# Jonathan E Allen

## List of Publications by Year in Descending Order

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|---|---|---|---|
| **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 | Improved Protein-Ligand Binding Affinity Prediction with Structure-Based Deep Fusion Inference. *Journal of Chemical Information and Modeling*, **2021**, 61, 1583-1592 | 6.1 | 24 |
| 48 | 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 | 1.8 | 3 |
| 47 | Discovery of Small-Molecule Inhibitors of SARS-CoV-2 Proteins Using a Computational and Experimental Pipeline. *Frontiers in Molecular Biosciences*, **2021**, 8, 678701 | 5.6 | 5 |
| 46 | A cross-study analysis of drug response prediction in cancer cell lines. *Briefings in Bioinformatics*, **2021**, | 13.4 | 7 |
| 45 | Machine Learning Models to Predict Inhibition of the Bile Salt Export Pump. *Journal of Chemical Information and Modeling*, **2021**, 61, 587-602 | 6.1 | 3 |
| 44 | AMPL: A Data-Driven Modeling Pipeline for Drug Discovery. *Journal of Chemical Information and Modeling*, **2020**, 60, 1955-1968 | 6.1 | 24 |
| 43 | Machine learning and ligand binding predictions: A review of data, methods, and obstacles. *Biochimica Et Biophysica Acta - General Subjects*, **2020**, 1864, 129545 | 4 | 9 |
| 42 | Binding Affinity Prediction by Pairwise Function Based on Neural Network. *Journal of Chemical Information and Modeling*, **2020**, 60, 2766-2772 | 6.1 | 19 |
| 41 | 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, | 6.6 | 4 |
| 40 | Quantifying Overfitting Potential in Drug Binding Datasets. *Lecture Notes in Computer Science*, **2020**, 585-598 | 0.9 | 1 |
| 39 | Predicting Small Molecule Transfer Free Energies by Combining Molecular Dynamics Simulations and Deep Learning. *Journal of Chemical Information and Modeling*, **2020**, 60, 5375-5381 | 6.1 | 13 |
| 38 | FDA-ARGOS is a database with public quality-controlled reference genomes for diagnostic use and regulatory science. *Nature Communications*, **2019**, 10, 3313 | 17.4 | 42 |
| 37 | Multiscale analysis for patterns of Zika virus genotype emergence, spread, and consequence. *PLoS ONE*, **2019**, 14, e0225699 | 3.7 | 7 |
| 36 | Predicting tumor cell line response to drug pairs with deep learning. *BMC Bioinformatics*, **2018**, 19, 486 | 3.6 | 51 |
| 35 | A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. *PLoS ONE*, **2018**, 13, e0209683 | 3.7 | 12 |
| 34 | Gene expression analysis of whole blood RNA from pigs infected with low and high pathogenic African swine fever viruses. *Scientific Reports*, **2017**, 7, 10115 | 4.9 | 23 |
| 33 | Draft Genome Sequences from a Novel Clade of Strains, Isolated from the International Space Station. *Genome Announcements*, **2017**, 5, | | 9 |

| 32 | Whole metagenome profiles of particulates collected from the International Space Station. *Microbiome*, **2017**, 5, 81 | 16.6 | 28 |
|----|----|----|----|
| 31 | A molecular portrait of maternal sepsis from Byzantine Troy. *ELife*, **2017**, 6, | 8.9 | 26 |
| 30 | Sendai virus intra-host population dynamics and host immunocompetence influence viral virulence during passage. *Virus Evolution*, **2016**, 2, vew008 | 3.7 | 5 |
| 29 | Characterization of Genetic Variability of Venezuelan Equine Encephalitis Viruses. *PLoS ONE*, **2016**, 11, e0152604 | 3.7 | 6 |
| 28 | Middle East Respiratory Syndrome Coronavirus Intra-Host Populations Are Characterized by Numerous High Frequency Variants. *PLoS ONE*, **2016**, 11, e0146251 | 3.7 | 12 |
| 27 | Draft Genome Sequences of Biosafety Level 2 Opportunistic Pathogens Isolated from the Environmental Surfaces of the International Space Station. *Genome Announcements*, **2016**, 4, | | 9 |
| 26 | Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. *BMC Research Notes*, **2015**, 8, 682 | 2.3 | 18 |
| 25 | Using populations of human and microbial genomes for organism detection in metagenomes. *Genome Research*, **2015**, 25, 1056-67 | 9.7 | 25 |
| 24 | Metagenomic analysis of the airborne environment in urban spaces. *Microbial Ecology*, **2015**, 69, 346-55 | 4.4 | 59 |
| 23 | Microbial profiling of combat wound infection through detection microarray and next-generation sequencing. *Journal of Clinical Microbiology*, **2014**, 52, 2583-94 | 9.7 | 38 |
| 22 | Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. *Scientific Reports*, **2014**, 4, 4245 | 4.9 | 38 |
| 21 | Forensic interpretation of molecular variation on networks of disease transmission and genetic inheritance. *Electrophoresis*, **2014**, 35, 3117-24 | 3.6 | 2 |
| 20 | Design and Optimization of a Metagenomics Analysis Workflow for NVRAM **2014**, | | 2 |
| 19 | Ultra-deep mutant spectrum profiling: improving sequencing accuracy using overlapping read pairs. *BMC Genomics*, **2013**, 14, 96 | 4.5 | 36 |
| 18 | Ultra-deep sequencing of intra-host rabies virus populations during cross-species transmission. *PLoS Neglected Tropical Diseases*, **2013**, 7, e2555 | 4.8 | 33 |
| 17 | Scalable metagenomic taxonomy classification using a reference genome database. *Bioinformatics*, **2013**, 29, 2253-60 | 7.2 | 127 |
| 16 | The role of viral population diversity in adaptation of bovine coronavirus to new host environments. *PLoS ONE*, **2013**, 8, e52752 | 3.7 | 28 |
| 15 | Design of Genomic Signatures for Pathogen Identification and Characterization **2011**, 493-508 | | |

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| 14 | Conserved amino acid markers from past influenza pandemic strains. *BMC Microbiology*, **2009**, 9, 77 | 4.5 | 30 |
| 13 | DNA signatures for detecting genetic engineering in bacteria. *Genome Biology*, **2008**, 9, R56 | 18.3 | 7 |
| 12 | Automated eukaryotic gene structure annotation using EVidenceModeler and the Program to Assemble Spliced Alignments. *Genome Biology*, **2008**, 9, R7 | 18.3 | 1212 |
| 11 | Draft genome of the filarial nematode parasite Brugia malayi. *Science*, **2007**, 317, 1756-60 | 33.3 | 513 |
| 10 | A phylogenetic generalized hidden Markov model for predicting alternatively spliced exons. *Algorithms for Molecular Biology*, **2006**, 1, 14 | 1.8 | 8 |
| 9 | JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. *Genome Biology*, **2006**, 7 Suppl 1, S9.1-13 | 18.3 | 50 |
| 8 | The genome of the basidiomycetous yeast and human pathogen Cryptococcus neoformans. *Science*, **2005**, 307, 1321-4 | 33.3 | 580 |
| 7 | Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes. *Science*, **2005**, 309, 134-7 | 33.3 | 259 |
| 6 | JIGSAW: integration of multiple sources of evidence for gene prediction. *Bioinformatics*, **2005**, 21, 3596-603 | | 127 |
| 5 | Computational gene prediction using multiple sources of evidence. *Genome Research*, **2004**, 14, 142-8 | 9.7 | 78 |
| 4 | Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14. *Nature*, **2002**, 419, 531-4 | 50.4 | 146 |
| 3 | Genome sequence of the human malaria parasite Plasmodium falciparum. *Nature*, **2002**, 419, 498-511 | 50.4 | 3336 |
| 2 | Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. *Nature*, **2002**, 419, 512-9 | 50.4 | 591 |
| 1 | FDA-ARGOS: A Public Quality-Controlled Genome Database Resource for Infectious Disease Sequencing Diagnostics and Regulatory Science Research | | 3 |