

Jonathan E Allen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4483188/publications.pdf>

Version: 2024-02-01

52
papers

10,509
citations

201674

27
h-index

182427

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 <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
2	Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , 2008, 9, R7.	9.6	2,484
3	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002, 419, 512-519.	27.8	666
4	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	12.6	664
5	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
6	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	309
7	Scalable metagenomic taxonomy classification using a reference genome database. <i>Bioinformatics</i> , 2013, 29, 2253-2260.	4.1	178
8	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	27.8	167
9	JIGSAW: integration of multiple sources of evidence for gene prediction. <i>Bioinformatics</i> , 2005, 21, 3596-3603.	4.1	147
10	Improved Protein-Ligand Binding Affinity Prediction with Structure-Based Deep Fusion Inference. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1583-1592.	5.4	140
11	Computational Gene Prediction Using Multiple Sources of Evidence. <i>Genome Research</i> , 2003, 14, 142-148.	5.5	110
12	FDA-ARGOS is a database with public quality-controlled reference genomes for diagnostic use and regulatory science. <i>Nature Communications</i> , 2019, 10, 3313.	12.8	101
13	Predicting tumor cell line response to drug pairs with deep learning. <i>BMC Bioinformatics</i> , 2018, 19, 486.	2.6	84
14	Metagenomic Analysis of the Airborne Environment in Urban Spaces. <i>Microbial Ecology</i> , 2015, 69, 346-355.	2.8	76
15	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. <i>Genome Biology</i> , 2006, 7, S9.	9.6	61
16	Whole metagenome profiles of particulates collected from the International Space Station. <i>Microbiome</i> , 2017, 5, 81.	11.1	54
17	AMPL: A Data-Driven Modeling Pipeline for Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1955-1968.	5.4	53
18	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. <i>Scientific Reports</i> , 2014, 4, 4245.	3.3	48

#	ARTICLE	IF	CITATIONS
19	Microbial Profiling of Combat Wound Infection through Detection Microarray and Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2583-2594.	3.9	47
20	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017, 6, .	6.0	46
21	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.	3.3	45
22	Ultra-Deep Sequencing of Intra-host Rabies Virus Populations during Cross-species Transmission. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2555.	3.0	43
23	Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. <i>BMC Genomics</i> , 2013, 14, 96.	2.8	40
24	Conserved amino acid markers from past influenza pandemic strains. <i>BMC Microbiology</i> , 2009, 9, 77.	3.3	39
25	Binding Affinity Prediction by Pairwise Function Based on Neural Network. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2766-2772.	5.4	39
26	Using populations of human and microbial genomes for organism detection in metagenomes. <i>Genome Research</i> , 2015, 25, 1056-1067.	5.5	37
27	A cross-study analysis of drug response prediction in cancer cell lines. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	37
28	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.	5.4	35
29	The Role of Viral Population Diversity in Adaptation of Bovine Coronavirus to New Host Environments. <i>PLoS ONE</i> , 2013, 8, e52752.	2.5	35
30	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.	3.5	22
31	Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. <i>BMC Research Notes</i> , 2015, 8, 682.	1.4	21
32	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.	3.7	21
33	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, .	0.8	20
34	Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants. <i>PLoS ONE</i> , 2016, 11, e0146251.	2.5	19
35	A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. <i>PLoS ONE</i> , 2018, 13, e0209683.	2.5	19
36	Machine learning and ligand binding predictions: A review of data, methods, and obstacles. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129545.	2.4	18

#	ARTICLE	IF	CITATIONS
37	Accelerators for Classical Molecular Dynamics Simulations of Biomolecules. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 4047-4069.	5.3	15
38	Draft Genome Sequences from a Novel Clade of <i>Bacillus cereus</i> <i>Sensu Lato</i> Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
39	Multiscale analysis for patterns of Zika virus genotype emergence, spread, and consequence. <i>PLoS ONE</i> , 2019, 14, e0225699.	2.5	12
40	DNA signatures for detecting genetic engineering in bacteria. <i>Genome Biology</i> , 2008, 9, R56.	9.6	11
41	A phylogenetic generalized hidden Markov model for predicting alternatively spliced exons. <i>Algorithms for Molecular Biology</i> , 2006, 1, 14.	1.2	10
42	Machine Learning Models to Predict Inhibition of the Bile Salt Export Pump. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 587-602.	5.4	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. <i>Journal of Virology</i> , 2020, 94, .	3.4	10
44	Characterization of Genetic Variability of Venezuelan Equine Encephalitis Viruses. <i>PLoS ONE</i> , 2016, 11, e0152604.	2.5	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 <i>in vivo</i> passage. <i>Virus Evolution</i> , 2016, 2, vew008.	4.9	5
48	Pose Classification Using Three-Dimensional Atomic Structure-Based Neural Networks Applied to Ion Channel Ligand Docking. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 2301-2315.	5.4	5
49	Forensic interpretation of molecular variation on networks of disease transmission and genetic inheritance. <i>Electrophoresis</i> , 2014, 35, 3117-3124.	2.4	2
50	GovMath. <i>Notices of the American Mathematical Society</i> , 2019, 66, 1.	0.2	2
51	Quantifying Overfitting Potential in Drug Binding Datasets. <i>Lecture Notes in Computer Science</i> , 2020, , 585-598.	1.3	1
52	Design of Genomic Signatures for Pathogen Identification and Characterization. , 2011, , 493-508.		0