Christopher G Knight

List of Publications by Year
in descending order

40 papers	2,195 citations	361045 20 h-index	344852 36 g-index
43 all docs	43 docs citations	43 times ranked	3504 citing authors

#	Article	IF	Citations
1	The lexicon of antimicrobial peptides: a complete set of arginine and tryptophan sequences. Communications Biology, 2021, 4, 605.	2.0	45
2	Cage and maternal effects on the bacterial communities of the murine gut. Scientific Reports, 2021, 11, 9841.	1.6	21
3	Does the Microbiome Affect the Outcome of Renal Transplantation?. Frontiers in Cellular and Infection Microbiology, 2020, 10, 558644.	1.8	13
4	Harnessing rhizosphere microbiomes for drought-resilient crop production. Science, 2020, 368, 270-274.	6.0	442
5	Morphological Phylogenetics Evaluated Using Novel Evolutionary Simulations. Systematic Biology, 2020, 69, 897-912.	2.7	26
6	Gut eosinophils and their impact on the mucusâ€resident microbiota. Immunology, 2019, 158, 194-205.	2.0	29
7	Measuring Microbial Mutation Rates with the Fluctuation Assay. Journal of Visualized Experiments, 2019, , .	0.2	9
8	Detecting macroecological patterns in bacterial communities across independent studies of global soils. Nature Microbiology, 2018, 3, 189-196.	5.9	136
9	Environmental pleiotropy and demographic history direct adaptation under antibiotic selection. Heredity, 2018, 121, 438-448.	1.2	7
10	Whole Genome Sequencing,de NovoAssembly and Phenotypic Profiling for the New Budding Yeast SpeciesSaccharomyces jurei. G3: Genes, Genomes, Genetics, 2018, 8, 2967-2977.	0.8	46
11	Opposing effects of final population density and stress on Escherichia coli mutation rate. ISME Journal, 2018, 12, 2981-2987.	4.4	8
12	Critical Mutation Rate has an Exponential Dependence on Population Size for Eukaryotic-length Genomes with Crossover. Scientific Reports, 2017, 7, 15519.	1.6	5
13	Spontaneous mutation rate is a plastic trait associated with population density across domains of life. PLoS Biology, 2017, 15, e2002731.	2.6	58
14	Critical mutation rate in a population with horizontal gene transfer. , 2017, , .		1
15	Variable Effects of Exposure to Formulated Microbicides on Antibiotic Susceptibility in Firmicutes and Proteobacteria. Applied and Environmental Microbiology, 2016, 82, 3591-3598.	1.4	21
16	Monotonicity of fitness landscapes and mutation rate control. Journal of Mathematical Biology, 2016, 73, 1491-1524.	0.8	6
17	Effect of summer daylight exposure and genetic background on growth in growth hormone-deficient children. Pharmacogenomics Journal, 2016, 16, 540-550.	0.9	18
18	Linkage disequilibrium network analysis (<scp>LD</scp>na) gives a global view of chromosomal inversions, local adaptation and geographic structure. Molecular Ecology Resources, 2015, 15, 1031-1045.	2.2	85

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19	Mutation rate plasticity in rifampicin resistance depends on Escherichia coli cellâ€“cell interactions. Nature Communications, 2014, 5, 3742.	5.8	69
20	Where antibiotic resistance mutations meet quorum-sensing. Microbial Cell, 2014, 1, 250-252.	1.4	7
21	Function-valued traits in evolution. Journal of the Royal Society Interface, 2013, 10, 20121032.	1.5	16
22	Critical Mutation Rate Has an Exponential Dependence on Population Size in Haploid and Diploid Populations. PLoS ONE, 2013, 8, e83438.	1.1	4
23	Absolute Quantification of the Glycolytic Pathway in Yeast:. Molecular and Cellular Proteomics, 2011, 10, M111.007633.	2.5	70
24	Testing temperatureâ€induced proteomic changes in the plantâ€associated bacterium Pseudomonas fluorescens SBW25. Environmental Microbiology Reports, 2010, 2, 396-402.	1.0	5
25	Elements of Computational Systems Biology. Eds. H. M. Lodhi & S. Muggleton. Wiley-Blackwell. 2010. 412 pages. ISBN 9780470180938. Price $115 (hardback).. Genetical Research, 2010, 92, 324-325.	0.3	0
26	Array-based evolution of DNA aptamers allows modelling of an explicit sequence-fitness landscape. Nucleic Acids Research, 2009, 37, e6-e6.	6.5	96
27	Making the right connections: biological networks in the light of evolution. BioEssays, 2009, 31, 1080-1090.	1.2	21
28	Genomic and genetic analyses of diversity and plant interactions of Pseudomonas fluorescens. Genome Biology, 2009, 10, R51.	13.9	370
29	Association of parameter, software, and hardware variation with large-scale behavior across 57,000 climate models. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12259-12264.	3.3	65
30	Adaptive Divergence in Experimental Populations of Pseudomonas fluorescens. III. Mutational Origins of Wrinkly Spreader Diversity. Genetics, 2007, 176, 441-453.	1.2	150
31	Integrated bioinformatic and phenotypic analysis of RpoN-dependent traits in the plant growth-promoting bacterium Pseudomonas fluorescens SBW25. Environmental Microbiology, 2007, 9, 3046-3064.	1.8	30
32	Unraveling adaptive evolution: how a single point mutation affects the protein coregulation network. Nature Genetics, 2006, 38, 1015-1022.	9.4	68
33	Pale Rock Sparrow Carpospiza brachydactyla in the Mount Lebanon range: modelling breeding habitat. Ibis, 2005, 147, 324-333.	1.0	6
34	From The Cover: Global analysis of predicted proteomes: Functional adaptation of physical properties. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8390-8395.	3.3	63
35	Evolution of germ-line signals that regulate growth and aging in nematodes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 769-774.	3.3	43
36	A novel mode of ecdysozoan growth in Caenorhabditis elegans. Evolution & Development, 2002, 4, 16-27.	1.1	82

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37	TESTING LIFE-HISTORY PLEIOTROPY IN CAENORHABDITIS ELEGANS. Evolution; International Journal of Organic Evolution, 2001, 55, 1795-1804.	1.1	37
38	TESTING LIFE-HISTORY PLEIOTROPY IN CAENORHABDITIS ELEGANS. Evolution; International Journal of Organic Evolution, 2001, 55, 1795.	1.1	5
39	The genetics of phenotypic innovation. , 0, , 91-104.		4
40	Optimal Mutation Rate Control under Selection in Hamming Spaces. , 0, , .		0