

John P Barton

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,268
citations

471371

17
h-index

526166

27
g-index

41
all docs

41
docs citations

41
times ranked

1710
citing authors

#	ARTICLE	IF	CITATIONS
1	Paired quantitative and qualitative assessment of the replication-competent HIV-1 reservoir and comparison with integrated proviral DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7908-E7916.	3.3	164
2	The Fitness Landscape of HIV-1 Gag: Advanced Modeling Approaches and Validation of Model Predictions by In Vitro Testing. <i>PLoS Computational Biology</i> , 2014, 10, e1003776.	1.5	125
3	Relative rate and location of intra-host HIV evolution to evade cellular immunity are predictable. <i>Nature Communications</i> , 2016, 7, 11660.	5.8	103
4	Fitness landscape of the human immunodeficiency virus envelope protein that is targeted by antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E564-E573.	3.3	101
5	Deconstruction of the Ras switching cycle through saturation mutagenesis. <i>ELife</i> , 2017, 6, .	2.8	95
6	Relationship between latent and rebound viruses in a clinical trial of anti-HIV-1 antibody 3BNC117. <i>Journal of Experimental Medicine</i> , 2018, 215, 2311-2324.	4.2	84
7	Spin models inferred from patient-derived viral sequence data faithfully describe HIV fitness landscapes. <i>Physical Review E</i> , 2013, 88, 062705.	0.8	78
8	Role of framework mutations and antibody flexibility in the evolution of broadly neutralizing antibodies. <i>ELife</i> , 2018, 7, .	2.8	72
9	Relationship between intact HIV-1 proviruses in circulating CD4 ⁺ T cells and rebound viruses emerging during treatment interruption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11341-E11348.	3.3	65
10	Characterization of Intact Proviruses in Blood and Lymph Node from HIV-Infected Individuals Undergoing Analytical Treatment Interruption. <i>Journal of Virology</i> , 2019, 93, .	1.5	49
11	Ising models for neural activity inferred via selective cluster expansion: structural and coding properties. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013, 2013, P03002.	0.9	32
12	Scaling laws describe memories of host-pathogen riposte in the HIV population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1965-1970.	3.3	32
13	Identification of drug resistance mutations in HIV from constraints on natural evolution. <i>Physical Review E</i> , 2016, 93, 022412.	0.8	31
14	MPL resolves genetic linkage in fitness inference from complex evolutionary histories. <i>Nature Biotechnology</i> , 2021, 39, 472-479.	9.4	26
15	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021, 6, e0009521.	1.7	26
16	Deconvolving mutational patterns of poliovirus outbreaks reveals its intrinsic fitness landscape. <i>Nature Communications</i> , 2020, 11, 377.	5.8	25
17	Predominance of positive epistasis among drug resistance-associated mutations in HIV-1 protease. <i>PLoS Genetics</i> , 2020, 16, e1009009.	1.5	25
18	On the Entropy of Protein Families. <i>Journal of Statistical Physics</i> , 2016, 162, 1267-1293.	0.5	22

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19	The Energy Costs of Insulators in Biochemical Networks. <i>Biophysical Journal</i> , 2013, 104, 1380-1390.	0.2	21
20	Rational design of vaccine targets and strategies for HIV: a crossroad of statistical physics, biology, and medicine. <i>Reports on Progress in Physics</i> , 2017, 80, 032601.	8.1	20
21	Inference of compressed Potts graphical models. <i>Physical Review E</i> , 2020, 101, 012309.	0.8	14
22	Modelling and in vitro testing of the HIV-1 Nef fitness landscape. <i>Virus Evolution</i> , 2019, 5, vez029.	2.2	11
23	Cross-serotypically conserved epitope recommendations for a universal T cell-based dengue vaccine. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008676.	1.3	11
24	Adenovirus-vectored vaccine containing multidimensionally conserved parts of the HIV proteome is immunogenic in rhesus macaques. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
25	MPFâ€œBML: a standalone GUI-based package for maximum entropy model inference. <i>Bioinformatics</i> , 2020, 36, 2278-2279.	1.8	5
26	Phase Diagram of a Generalized ABC Model on the Interval. <i>Journal of Statistical Physics</i> , 2011, 145, 763-784.	0.5	4
27	Correction for Rando et al., â€œPathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structureâ€œ. <i>MSystems</i> , 2022, , e0144721.	1.7	2
28	Studying Viral Populations with Tools from Quantum Spin Chains. <i>Journal of Statistical Physics</i> , 2021, 182, 1.	0.5	0
29	Cross-serotypically conserved epitope recommendations for a universal T cell-based dengue vaccine. , 2020, 14, e0008676.		0
30	Cross-serotypically conserved epitope recommendations for a universal T cell-based dengue vaccine. , 2020, 14, e0008676.		0
31	Cross-serotypically conserved epitope recommendations for a universal T cell-based dengue vaccine. , 2020, 14, e0008676.		0
32	Cross-serotypically conserved epitope recommendations for a universal T cell-based dengue vaccine. , 2020, 14, e0008676.		0