

Jonathan E Allen

List of Publications by Year in descending order

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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	A cross-study analysis of drug response prediction in cancer cell lines. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	37
2	Pose Classification Using Three-Dimensional Atomic Structure-Based Neural Networks Applied to Ion Channelâ€™Ligand Docking. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 2301-2315.	5.4	5
3	Accelerators for Classical Molecular Dynamics Simulations of Biomolecules. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 4047-4069.	5.3	15
4	Improved Proteinâ€™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
5	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
6	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
7	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
8	High-throughput virtual screening of small molecule inhibitors for SARS-CoV-2 protein targets with deep fusion models. , 2021, , .		7
9	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
10	AMPL: A Data-Driven Modeling Pipeline for Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1955-1968.	5.4	53
11	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
12	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
13	Quantifying Overfitting Potential in Drug Binding Datasets. <i>Lecture Notes in Computer Science</i> , 2020, , 585-598.	1.3	1
14	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
15	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
16	Multiscale analysis for patterns of Zika virus genotype emergence, spread, and consequence. <i>PLoS ONE</i> , 2019, 14, e0225699.	2.5	12
17	GovMath. <i>Notices of the American Mathematical Society</i> , 2019, 66, 1.	0.2	2
18	Predicting tumor cell line response to drug pairs with deep learning. <i>BMC Bioinformatics</i> , 2018, 19, 486.	2.6	84

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19	A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. PLoS ONE, 2018, 13, e0209683.	2.5	19
20	Gene expression analysis of whole blood RNA from pigs infected with low and high pathogenic African swine fever viruses. Scientific Reports, 2017, 7, 10115.	3.3	45
21	Draft Genome Sequences from a Novel Clade of <i>Bacillus cereus</i> <i>Sensu Lato</i> Strains, Isolated from the International Space Station. Genome Announcements, 2017, 5, .	0.8	14
22	Whole metagenome profiles of particulates collected from the International Space Station. Microbiome, 2017, 5, 81.	11.1	54
23	A molecular portrait of maternal sepsis from Byzantine Troy. ELife, 2017, 6, .	6.0	46
24	Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants. PLoS ONE, 2016, 11, e0146251.	2.5	19
25	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
26	Sendai virus intra-host population dynamics and host immunocompetence influence viral virulence during <i>in vivo</i> passage. Virus Evolution, 2016, 2, vew008.	4.9	5
27	Characterization of Genetic Variability of Venezuelan Equine Encephalitis Viruses. PLoS ONE, 2016, 11, e0152604.	2.5	7
28	Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. BMC Research Notes, 2015, 8, 682.	1.4	21
29	Using populations of human and microbial genomes for organism detection in metagenomes. Genome Research, 2015, 25, 1056-1067.	5.5	37
30	Metagenomic Analysis of the Airborne Environment in Urban Spaces. Microbial Ecology, 2015, 69, 346-355.	2.8	76
31	Forensic interpretation of molecular variation on networks of disease transmission and genetic inheritance. Electrophoresis, 2014, 35, 3117-3124.	2.4	2
32	Design and Optimization of a Metagenomics Analysis Workflow for NVRAM. , 2014, , .		5
33	Microbial Profiling of Combat Wound Infection through Detection Microarray and Next-Generation Sequencing. Journal of Clinical Microbiology, 2014, 52, 2583-2594.	3.9	47
34	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. Scientific Reports, 2014, 4, 4245.	3.3	48
35	Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. BMC Genomics, 2013, 14, 96.	2.8	40
36	Ultra-Deep Sequencing of Intra-host Rabies Virus Populations during Cross-species Transmission. PLoS Neglected Tropical Diseases, 2013, 7, e2555.	3.0	43

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37	Scalable metagenomic taxonomy classification using a reference genome database. <i>Bioinformatics</i> , 2013, 29, 2253-2260.	4.1	178
38	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
39	Design of Genomic Signatures for Pathogen Identification and Characterization. , 2011, , 493-508.		0
40	Conserved amino acid markers from past influenza pandemic strains. <i>BMC Microbiology</i> , 2009, 9, 77.	3.3	39
41	DNA signatures for detecting genetic engineering in bacteria. <i>Genome Biology</i> , 2008, 9, R56.	9.6	11
42	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
43	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
44	A phylogenetic generalized hidden Markov model for predicting alternatively spliced exons. <i>Algorithms for Molecular Biology</i> , 2006, 1, 14.	1.2	10
45	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
46	JIGSAW: integration of multiple sources of evidence for gene prediction. <i>Bioinformatics</i> , 2005, 21, 3596-3603.	4.1	147
47	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	12.6	664
48	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	309
49	Computational Gene Prediction Using Multiple Sources of Evidence. <i>Genome Research</i> , 2003, 14, 142-148.	5.5	110
50	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	27.8	167
51	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
52	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