

Jonathan E Allen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

7,698
citations

24
h-index

58
g-index

58
ext. papers

9,312
ext. citations

10.8
avg, IF

4.69
L-index

#	Paper	IF	Citations
49	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002 , 419, 498-511	50.4	3336
48	Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , 2008 , 9, R7	18.3	1212
47	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002 , 419, 512-9	50.4	591
46	The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005 , 307, 1321-4	33.3	580
45	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , 2007 , 317, 1756-60	33.3	513
44	Genome sequence of <i>Theileria parva</i> , a bovine pathogen that transforms lymphocytes. <i>Science</i> , 2005 , 309, 134-7	33.3	259
43	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002 , 419, 531-4	50.4	146
42	Scalable metagenomic taxonomy classification using a reference genome database. <i>Bioinformatics</i> , 2013 , 29, 2253-60	7.2	127
41	JIGSAW: integration of multiple sources of evidence for gene prediction. <i>Bioinformatics</i> , 2005 , 21, 3596-603	6.3	127
40	Computational gene prediction using multiple sources of evidence. <i>Genome Research</i> , 2004 , 14, 142-8	9.7	78
39	Metagenomic analysis of the airborne environment in urban spaces. <i>Microbial Ecology</i> , 2015 , 69, 346-55	4.4	59
38	Predicting tumor cell line response to drug pairs with deep learning. <i>BMC Bioinformatics</i> , 2018 , 19, 486	3.6	51
37	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S9.1-13	18.3	50
36	FDA-ARGOS is a database with public quality-controlled reference genomes for diagnostic use and regulatory science. <i>Nature Communications</i> , 2019 , 10, 3313	17.4	42
35	Microbial profiling of combat wound infection through detection microarray and next-generation sequencing. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 2583-94	9.7	38
34	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. <i>Scientific Reports</i> , 2014 , 4, 4245	4.9	38
33	Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. <i>BMC Genomics</i> , 2013 , 14, 96	4.5	36

32	Ultra-deep sequencing of intra-host rabies virus populations during cross-species transmission. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2555	4.8	33
31	Conserved amino acid markers from past influenza pandemic strains. <i>BMC Microbiology</i> , 2009 , 9, 77	4.5	30
30	Whole metagenome profiles of particulates collected from the International Space Station. <i>Microbiome</i> , 2017 , 5, 81	16.6	28
29	The role of viral population diversity in adaptation of bovine coronavirus to new host environments. <i>PLoS ONE</i> , 2013 , 8, e52752	3.7	28
28	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017 , 6,	8.9	26
27	Using populations of human and microbial genomes for organism detection in metagenomes. <i>Genome Research</i> , 2015 , 25, 1056-67	9.7	25
26	AMPL: A Data-Driven Modeling Pipeline for Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 1955-1968	6.1	24
25	Improved Protein-Ligand Binding Affinity Prediction with Structure-Based Deep Fusion Inference. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 1583-1592	6.1	24
24	Gene expression analysis of whole blood RNA from pigs infected with low and high pathogenic African swine fever viruses. <i>Scientific Reports</i> , 2017 , 7, 10115	4.9	23
23	Binding Affinity Prediction by Pairwise Function Based on Neural Network. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 2766-2772	6.1	19
22	Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. <i>BMC Research Notes</i> , 2015 , 8, 682	2.3	18
21	Predicting Small Molecule Transfer Free Energies by Combining Molecular Dynamics Simulations and Deep Learning. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 5375-5381	6.1	13
20	Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants. <i>PLoS ONE</i> , 2016 , 11, e0146251	3.7	12
19	A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. <i>PLoS ONE</i> , 2018 , 13, e0209683	3.7	12
18	Machine learning and ligand binding predictions: A review of data, methods, and obstacles. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020 , 1864, 129545	4	9
17	Draft Genome Sequences from a Novel Clade of Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , 2017 , 5,		9
16	Draft Genome Sequences of Biosafety Level 2 Opportunistic Pathogens Isolated from the Environmental Surfaces of the International Space Station. <i>Genome Announcements</i> , 2016 , 4,		9
15	A phylogenetic generalized hidden Markov model for predicting alternatively spliced exons. <i>Algorithms for Molecular Biology</i> , 2006 , 1, 14	1.8	8

14	DNA signatures for detecting genetic engineering in bacteria. <i>Genome Biology</i> , 2008 , 9, R56	18.3	7
13	Multiscale analysis for patterns of Zika virus genotype emergence, spread, and consequence. <i>PLoS ONE</i> , 2019 , 14, e0225699	3.7	7
12	A cross-study analysis of drug response prediction in cancer cell lines. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	7
11	Characterization of Genetic Variability of Venezuelan Equine Encephalitis Viruses. <i>PLoS ONE</i> , 2016 , 11, e0152604	3.7	6
10	Sendai virus intra-host population dynamics and host immunocompetence influence viral virulence during passage. <i>Virus Evolution</i> , 2016 , 2, vew008	3.7	5
9	Discovery of Small-Molecule Inhibitors of SARS-CoV-2 Proteins Using a Computational and Experimental Pipeline. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 678701	5.6	5
8	Two Sides of a Coin: a Zika Virus Mutation Selected in Pregnant Rhesus Macaques Promotes Fetal Infection in Mice but at a Cost of Reduced Fitness in Nonpregnant Macaques and Diminished Transmissibility by Vectors. <i>Journal of Virology</i> , 2020 , 94,	6.6	4
7	FDA-ARGOS: A Public Quality-Controlled Genome Database Resource for Infectious Disease Sequencing Diagnostics and Regulatory Science Research		3
6	Enabling rapid COVID-19 small molecule drug design through scalable deep learning of generative models. <i>International Journal of High Performance Computing Applications</i> , 2021 , 35, 469-482	1.8	3
5	Machine Learning Models to Predict Inhibition of the Bile Salt Export Pump. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 587-602	6.1	3
4	Forensic interpretation of molecular variation on networks of disease transmission and genetic inheritance. <i>Electrophoresis</i> , 2014 , 35, 3117-24	3.6	2
3	Design and Optimization of a Metagenomics Analysis Workflow for NVRAM 2014 ,		2
2	Quantifying Overfitting Potential in Drug Binding Datasets. <i>Lecture Notes in Computer Science</i> , 2020 , 585-598	0.9	1
1	Design of Genomic Signatures for Pathogen Identification and Characterization 2011 , 493-508		