

# Fiona Sl Brinkman

## List of Publications by Year in descending order

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Version: 2024-02-01

76  
papers

21,316  
citations

34105

52  
h-index

69250

77  
g-index

96  
all docs

96  
docs citations

96  
times ranked

27654  
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen. <i>Nature</i> , 2000, 406, 959-964.	27.8	3,943
2	CARD 2017: expansion and model-centric curation of the comprehensive antibiotic resistance database. <i>Nucleic Acids Research</i> , 2017, 45, D566-D573.	14.5	2,063
3	PSORTb 3.0: improved protein subcellular localization prediction with refined localization subcategories and predictive capabilities for all prokaryotes. <i>Bioinformatics</i> , 2010, 26, 1608-1615.	4.1	2,044
4	IslandViewer 4: expanded prediction of genomic islands for larger-scale datasets. <i>Nucleic Acids Research</i> , 2017, 45, W30-W35.	14.5	1,251
5	InnateDB: systems biology of innate immunity and beyond—recent updates and continuing curation. <i>Nucleic Acids Research</i> , 2013, 41, D1228-D1233.	14.5	1,073
6	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
7	PSORTb v.2.0: Expanded prediction of bacterial protein subcellular localization and insights gained from comparative proteome analysis. <i>Bioinformatics</i> , 2005, 21, 617-623.	4.1	677
8	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	27.0	665
9	The complete genome of <i>Rhodococcus</i> sp. RHA1 provides insights into a catabolic powerhouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15582-15587.	7.1	586
10	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	19.0	500
11	Modulation of the TLR-Mediated Inflammatory Response by the Endogenous Human Host Defense Peptide LL-37. <i>Journal of Immunology</i> , 2006, 176, 2455-2464.	0.8	491
12	IslandViewer: an integrated interface for computational identification and visualization of genomic islands. <i>Bioinformatics</i> , 2009, 25, 664-665.	4.1	398
13	PSORT-B: improving protein subcellular localization prediction for Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 3613-3617.	14.5	383
14	IslandPath: aiding detection of genomic islands in prokaryotes. <i>Bioinformatics</i> , 2003, 19, 418-420.	4.1	344
15	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. <i>Molecular Systems Biology</i> , 2008, 4, 218.	7.2	330
16	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i> . <i>Genome Research</i> , 2009, 19, 12-23.	5.5	317
17	IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis: Figure 1.. <i>Nucleic Acids Research</i> , 2015, 43, W104-W108.	14.5	316
18	Function of <i>Pseudomonas</i> Porins in Uptake and Efflux. <i>Annual Review of Microbiology</i> , 2002, 56, 17-38.	7.3	283

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19	PSICQUIC and PSIScore: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
20	Detecting genomic islands using bioinformatics approaches. <i>Nature Reviews Microbiology</i> , 2010, 8, 373-382.	28.6	257
21	Evaluation of genomic island predictors using a comparative genomics approach. <i>BMC Bioinformatics</i> , 2008, 9, 329.	2.6	255
22	The Burkholderia Genome Database: facilitating flexible queries and comparative analyses. <i>Bioinformatics</i> , 2008, 24, 2803-2804.	4.1	245
23	Evidence of a Large Novel Gene Pool Associated with Prokaryotic Genomic Islands. <i>PLoS Genetics</i> , 2005, 1, e62.	3.5	219
24	Contribution of the PhoP-PhoQ and PmrA-PmrB Two-Component Regulatory Systems to Mg <sup>2+</sup> -Induced Gene Regulation in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2006, 188, 3995-4006.	2.2	188
25	Methods for predicting bacterial protein subcellular localization. <i>Nature Reviews Microbiology</i> , 2006, 4, 741-751.	28.6	154
26	Construction of a mini-Tn <sup>5</sup> -luxCDABE mutant library in <i>Pseudomonas aeruginosa</i> PAO1: A tool for identifying differentially regulated genes. <i>Genome Research</i> , 2005, 15, 583-589.	5.5	150
27	Avian beta-defensin nomenclature: A community proposed update. <i>Immunology Letters</i> , 2007, 110, 86-89.	2.5	138
28	Enabling a systems biology approach to immunology: focus on innate immunity. <i>Trends in Immunology</i> , 2009, 30, 249-262.	6.8	122
29	The Association of Virulence Factors with Genomic Islands. <i>PLoS ONE</i> , 2009, 4, e8094.	2.5	119
30	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. <i>Microbial Genomics</i> , 2017, 3, e000116.	2.0	119
31	Aminoglycoside Efflux in <i>Pseudomonas aeruginosa</i> : Involvement of Novel Outer Membrane Proteins. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 1101-1111.	3.2	115
32	Evidence That Plant-Like Genes in <i>Chlamydia</i> Species Reflect an Ancestral Relationship between <i>Chlamydiaceae</i> , <i>Cyanobacteria</i> , and the Chloroplast. <i>Genome Research</i> , 2002, 12, 1159-1167.	5.5	114
33	Effect of Stress on Viral-Bacterial Synergy in Bovine Respiratory Disease: Novel Mechanisms to Regulate Inflammation. <i>Comparative and Functional Genomics</i> , 2005, 6, 244-250.	2.0	105
34	Genome-wide identification of <i>Pseudomonas aeruginosa</i> exported proteins using a consensus computational strategy combined with a laboratory-based PhoA fusion screen. <i>Genome Research</i> , 2005, 15, 321-329.	5.5	103
35	Computer-aided biotechnology: from immuno-informatics to reverse vaccinology. <i>Trends in Biotechnology</i> , 2008, 26, 190-200.	9.3	101
36	Bovine and human cathelicidin cationic host defense peptides similarly suppress transcriptional responses to bacterial lipopolysaccharide. <i>Journal of Leukocyte Biology</i> , 2006, 80, 1563-1574.	3.3	93

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37	PSORTdb: expanding the bacteria and archaea protein subcellular localization database to better reflect diversity in cell envelope structures. <i>Nucleic Acids Research</i> , 2016, 44, D663-D668.	14.5	90
38	Lateral Gene Transfer and Metabolic Adaptation in the Human Parasite <i>Trichomonas vaginalis</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1769-1773.	8.9	88
39	IslandViewer update: improved genomic island discovery and visualization. <i>Nucleic Acids Research</i> , 2013, 41, W129-W132.	14.5	87
40	Proteomic, Microarray, and Signature-Tagged Mutagenesis Analyses of Anaerobic <i>Pseudomonas aeruginosa</i> at pH 6.5, Likely Representing Chronic, Late-Stage Cystic Fibrosis Airway Conditions. <i>Journal of Bacteriology</i> , 2008, 190, 2739-2758.	2.2	86
41	Phylogenetic analysis of carbamoylphosphate synthetase genes: complex evolutionary history includes an internal duplication within a gene which can root the tree of life. <i>Molecular Biology and Evolution</i> , 1996, 13, 970-977.	8.9	84
42	Effective Adjunctive Therapy by an Innate Defense Regulatory Peptide in a Preclinical Model of Severe Malaria. <i>Science Translational Medicine</i> , 2012, 4, 135ra64.	12.4	81
43	Improving the specificity of high-throughput ortholog prediction. <i>BMC Bioinformatics</i> , 2006, 7, 270.	2.6	80
44	Raloxifene attenuates <i>Pseudomonas aeruginosa</i> pyocyanin production and virulence. <i>International Journal of Antimicrobial Agents</i> , 2012, 40, 246-251.	2.5	79
45	OrthoLugeDB: a bacterial and archaeal orthology resource for improved comparative genomic analysis. <i>Nucleic Acids Research</i> , 2013, 41, D366-D376.	14.5	73
46	Curating the innate immunity interactome. <i>BMC Systems Biology</i> , 2010, 4, 117.	3.0	68
47	Identification of the Regulatory Logic Controlling <i>Salmonella</i> Pathoadaptation by the SsrA-SsrB Two-Component System. <i>PLoS Genetics</i> , 2010, 6, e1000875.	3.5	67
48	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic islands. <i>Microbial Genomics</i> , 2020, 6, .	2.0	67
49	Genetic and Molecular Analysis of GogB, a Phage-encoded Type III-secreted Substrate in <i>Salmonella enterica</i> Serovar Typhimurium with Autonomous Expression from its Associated Phage. <i>Journal of Molecular Biology</i> , 2005, 348, 817-830.	4.2	66
50	Functional Characterization of a Catabolic Plasmid from Polychlorinated- Biphenyl-Degrading <i>Rhodococcus</i> sp. Strain RHA1. <i>Journal of Bacteriology</i> , 2004, 186, 7783-7795.	2.2	65
51	Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures. <i>PeerJ</i> , 2013, 1, e229.	2.0	64
52	The Amino Terminus of <i>Pseudomonas aeruginosa</i> Outer Membrane Protein OprF Forms Channels in Lipid Bilayer Membranes: Correlation with a Three-Dimensional Model. <i>Journal of Bacteriology</i> , 2000, 182, 5251-5255.	2.2	63
53	Evaluation of a Structural Model of <i>Pseudomonas aeruginosa</i> Outer Membrane Protein OprM, an Efflux Component Involved in Intrinsic Antibiotic Resistance. <i>Journal of Bacteriology</i> , 2001, 183, 367-374.	2.2	63
54	Genes, the environment and personalized medicine. <i>EMBO Reports</i> , 2014, 15, 736-739.	4.5	42

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55	Evolutionary Relationships among Virulence-Associated Histidine Kinases. <i>Infection and Immunity</i> , 2001, 69, 5207-5211.	2.2	40
56	Assessing the precision of high-throughput computational and laboratory approaches for the genome-wide identification of protein subcellular localization in bacteria. <i>BMC Genomics</i> , 2005, 6, 162.	2.8	40
57	The proportional lack of archaeal pathogens: Do viruses/phages hold the key?. <i>BioEssays</i> , 2011, 33, 248-254.	2.5	40
58	Phylogeny of Na <sup>+</sup> /Ca <sup>2+</sup> exchanger (NCX) genes from genomic data identifies new gene duplications and a new family member in fish species. <i>Physiological Genomics</i> , 2005, 21, 161-173.	2.3	29
59	PhyloBLAST: facilitating phylogenetic analysis of BLAST results. <i>Bioinformatics</i> , 2001, 17, 385-387.	4.1	26
60	Baseline Practices for the Application of Genomic Data Supporting Regulatory Food Safety. <i>Journal of AOAC INTERNATIONAL</i> , 2017, 100, 721-731.	1.5	25
61	The Human Transcriptome During Nontyphoid Salmonella and HIV Coinfection Reveals Attenuated NF- $\kappa$ B-Mediated Inflammation and Persistent Cell Cycle Disruption. <i>Journal of Infectious Diseases</i> , 2011, 204, 1237-1245.	4.0	24
62	Disruption of the Gut Microbiota With Antibiotics Exacerbates Acute Vascular Rejection. <i>Transplantation</i> , 2018, 102, 1085-1095.	1.0	24
63	Molecular analyses of disease pathogenesis: Application of bovine microarrays. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 277-287.	1.2	17
64	MicrobeDB: a locally maintainable database of microbial genomic sequences. <i>Bioinformatics</i> , 2012, 28, 1947-1948.	4.1	15
65	Identification of oprG, a gene encoding a major outer membrane protein of <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 1999, 43, 607-608.	3.0	14
66	GenomeD3Plot: a library for rich, interactive visualizations of genomic data in web applications: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 3348-3349.	4.1	13
67	B Cells With High Side Scatter Parameter by Flow Cytometry Correlate With Inferior Survival in Diffuse Large B-Cell Lymphoma. <i>American Journal of Clinical Pathology</i> , 2012, 137, 805-814.	0.7	12
68	G-protein-coupled receptor independent, immunomodulatory properties of chemokine CXCL9. <i>Cellular Immunology</i> , 2010, 261, 105-113.	3.0	10
69	Bioinformatic detection of horizontally transferred DNA in bacterial genomes. <i>F1000 Biology Reports</i> , 2009, 1, 25.	4.0	9
70	Personalized Genetic Testing and Norovirus Susceptibility. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2014, 25, 222-224.	1.9	7
71	The <i>Pseudomonas aeruginosa</i> whole genome sequence: A 20th anniversary celebration. <i>Advances in Microbial Physiology</i> , 2021, 79, 25-88.	2.4	7
72	Population genomics: modeling the new and a renaissance of the old. <i>Current Opinion in Microbiology</i> , 2008, 11, 439-441.	5.1	4

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73	Eleven High-Quality Reference Genome Sequences and 360 Draft Assemblies of Shiga Toxin-Producing <i>Escherichia coli</i> Isolates from Human, Food, Animal, and Environmental Sources in Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
74	A statistical approach to high-throughput screening of predicted orthologs. <i>Computational Statistics and Data Analysis</i> , 2011, 55, 935-943.	1.2	2
75	Transcriptome comparison of dengue-susceptible and -resistant field derived strains of Colombian <i>Aedes aegypti</i> using RNA-sequencing. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2021, 116, e200547.	1.6	2
76	Dysbiosis of the Female Murine Gut Microbiome Exacerbates Neutrophil-Mediated Vascular Allograft Injury by Affecting Immunoregulation by Acetate. <i>Transplantation</i> , 2022, Publish Ahead of Print, .	1.0	1