

# John Archer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/580107/publications.pdf>

Version: 2024-02-01

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	Persistent HIV-1 replication maintains the tissue reservoir during therapy. <i>Nature</i> , 2016, 530, 51-56.	27.8	550
2	16S rDNA Phylogeny and Ultrastructural Characterization of <i>Wolbachia</i> Intracellular Bacteria of the Filarial Nematodes <i>Brugia malayi</i> , <i>B. pahangi</i> , and <i>Wuchereria bancrofti</i> . <i>Experimental Parasitology</i> , 1999, 91, 356-361.	1.2	108
3	Detection of low-frequency pretherapy chemokine (CXC motif) receptor 4 (CXCR4)-using HIV-1 with ultra-deep pyrosequencing. <i>Aids</i> , 2009, 23, 1209-1218.	2.2	104
4	Human APOBEC3 Induced Mutation of Human Immunodeficiency Virus Type-1 Contributes to Adaptation and Evolution in Natural Infection. <i>PLoS Pathogens</i> , 2014, 10, e1004281.	4.7	83
5	Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. <i>PLoS ONE</i> , 2012, 7, e49602.	2.5	78
6	The Evolutionary Analysis of Emerging Low Frequency HIV-1 CXCR4 Using Variants through Time—An Ultra-Deep Approach. <i>PLoS Computational Biology</i> , 2010, 6, e1001022.	3.2	72
7	Molecular Mechanisms of Recombination Restriction in the Envelope Gene of the Human Immunodeficiency Virus. <i>PLoS Pathogens</i> , 2009, 5, e1000418.	4.7	70
8	Preclinical development of an oral anti- <i>Wolbachia</i> macrolide drug for the treatment of lymphatic filariasis and onchocerciasis. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	67
9	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. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2167-2185.	3.2	61
10	Identifying the Important HIV-1 Recombination Breakpoints. <i>PLoS Computational Biology</i> , 2008, 4, e1000178.	3.2	58
11	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. <i>BMC Bioinformatics</i> , 2012, 13, 47.	2.6	58
12	AWZ1066S, a highly specific anti- <i>Wolbachia</i> drug candidate for a short-course treatment of filariasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1414-1419.	7.1	57
13	Sequence determinants of breakpoint location during HIV-1 intersubtype recombination. <i>Nucleic Acids Research</i> , 2006, 34, 5203-5216.	14.5	53
14	VTBuilder: a tool for the assembly of multi isoform transcriptomes. <i>BMC Bioinformatics</i> , 2014, 15, 389.	2.6	36
15	Understanding the diversification of HIV-1 groups M and O. <i>Aids</i> , 2007, 21, 1693-1700.	2.2	32
16	Signatures of Selection on Standing Genetic Variation Underlie Athletic and Navigational Performance in Racing Pigeons. <i>Molecular Biology and Evolution</i> , 2018, 35, 1176-1189.	8.9	25
17	Back to basics — how the evolution of the extracellular matrix underpinned vertebrate evolution. <i>International Journal of Experimental Pathology</i> , 2009, 90, 95-100.	1.3	24
18	<i>CTree</i> : comparison of clusters between phylogenetic trees made easy. <i>Bioinformatics</i> , 2007, 23, 2952-2953.	4.1	21

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19	Sensitive Cell-Based Assay for Determination of Human Immunodeficiency Virus Type 1 Coreceptor Tropism. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1517-1527.	3.9	18
20	Eosinophil-Mediated Immune Control of Adult Filarial Nematode Infection Can Proceed in the Absence of IL-4 Receptor Signaling. <i>Journal of Immunology</i> , 2020, 205, 731-740.	0.8	14
21	Structural Requirements for Dihydrobenzoxazepinone Anthelmintics: Actions against Medically Important and Model Parasites: <i>Trichuris muris</i> , <i>Brugia malayi</i> , <i>Heligmosomoides polygyrus</i> , and <i>Schistosoma mansoni</i> . <i>ACS Infectious Diseases</i> , 2021, 7, 1260-1274.	3.8	13
22	Transcriptome annotation and characterization of novel toxins in six scorpion species. <i>BMC Genomics</i> , 2019, 20, 645.	2.8	9
23	Validation of ultrasound bioimaging to predict worm burden and treatment efficacy in preclinical filariasis drug screening models. <i>Scientific Reports</i> , 2018, 8, 5910.	3.3	8
24	Lorenzo-Redondo et al. reply. <i>Nature</i> , 2017, 551, E10-E10.	27.8	5
25	Independent evolution of song diversity and song motor performance in canaries, goldfinches and allies indicates clade-specific trade-offs in birdsong. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1170-1185.	2.3	5
26	CStone: A de novo transcriptome assembler for short-read data that identifies non-chimeric contigs based on underlying graph structure. <i>PLoS Computational Biology</i> , 2021, 17, e1009631.	3.2	5
27	Using Knowledge of Protein Structural Constraints to Predict the Evolution of HIV-1. <i>Journal of Molecular Biology</i> , 2011, 410, 1023-1034.	4.2	4
28	A non-lethal method for studying scorpion venom gland transcriptomes, with a review of potentially suitable taxa to which it can be applied. <i>PLoS ONE</i> , 2021, 16, e0258712.	2.5	3
29	A mouse infection model and long-term lymphatic endothelium co-culture system to evaluate drugs against adult <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010474.	3.0	2
30	Quantification of the effects of chimerism on read mapping, differential expression and annotation following short-read de novo assembly.. <i>F1000Research</i> , 0, 11, 120.	1.6	1
31	The genetics of adaptation in freshwater Eurasian shad ( <i>Alosa</i> ). <i>Ecology and Evolution</i> , 2022, 12, .	1.9	1
32	CView: A network based tool for enhanced alignment visualization. <i>PLoS ONE</i> , 2022, 17, e0259726.	2.5	1