Fiona Sl Brinkman

List of Publications by Year
in descending order

76 papers	21,316 citations	34016 52 h-index	69108 77 g-index
96 all docs	96 docs citations	96 times ranked	27654 citing authors

#	Article	IF	Citations
1	Dysbiosis of the Female Murine Gut Microbiome Exacerbates Neutrophil-Mediated Vascular Allograft Injury by Affecting Immunoregulation by Acetate. Transplantation, 2022, Publish Ahead of Print, .	0.5	1
2	Transcriptome comparison of dengue-susceptible and -resistant field derived strains of Colombian Aedes aegypti using RNA-sequencing. Memorias Do Instituto Oswaldo Cruz, 2021, 116, e200547.	0.8	2
3	The Pseudomonas aeruginosa whole genome sequence: A 20th anniversary celebration. Advances in Microbial Physiology, 2021, 79, 25-88.	1.0	7
4	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic Islands. Microbial Genomics, 2020, 6, .	1.0	67
5	Eleven High-Quality Reference Genome Sequences and 360 Draft Assemblies of Shiga Toxin-Producing Escherichia coli Isolates from Human, Food, Animal, and Environmental Sources in Canada. Microbiology Resource Announcements, 2019, 8, .	0.3	4
6	Disruption of the Gut Microbiota With Antibiotics Exacerbates Acute Vascular Rejection. Transplantation, 2018, 102, 1085-1095.	0.5	24
7	IslandViewer 4: expanded prediction of genomic islands for larger-scale datasets. Nucleic Acids Research, 2017, 45, W30-W35.	6.5	1,251
8	Baseline Practices for the Application of Genomic Data Supporting Regulatory Food Safety. Journal of AOAC INTERNATIONAL, 2017, 100, 721-731.	0.7	25
9	CARD 2017: expansion and model-centric curation of the comprehensive antibiotic resistance database. Nucleic Acids Research, 2017, 45, D566-D573.	6.5	2,063
10	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. Microbial Genomics, 2017, 3, e000116.	1.0	119
11	PSORTdb: expanding the bacteria and archaea protein subcellular localization database to better reflect diversity in cell envelope structures. Nucleic Acids Research, 2016, 44, D663-D668.	6.5	90
12	GenomeD3Plot: a library for rich, interactive visualizations of genomic data in web applications: Fig. 1.. Bioinformatics, 2015, 31, 3348-3349.	1.8	13
13	IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis: Figure 1.. Nucleic Acids Research, 2015, 43, W104-W108.	6.5	316
14	Personalized Genetic Testing and Norovirus Susceptibility. Canadian Journal of Infectious Diseases and Medical Microbiology, 2014, 25, 222-224.	0.7	7
15	Genes, the environment and personalized medicine. EMBO Reports, 2014, 15, 736-739.	2.0	42
16	IslandViewer update: improved genomic island discovery and visualization. Nucleic Acids Research, 2013, 41, W129-W132.	6.5	87
17	InnateDB: systems biology of innate immunity and beyond—recent updates and continuing curation. Nucleic Acids Research, 2013, 41, D1228-D1233.	6.5	1,073
18	OrthologeDB: a bacterial and archaeal orthology resource for improved comparative genomic analysis. Nucleic Acids Research, 2013, 41, D366-D376.	6.5	73

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19	Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures. PeerJ, 2013, 1, e229.	0.9	64
20	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	9.0	500
21	MicrobeDB: a locally maintainable database of microbial genomic sequences. Bioinformatics, 2012, 28, 1947-1948.	1.8	15
22	Effective Adjunctive Therapy by an Innate Defense Regulatory Peptide in a Preclinical Model of Severe Malaria. Science Translational Medicine, 2012, 4, 135ra64.	5.8	81
23	B Cells With High Side Scatter Parameter by Flow Cytometry Correlate With Inferior Survival in Diffuse Large B-Cell Lymphoma. American Journal of Clinical Pathology, 2012, 137, 805-814.	0.4	12
24	Raloxifene attenuates Pseudomonas aeruginosa pyocyanin production and virulence. International Journal of Antimicrobial Agents, 2012, 40, 246-251.	1.1	79
25	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	9.0	274
26	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. New England Journal of Medicine, 2011, 364, 730-739.	13.9	665
27	The proportional lack of archaeal pathogens: Do viruses/phages hold the key?. BioEssays, 2011, 33, 248-254.	1.2	40
28	A statistical approach to high-throughput screening of predicted orthologs. Computational Statistics and Data Analysis, 2011, 55, 935-943.	0.7	2
29	The Human Transcriptome During Nontyphoid Salmonella and HIV Coinfection Reveals Attenuated NFκB-Mediated Inflammation and Persistent Cell Cycle Disruption. Journal of Infectious Diseases, 2011, 204, 1237-1245.	1.9	24
30	G-protein-coupled receptor independent, immunomodulatory properties of chemokine CXCL9. Cellular Immunology, 2010, 261, 105-113.	1.4	10
31	Curating the innate immunity interactome. BMC Systems Biology, 2010, 4, 117.	3.0	68
32	Detecting genomic islands using bioinformatics approaches. Nature Reviews Microbiology, 2010, 8, 373-382.	13.6	257
33	Identification of the Regulatory Logic Controlling Salmonella Pathoadaptation by the SsrA-SsrB Two-Component System. PLoS Genetics, 2010, 6, e1000875.	1.5	67
34	PSORTb 3.0: improved protein subcellular localization prediction with refined localization subcategories and predictive capabilities for all prokaryotes. Bioinformatics, 2010, 26, 1608-1615.	1.8	2,044
35	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i>. Genome Research, 2009, 19, 12-23.	2.4	317
36	The Association of Virulence Factors with Genomic Islands. PLoS ONE, 2009, 4, e8094.	1.1	119

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37	IslandViewer: an integrated interface for computational identification and visualization of genomic islands. Bioinformatics, 2009, 25, 664-665.	1.8	398
38	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
39	Enabling a systems biology approach to immunology: focus on innate immunity. Trends in Immunology, 2009, 30, 249-262.	2.9	122
40	Bioinformatic detection of horizontally transferred DNA in bacterial genomes. F1000 Biology Reports, 2009, 1, 25.	4.0	9
41	Evaluation of genomic island predictors using a comparative genomics approach. BMC Bioinformatics, 2008, 9, 329.	1.2	255
42	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. Trends in Biotechnology, 2008, 26, 190-200.	4.9	101
43	Population genomics: modeling the new and a renaissance of the old. Current Opinion in Microbiology, 2008, 11, 439-441.	2.3	4
44	The Burkholderia Genome Database: facilitating flexible queries and comparative analyses. Bioinformatics, 2008, 24, 2803-2804.	1.8	245
45	Proteomic, Microarray, and Signature-Tagged Mutagenesis Analyses of Anaerobic *Pseudomonas aeruginosa* at pH 6.5, Likely Representing Chronic, Late-Stage Cystic Fibrosis Airway Conditions. Journal of Bacteriology, 2008, 190, 2739-2758.	1.0	86
46	InnateDB: facilitating systems–level analyses of the mammalian innate immune response. Molecular Systems Biology, 2008, 4, 218.	3.2	330
47	Avian beta-defensin nomenclature: A community proposed update. Immunology Letters, 2007, 110, 86-89.	1.1	138
48	Bovine and human cathelicidin cationic host defense peptides similarly suppress transcriptional responses to bacterial lipopolysaccharide. Journal of Leukocyte Biology, 2006, 80, 1563-1574.	1.5	93
49	Modulation of the TLR-Mediated Inflammatory Response by the Endogenous Human Host Defense Peptide LL-37. Journal of Immunology, 2006, 176, 2455-2464.	0.4	491
50	Contribution of the PhoP-PhoQ and PmrA-PmrB Two-Component Regulatory Systems to Mg 2+ -Induced Gene Regulation in Pseudomonas aeruginosa. Journal of Bacteriology, 2006, 188, 3995-4006.	1.0	188
51	The complete genome of Rhodococcus sp. RHA1 provides insights into a catabolic powerhouse. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15582-15587.	3.3	586
52	Methods for predicting bacterial protein subcellular localization. Nature Reviews Microbiology, 2006, 4, 741-751.	13.6	154
53	Improving the specificity of high-throughput ortholog prediction. BMC Bioinformatics, 2006, 7, 270.	1.2	80
54	Assessing the precision of high-throughput computational and laboratory approaches for the genome-wide identification of protein subcellular localization in bacteria. BMC Genomics, 2005, 6, 162.	1.2	40

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55	Effect of Stress on Viral–Bacterial Synergy in Bovine Respiratory Disease: Novel Mechanisms to Regulate Inflammation. Comparative and Functional Genomics, 2005, 6, 244-250.	2.0	105
56	Evidence of a Large Novel Gene Pool Associated with Prokaryotic Genomic Islands. PLoS Genetics, 2005, 1, e62.	1.5	219
57	PSORTb v.2.0: Expanded prediction of bacterial protein subcellular localization and insights gained from comparative proteome analysis. Bioinformatics, 2005, 21, 617-623.	1.8	677
58	Phylogeny of Na+/Ca2+ exchanger (NCX) genes from genomic data identifies new gene duplications and a new family member in fish species. Physiological Genomics, 2005, 21, 161-173.	1.0	29
59	Genome-wide identification of Pseudomonas aeruginosa exported proteins using a consensus computational strategy combined with a laboratory-based PhoA fusion screen. Genome Research, 2005, 15, 321-329.	2.4	103
60	Construction of a mini-Tn5-luxCDABE mutant library in Pseudomonas aeruginosa PAO1: A tool for identifying differentially regulated genes. Genome Research, 2005, 15, 583-589.	2.4	150
61	Genetic and Molecular Analysis of GogB, a Phage-encoded Type III-secreted Substrate in Salmonella enterica Serovar Typhimurium with Autonomous Expression from its Associated Phage. Journal of Molecular Biology, 2005, 348, 817-830.	2.0	66
62	Molecular analyses of disease pathogenesis: Application of bovine microarrays. Veterinary Immunology and Immunopathology, 2005, 105, 277-287.	0.5	17
63	Functional Characterization of a Catabolic Plasmid from Polychlorinated- Biphenyl-Degrading Rhodococcus sp. Strain RHA1. Journal of Bacteriology, 2004, 186, 7783-7795.	1.0	65
64	IslandPath: aiding detection of genomic islands in prokaryotes. Bioinformatics, 2003, 19, 418-420.	1.8	344
65	Aminoglycoside Efflux in Pseudomonas aeruginosa : Involvement of Novel Outer Membrane Proteins. Antimicrobial Agents and Chemotherapy, 2003, 47, 1101-1111.	1.4	115
66	PSORT-B: improving protein subcellular localization prediction for Gram-negative bacteria. Nucleic Acids Research, 2003, 31, 3613-3617.	6.5	383
67	Evidence That Plant-Like Genes in Chlamydia Species Reflect an Ancestral Relationship between Chlamydiaceae, Cyanobacteria, and the Chloroplast. Genome Research, 2002, 12, 1159-1167.	2.4	114
68	Function ofPseudomonasPorins in Uptake and Efflux. Annual Review of Microbiology, 2002, 56, 17-38.	2.9	283
69	PhyloBLAST: facilitating phylogenetic analysis of BLAST results. Bioinformatics, 2001, 17, 385-387.	1.8	26
70	Evolutionary Relationships among Virulence-Associated Histidine Kinases. Infection and Immunity, 2001, 69, 5207-5211.	1.0	40
71	Evaluation of a Structural Model of Pseudomonas aeruginosa Outer Membrane Protein OprM, an Efflux Component Involved in Intrinsic Antibiotic Resistance. Journal of Bacteriology, 2001, 183, 367-374.	1.0	63
72	Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen. Nature, 2000, 406, 959-964.	13.7	3,943

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73	The Amino Terminus of Pseudomonas aeruginosa Outer Membrane Protein OprF Forms Channels in Lipid Bilayer Membranes: Correlation with a Three-Dimensional Model. Journal of Bacteriology, 2000, 182, 5251-5255.	1.0	63
74	Lateral Gene Transfer and Metabolic Adaptation in the Human Parasite Trichomonas vaginalis. Molecular Biology and Evolution, 2000, 17, 1769-1773.	3.5	88
75	Identification of oprG, a gene encoding a major outer membrane protein of Pseudomonas aeruginosa. Journal of Antimicrobial Chemotherapy, 1999, 43, 607-608.	1.3	14
76	Phylogenetic analysis of carbamoylphosphate synthetase genes: complex evolutionary history includes an internal duplication within a gene which can root the tree of life. Molecular Biology and Evolution, 1996, 13, 970-977.	3.5	84