
47	Benchmarking Tree and Ancestral Sequence Inference for B Cell Receptor Sequences. <i>Frontiers in Immunology</i> , 2018, 9, 2451.	4.8	26
48	Human T cell receptor occurrence patterns encode immune history, genetic background, and receptor specificity. <i>ELife</i> , 2018, 7, .	6.0	124
49	Predicting B cell receptor substitution profiles using public repertoire data. <i>PLoS Computational Biology</i> , 2018, 14, e1006388.	3.2	8
50	The Bayesian optimist's guide to adaptive immune receptor repertoire analysis. <i>Immunological Reviews</i> , 2018, 284, 148-166.	6.0	12
51	Consistency and convergence rate of phylogenetic inference via regularization. <i>Annals of Statistics</i> , 2018, 46, 1481-1512.	2.6	5
52	Comment on "A Database of Human Immune Receptor Alleles Recovered from Population Sequencing Data". <i>Journal of Immunology</i> , 2017, 198, 3371-3373.	0.8	46
53	On the enumeration of tanglegrams and tangled chains. <i>Journal of Combinatorial Theory - Series A</i> , 2017, 146, 239-263.	0.8	7
54	Ricci-Ollivier curvature of the rooted phylogenetic subtree-prune-regraft graph. <i>Theoretical Computer Science</i> , 2017, 699, 1-20.	0.9	10

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55	Does Postoperative Glenoid Retroversion Affect the 2-Year Clinical and Radiographic Outcomes for Total Shoulder Arthroplasty?. <i>Clinical Orthopaedics and Related Research</i> , 2017, 475, 2726-2739.	1.5	53
56	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
57	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. <i>Frontiers in Immunology</i> , 2017, 8, 1418.	4.8	102
58	What Factors are Predictive of Patient-reported Outcomes? A Prospective Study of 337 Shoulder Arthroplasties. <i>Clinical Orthopaedics and Related Research</i> , 2016, 474, 2496-2510.	1.5	90
59	Consistency of VDJ Rearrangement and Substitution Parameters Enables Accurate B Cell Receptor Sequence Annotation. <i>PLoS Computational Biology</i> , 2016, 12, e1004409.	3.2	130
60	Likelihood-Based Inference of B Cell Clonal Families. <i>PLoS Computational Biology</i> , 2016, 12, e1005086.	3.2	93
61	Bacterial Composition of the Human Upper Gastrointestinal Tract Microbiome Is Dynamic and Associated with Genomic Instability in a Barrett's Esophagus Cohort. <i>PLoS ONE</i> , 2015, 10, e0129055.	2.5	107
62	Non-Human Primates Harbor Diverse Mammalian and Avian Astroviruses Including Those Associated with Human Infections. <i>PLoS Pathogens</i> , 2015, 11, e1005225.	4.7	68
63	Quantifying MCMC Exploration of Phylogenetic Tree Space. <i>Systematic Biology</i> , 2015, 64, 472-491.	5.6	71
64	The evolution within us. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140235.	4.0	34
65	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
66	Phylogenetics and the Human Microbiome. <i>Systematic Biology</i> , 2015, 64, e26-e41.	5.6	36
67	Propionibacterium Persists in the Skin Despite Standard Surgical Preparation. <i>Journal of Bone and Joint Surgery - Series A</i> , 2014, 96, 1447-1450.	3.0	150
68	Minimizing the Average Distance to a Closest Leaf in a Phylogenetic Tree. <i>Systematic Biology</i> , 2013, 62, 824-836.	5.6	11
69	High-throughput sequencing of B- and T-lymphocyte antigen receptors in hematology. <i>Blood</i> , 2013, 122, 19-22.	1.4	33
70	The mean and variance of phylogenetic diversity under rarefaction. <i>Methods in Ecology and Evolution</i> , 2013, 4, 566-572.	5.2	50
71	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
72	nestly: a framework for running software with nested parameter choices and aggregating results. <i>Bioinformatics</i> , 2013, 29, 387-388.	4.1	7

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73	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
74	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
75	A Format for Phylogenetic Placements. <i>PLoS ONE</i> , 2012, 7, e31009.	2.5	60
76	ppplacer: linear time maximum-likelihood and Bayesian phylogenetic placement of sequences onto a fixed reference tree. <i>BMC Bioinformatics</i> , 2010, 11, 538.	2.6	901
77	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
78	A Method for Investigating Relative Timing Information on Phylogenetic Trees. <i>Systematic Biology</i> , 2009, 58, 167-183.	5.6	30
79	Healing of reamed glenoid bone articulating with a metal humeral hemiarthroplasty: A canine model. <i>Journal of Orthopaedic Research</i> , 2005, 23, 18-26.	2.3	55