John Archer

List of Publications by Year
in descending order

32 papers	1,646 citations	430874 18 h-index	477307 29 g-index
34 all docs	34 docs citations	34 times ranked	2953 citing authors

#	Article	IF	Citations
1	The genetics of adaptation in freshwater Eurasian shad (*Alosa*). Ecology and Evolution, 2022, 12, .	1.9	1
2	CView: A network based tool for enhanced alignment visualization. PLoS ONE, 2022, 17, e0259726.	2.5	1
3	A mouse infection model and long-term lymphatic endothelium co-culture system to evaluate drugs against adult Brugia malayi. PLoS Neglected Tropical Diseases, 2022, 16, e0010474.	3.0	2
4	Structural Requirements for Dihydrobenzoxazepinone Anthelmintics: Actions against Medically Important and Model Parasites: *Trichuris muris*, *Brugia malayi*, *Heligmosomoides polygyrus*, and *Schistosoma mansoni*. ACS Infectious Diseases, 2021, 7, 1260-1274.	3.8	13
5	CStone: A de novo transcriptome assembler for short-read data that identifies non-chimeric contigs based on underlying graph structure. PLoS Computational Biology, 2021, 17, e1009631.	3.2	5
6	A non-lethal method for studying scorpion venom gland transcriptomes, with a review of potentially suitable taxa to which it can be applied. PLoS ONE, 2021, 16, e0258712.	2.5	3
7	Eosinophil-Mediated Immune Control of Adult Filarial Nematode Infection Can Proceed in the Absence of IL-4 Receptor Signaling. Journal of Immunology, 2020, 205, 731-740.	0.8	14
8	Independent evolution of song diversity and song motor performance in canaries, goldfinches and allies indicates clade‐specific trade‐offs in birdsong. Evolution; International Journal of Organic Evolution, 2020, 74, 1170-1185.	2.3	5
9	Transcriptome annotation and characterization of novel toxins in six scorpion species. BMC Genomics, 2019, 20, 645.	2.8	9
10	Preclinical development of an oral anti-*Wolbachia* macrolide drug for the treatment of lymphatic filariasis and onchocerciasis. Science Translational Medicine, 2019, 11, .	12.4	67
11	AWZ1066S, a highly specific anti-*Wolbachia* drug candidate for a short-course treatment of filariasis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1414-1419.	7.1	57
12	Validation of ultrasound bioimaging to predict worm burden and treatment efficacy in preclinical filariasis drug screening models. Scientific Reports, 2018, 8, 5910.	3.3	8
13	Signatures of Selection on Standing Genetic Variation Underlie Athletic and Navigational Performance in Racing Pigeons. Molecular Biology and Evolution, 2018, 35, 1176-1189.	8.9	25
14	Lorenzo-Redondo et al. reply. Nature, 2017, 551, E10-E10.	27.8	5
15	Persistent HIV-1 replication maintains the tissue reservoir during therapy. Nature, 2016, 530, 51-56.	27.8	550
16	Human APOBEC3 Induced Mutation of Human Immunodeficiency Virus Type-1 Contributes to Adaptation and Evolution in Natural Infection. PLoS Pathogens, 2014, 10, e1004281.	4.7	83
17	VTBuilder: a tool for the assembly of multi isoform transcriptomes. BMC Bioinformatics, 2014, 15, 389.	2.6	36
18	Sensitive Deep-Sequencing-Based HIV-1 Genotyping Assay To Simultaneously Determine Susceptibility to Protease, Reverse Transcriptase, Integrase, and Maturation Inhibitors, as Well as HIV-1 Coreceptor Tropism. Antimicrobial Agents and Chemotherapy, 2014, 58, 2167-2185.	3.2	61

#	Article	IF	Citations
19	Sensitive Cell-Based Assay for Determination of Human Immunodeficiency Virus Type 1 Coreceptor Tropism. Journal of Clinical Microbiology, 2013, 51, 1517-1527.	3.9	18
20	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. BMC Bioinformatics, 2012, 13, 47.	2.6	58
21	Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. PLoS ONE, 2012, 7, e49602.	2.5	78
22	Using Knowledge of Protein Structural Constraints to Predict the Evolution of HIV-1. Journal of Molecular Biology, 2011, 410, 1023-1034.	4.2	4
23	The Evolutionary Analysis of Emerging Low Frequency HIV-1 CXCR4 Using Variants through Time—An Ultra-Deep Approach. PLoS Computational Biology, 2010, 6, e1001022.	3.2	72
24	Molecular Mechanisms of Recombination Restriction in the Envelope Gene of the Human Immunodeficiency Virus. PLoS Pathogens, 2009, 5, e1000418.	4.7	70
25	Back to basics – how the evolution of the extracellular matrix underpinned vertebrate evolution. International Journal of Experimental Pathology, 2009, 90, 95-100.	1.3	24
26	Detection of low-frequency pretherapy chemokine (CXC motif) receptor 4 (CXCR4)-using HIV-1 with ultra-deep pyrosequencing. Aids, 2009, 23, 1209-1218.	2.2	104
27	Identifying the Important HIV-1 Recombination Breakpoints. PLoS Computational Biology, 2008, 4, e1000178.	3.2	58
28	<i>CTree</i>: comparison of clusters between phylogenetic trees made easy. Bioinformatics, 2007, 23, 2952-2953.	4.1	21
29	Understanding the diversification of HIV-1 groups M and O. Aids, 2007, 21, 1693-1700.	2.2	32
30	Sequence determinants of breakpoint location during HIV-1 intersubtype recombination. Nucleic Acids Research, 2006, 34, 5203-5216.	14.5	53
31	16S rDNA Phylogeny and Ultrastructural Characterization ofWolbachiaIntracellular Bacteria of the Filarial NematodesBrugia malayi,B. pahangi, andWuchereria bancrofti. Experimental Parasitology, 1999, 91, 356-361.	1.2	108
32	Quantification of the effects of chimerism on read mapping, differential expression and annotation following short-read de novo assembly.. F1000Research, 0, 11, 120.	1.6	1