

Christina L Burch

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,146
citations

279701

23
h-index

360920

35
g-index

39
all docs

39
docs citations

39
times ranked

3560
citing authors

#	ARTICLE	IF	CITATIONS
1	Recombination drives the evolution of mutational robustness. <i>Current Opinion in Systems Biology</i> , 2019, 13, 142-149.	1.3	9
2	Population structure promotes the evolution of costly sex in artificial gene networks. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1089-1100.	1.1	4
3	Evolutionary pathways to NS5A inhibitor resistance in genotype 1 hepatitis C virus. <i>Antiviral Research</i> , 2018, 158, 45-51.	1.9	3
4	The emergence of performance trade-offs during local adaptation: insights from experimental evolution. <i>Molecular Ecology</i> , 2017, 26, 1720-1733.	2.0	99
5	Permissivity of Dipeptidyl Peptidase 4 Orthologs to Middle East Respiratory Syndrome Coronavirus Is Governed by Glycosylation and Other Complex Determinants. <i>Journal of Virology</i> , 2017, 91, .	1.5	38
6	An Evolving Genetic Architecture Interacts with Hill's Robertson Interference to Determine the Benefit of Sex. <i>Genetics</i> , 2016, 203, 923-936.	1.2	20
7	Evolutionary rescue and the coexistence of generalist and specialist competitors: an experimental test. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151932.	1.2	24
8	Coronavirus Host Range Expansion and Middle East Respiratory Syndrome Coronavirus Emergence: Biochemical Mechanisms and Evolutionary Perspectives. <i>Annual Review of Virology</i> , 2015, 2, 95-117.	3.0	75
9	Dominance Effects of Deleterious and Beneficial Mutations in a Single Gene of the RNA Virus ϕ 6. <i>PLoS ONE</i> , 2014, 9, e97717.	1.1	4
10	Competition and the origins of novelty: experimental evolution of niche-width expansion in a virus. <i>Biology Letters</i> , 2013, 9, 20120616.	1.0	62
11	Comparison of SIV and HIV-1 Genomic RNA Structures Reveals Impact of Sequence Evolution on Conserved and Non-Conserved Structural Motifs. <i>PLoS Pathogens</i> , 2013, 9, e1003294.	2.1	83
12	Deconvolution estimation of mixture distributions with boundaries. <i>Electronic Journal of Statistics</i> , 2013, 7, 323-341.	0.4	11
13	Direct deconvolution density estimation of a mixture distribution motivated by mutation effects distribution. <i>Journal of Nonparametric Statistics</i> , 2010, 22, 1-22.	0.4	14
14	Genetic Architecture and the Evolution of Sex. <i>Journal of Heredity</i> , 2010, 101, S142-S157.	1.0	24
15	Hotter Is Better and Broader: Thermal Sensitivity of Fitness in a Population of Bacteriophages. <i>American Naturalist</i> , 2009, 173, 419-430.	1.0	112
16	Major Coexisting Human Immunodeficiency Virus Type 1 <i>env</i> Gene Subpopulations in the Peripheral Blood Are Produced by Cells with Similar Turnover Rates and Show Little Evidence of Genetic Compartmentalization. <i>Journal of Virology</i> , 2009, 83, 4068-4080.	1.5	15
17	ORIGINAL ARTICLE: Coinfection rates in ϕ 6 bacteriophage are enhanced by virus-induced changes in host cells. <i>Evolutionary Applications</i> , 2009, 2, 24-31.	1.5	10
18	Architecture and secondary structure of an entire HIV-1 RNA genome. <i>Nature</i> , 2009, 460, 711-716.	13.7	719

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19	Cross-sectional characterization of HIV-1 env compartmentalization in cerebrospinal fluid over the full disease course. <i>Aids</i> , 2009, 23, 907-915.	1.0	94
20	Beneficial Fitness Effects Are Not Exponential for Two Viruses. <i>Journal of Molecular Evolution</i> , 2008, 67, 368-376.	0.8	97
21	Compensatory Evolution in RNA Secondary Structures Increases Substitution Rate Variation among Sites. <i>Molecular Biology and Evolution</i> , 2008, 25, 1778-1787.	3.5	18
22	The molecular epidemiology of HIV-1 envelope diversity during HIV-1 subtype C vertical transmission in Malawian mother-infant pairs. <i>Aids</i> , 2008, 22, 863-871.	1.0	26
23	Optimal Foraging Predicts the Ecology but Not the Evolution of Host Specialization in Bacteriophages. <i>PLoS ONE</i> , 2008, 3, e1946.	1.1	35
24	High Frequency of Mutations That Expand the Host Range of an RNA Virus. <i>Genetics</i> , 2007, 176, 1013-1022.	1.2	77
25	Experimental Estimate of the Abundance and Effects of Nearly Neutral Mutations in the RNA Virus ϕ 6. <i>Genetics</i> , 2007, 176, 467-476.	1.2	28
26	EVOLUTION OF HOST SPECIFICITY DRIVES REPRODUCTIVE ISOLATION AMONG RNA VIRUSES. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 2614-2622.	1.1	85
27	The Genetic Basis of Thermal Reaction Norm Evolution in Lab and Natural Phage Populations. <i>PLoS Biology</i> , 2006, 4, e201.	2.6	81
28	Sexual reproduction selects for robustness and negative epistasis in artificial gene networks. <i>Nature</i> , 2006, 440, 87-90.	13.7	211
29	Pleiotropic Costs of Niche Expansion in the RNA Bacteriophage ϕ 6. <i>Genetics</i> , 2006, 172, 751-757.	1.2	179
30	Epistasis and Its Relationship to Canalization in the RNA Virus ϕ 6. <i>Genetics</i> , 2004, 167, 559-567.	1.2	119
31	Patterns of epistasis in RNA viruses: a review of the evidence from vaccine design. <i>Journal of Evolutionary Biology</i> , 2003, 16, 1223-1235.	0.8	32
32	Kin Selection and Parasite Evolution: Higher and Lower Virulence with Hard and Soft Selection. <i>Quarterly Review of Biology</i> , 2000, 75, 261-275.	0.0	131
33	Evolvability of an RNA virus is determined by its mutational neighbourhood. <i>Nature</i> , 2000, 406, 625-628.	13.7	259
34	Evolution by Small Steps and Rugged Landscapes in the RNA Virus ϕ 6. <i>Genetics</i> , 1999, 151, 921-927.	1.2	292
35	Hybrid Frequencies Confirm Limit to Coinfection in the RNA Bacteriophage ϕ 6. <i>Journal of Virology</i> , 1999, 73, 2420-2424.	1.5	49