John P Barton

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Paired quantitative and qualitative assessment of the replication-competent HIV-1 reservoir and comparison with integrated proviral DNA. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7908-E7916.	7.1	164
2	The Fitness Landscape of HIV-1 Gag: Advanced Modeling Approaches and Validation of Model Predictions by In Vitro Testing. PLoS Computational Biology, 2014, 10, e1003776.	3.2	125
3	Relative rate and location of intra-host HIV evolution to evade cellular immunity are predictable. Nature Communications, 2016, 7, 11660.	12.8	103
4	Fitness landscape of the human immunodeficiency virus envelope protein that is targeted by antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E564-E573.	7.1	101
5	Deconstruction of the Ras switching cycle through saturation mutagenesis. ELife, 2017, 6, .	6.0	95
6	Relationship between latent and rebound viruses in a clinical trial of anti–HIV-1 antibody 3BNC117. Journal of Experimental Medicine, 2018, 215, 2311-2324.	8.5	84
7	Spin models inferred from patient-derived viral sequence data faithfully describe HIV fitness landscapes. Physical Review E, 2013, 88, 062705.	2.1	78
8	Role of framework mutations and antibody flexibility in the evolution of broadly neutralizing antibodies. ELife, 2018, 7, .	6.0	72
9	Relationship between intact HIV-1 proviruses in circulating CD4 ⁺ T cells and rebound viruses emerging during treatment interruption. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11341-E11348.	7.1	65
10	Characterization of Intact Proviruses in Blood and Lymph Node from HIV-Infected Individuals Undergoing Analytical Treatment Interruption. Journal of Virology, 2019, 93, .	3.4	49
11	Ising models for neural activity inferred via selective cluster expansion: structural and coding properties. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P03002.	2.3	32
12	Scaling laws describe memories of host–pathogen riposte in the HIV population. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1965-1970.	7.1	32
13	Identification of drug resistance mutations in HIV from constraints on natural evolution. Physical Review E, 2016, 93, 022412.	2.1	31
14	MPL resolves genetic linkage in fitness inference from complex evolutionary histories. Nature Biotechnology, 2021, 39, 472-479.	17.5	26
15	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. MSystems, 2021, 6, e0009521.	3.8	26
16	Deconvolving mutational patterns of poliovirus outbreaks reveals its intrinsic fitness landscape. Nature Communications, 2020, 11, 377.	12.8	25
17	Predominance of positive epistasis among drug resistance-associated mutations in HIV-1 protease. PLoS Genetics, 2020, 16, e1009009.	3.5	25
18	On the Entropy of Protein Families. Journal of Statistical Physics, 2016, 162, 1267-1293.	1.2	22

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19	The Energy Costs of Insulators in Biochemical Networks. Biophysical Journal, 2013, 104, 1380-1390.	0.5	21
20	Rational design of vaccine targets and strategies for HIV: a crossroad of statistical physics, biology, and medicine. Reports on Progress in Physics, 2017, 80, 032601.	20.1	20
21	Inference of compressed Potts graphical models. Physical Review E, 2020, 101, 012309.	2.1	14
22	Modelling and in vitro testing of the HIV-1 Nef fitness landscape. Virus Evolution, 2019, 5, vez029.	4.9	11
23	Cross-serotypically conserved epitope recommendations for a universal T cell-based dengue vaccine. PLoS Neglected Tropical Diseases, 2020, 14, e0008676.	3.0	11
24	Adenovirus-vectored vaccine containing multidimensionally conserved parts of the HIV proteome is immunogenic in rhesus macaques. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
25	MPF–BML: a standalone GUI-based package for maximum entropy model inference. Bioinformatics, 2020, 36, 2278-2279.	4.1	5
26	Phase Diagram of a Generalized ABC Model on the Interval. Journal of Statistical Physics, 2011, 145, 763-784.	1.2	4
27	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure― MSystems, 2022, , e0144721.	3.8	2
28	Studying Viral Populations with Tools from Quantum Spin Chains. Journal of Statistical Physics, 2021, 182, 1.	1.2	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