Jonathan E Allen

List of Publications by Year
in descending order

52 papers	10,509 citations	201385 27 h-index	182168 51 g-index
58 all docs	58 docs citations	58 times ranked	14697 citing authors

#	Article	IF	Citations
1	Genome sequence of the human malaria parasite Plasmodium falciparum. Nature, 2002, 419, 498-511.	13.7	3,881
2	Automated eukaryotic gene structure annotation using EVidenceModeler and the Program to Assemble Spliced Alignments. Genome Biology, 2008, 9, R7.	13.9	2,484
3	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. Nature, 2002, 419, 512-519.	13.7	666
4	The Genome of the Basidiomycetous Yeast and Human Pathogen Cryptococcus neoformans. Science, 2005, 307, 1321-1324.	6.0	664
5	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i>. Science, 2007, 317, 1756-1760.	6.0	571
6	Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms Lymphocytes. Science, 2005, 309, 134-137.	6.0	309
7	Scalable metagenomic taxonomy classification using a reference genome database. Bioinformatics, 2013, 29, 2253-2260.	1.8	178
8	Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14. Nature, 2002, 419, 531-534.	13.7	167
9	JIGSAW: integration of multiple sources of evidence for gene prediction. Bioinformatics, 2005, 21, 3596-3603.	1.8	147
10	Improved Protein–Ligand Binding Affinity Prediction with Structure-Based Deep Fusion Inference. Journal of Chemical Information and Modeling, 2021, 61, 1583-1592.	2.5	140
11	Computational Gene Prediction Using Multiple Sources of Evidence. Genome Research, 2003, 14, 142-148.	2.4	110
12	FDA-ARGOS is a database with public quality-controlled reference genomes for diagnostic use and regulatory science. Nature Communications, 2019, 10, 3313.	5.8	101
13	Predicting tumor cell line response to drug pairs with deep learning. BMC Bioinformatics, 2018, 19, 486.	1.2	84
14	Metagenomic Analysis of the Airborne Environment in Urban Spaces. Microbial Ecology, 2015, 69, 346-355.	1.4	76
15	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. Genome Biology, 2006, 7, S9.	13.9	61
16	Whole metagenome profiles of particulates collected from the International Space Station. Microbiome, 2017, 5, 81.	4.9	54
17	AMPL: A Data-Driven Modeling Pipeline for Drug Discovery. Journal of Chemical Information and Modeling, 2020, 60, 1955-1968.	2.5	53
18	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. Scientific Reports, 2014, 4, 4245.	1.6	48

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19	Microbial Profiling of Combat Wound Infection through Detection Microarray and Next-Generation Sequencing. Journal of Clinical Microbiology, 2014, 52, 2583-2594.	1.8	47
20	A molecular portrait of maternal sepsis from Byzantine Troy. ELife, 2017, 6, .	2.8	46
21	Gene expression analysis of whole blood RNA from pigs infected with low and high pathogenic African swine fever viruses. Scientific Reports, 2017, 7, 10115.	1.6	45
22	Ultra-Deep Sequencing of Intra-host Rabies Virus Populations during Cross-species Transmission. PLoS Neglected Tropical Diseases, 2013, 7, e2555.	1.3	43
23	Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. BMC Genomics, 2013, 14, 96.	1.2	40
24	Conserved amino acid markers from past influenza pandemic strains. BMC Microbiology, 2009, 9, 77.	1.3	39
25	Binding Affinity Prediction by Pairwise Function Based on Neural Network. Journal of Chemical Information and Modeling, 2020, 60, 2766-2772.	2.5	39
26	Using populations of human and microbial genomes for organism detection in metagenomes. Genome Research, 2015, 25, 1056-1067.	2.4	37
27	A cross-study analysis of drug response prediction in cancer cell lines. Briefings in Bioinformatics, 2022, 23, .	3.2	37
28	Predicting Small Molecule Transfer Free Energies by Combining Molecular Dynamics Simulations and Deep Learning. Journal of Chemical Information and Modeling, 2020, 60, 5375-5381.	2.5	35
29	The Role of Viral Population Diversity in Adaptation of Bovine Coronavirus to New Host Environments. PLoS ONE, 2013, 8, e52752.	1.1	35
30	Discovery of Small-Molecule Inhibitors of SARS-CoV-2 Proteins Using a Computational and Experimental Pipeline. Frontiers in Molecular Biosciences, 2021, 8, 678701.	1.6	22
31	Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. BMC Research Notes, 2015, 8, 682.	0.6	21
32	Enabling rapid COVID-19 small molecule drug design through scalable deep learning of generative models. International Journal of High Performance Computing Applications, 2021, 35, 469-482.	2.4	21
33	Draft Genome Sequences of Biosafety Level 2 Opportunistic Pathogens Isolated from the Environmental Surfaces of the International Space Station. Genome Announcements, 2016, 4, .	0.8	20
34	Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants. PLoS ONE, 2016, 11, e0146251.	1.1	19
35	A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. PLoS ONE, 2018, 13, e0209683.	1.1	19
36	Machine learning and ligand binding predictions: A review of data, methods, and obstacles. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129545.	1.1	18

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37	Accelerators for Classical Molecular Dynamics Simulations of Biomolecules. Journal of Chemical Theory and Computation, 2022, 18, 4047-4069.	2.3	15
38	Draft Genome Sequences from a Novel Clade of Bacillus cereus *Sensu Lato* Strains, Isolated from the International Space Station. Genome Announcements, 2017, 5, .	0.8	14
39	Multiscale analysis for patterns of Zika virus genotype emergence, spread, and consequence. PLoS ONE, 2019, 14, e0225699.	1.1	12
40	DNA signatures for detecting genetic engineering in bacteria. Genome Biology, 2008, 9, R56.	13.9	11
41	A phylogenetic generalized hidden Markov model for predicting alternatively spliced exons. Algorithms for Molecular Biology, 2006, 1, 14.	0.3	10
42	Machine Learning Models to Predict Inhibition of the Bile Salt Export Pump. Journal of Chemical Information and Modeling, 2021, 61, 587-602.	2.5	10
43	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. Journal of Virology, 2020, 94, .	1.5	10
44	Characterization of Genetic Variability of Venezuelan Equine Encephalitis Viruses. PLoS ONE, 2016, 11, e0152604.	1.1	7
45	High-throughput virtual screening of small molecule inhibitors for SARS-CoV-2 protein targets with deep fusion models. , 2021, , .		7
46	Design and Optimization of a Metagenomics Analysis Workflow for NVRAM. , 2014, , .		5
47	Sendai virus intra-host population dynamics and host immunocompetence influence viral virulence during *in vivo* passage. Virus Evolution, 2016, 2, vew008.	2.2	5
48	Pose Classification Using Three-Dimensional Atomic Structure-Based Neural Networks Applied to Ion Channel–Ligand Docking. Journal of Chemical Information and Modeling, 2022, 62, 2301-2315.	2.5	5
49	Forensic interpretation of molecular variation on networks of disease transmission and genetic inheritance. Electrophoresis, 2014, 35, 3117-3124.	1.3	2
50	GovMath. Notices of the American Mathematical Society, 2019, 66, 1.	0.1	2
51	Quantifying Overfitting Potential in Drug Binding Datasets. Lecture Notes in Computer Science, 2020, , 585-598.	1.0	1
52	Design of Genomic Signatures for Pathogen Identification and Characterization. , 2011, , 493-508.		0