

# David Powell

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

2,521  
citations

172457

29  
h-index

214800

47  
g-index

65  
all docs

65  
docs citations

65  
times ranked

4802  
citing authors

#	ARTICLE	IF	CITATIONS
1	Age-Related Decline in Primary CD8+ T Cell Responses Is Associated with the Development of Senescence in Virtual Memory CD8+ T Cells. <i>Cell Reports</i> , 2018, 23, 3512-3524.	6.4	194
2	Glucose Homeostasis Is Important for Immune Cell Viability during <i>Candida</i> Challenge and Host Survival of Systemic Fungal Infection. <i>Cell Metabolism</i> , 2018, 27, 988-1006.e7.	16.2	162
3	Construction and analysis of chromosomal <i>Clostridium difficile</i> mutants. <i>Molecular Microbiology</i> , 2006, 61, 1335-1351.	2.5	149
4	Function of the Cytochrome bc 1 - aa 3 Branch of the Respiratory Network in Mycobacteria and Network Adaptation Occurring in Response to Its Disruption. <i>Journal of Bacteriology</i> , 2005, 187, 6300-6308.	2.2	133
5	Reprogramming Roadmap reveals route to human induced trophoblast stem cells. <i>Nature</i> , 2020, 586, 101-107.	27.8	131
6	Effects of Temperature on Gene Expression Patterns in <i>Leptospira interrogans</i> Serovar Lai as Assessed by Whole-Genome Microarrays. <i>Infection and Immunity</i> , 2006, 74, 5848-5859.	2.2	128
7	Mesenchymal stromal cell apoptosis is required for their therapeutic function. <i>Nature Communications</i> , 2021, 12, 6495.	12.8	91
8	Identification of Novel <i>Acinetobacter baumannii</i> Type VI Secretion System Antibacterial Effector and Immunity Pairs. <i>Infection and Immunity</i> , 2018, 86, .	2.2	88
9	The transcriptomic response of <i>Acinetobacter baumannii</i> to colistin and doripenem alone and in combination in an <i>in vitro</i> pharmacokinetics/pharmacodynamics model. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1303-1313.	3.0	85
10	Global Gene Expression in Skeletal Muscle from Well-Trained Strength and Endurance Athletes. <i>Medicine and Science in Sports and Exercise</i> , 2009, 41, 546-565.	0.4	82
11	Mesenchymal Niche-Derived Neuregulin-1 Drives Intestinal Stem Cell Proliferation and Regeneration of Damaged Epithelium. <i>Cell Stem Cell</i> , 2020, 27, 646-662.e7.	11.1	82
12	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015, 6, e00080.	4.1	81
13	PAT-seq: a method to study the integration of 3' UTR dynamics with gene expression in the eukaryotic transcriptome. <i>Rna</i> , 2015, 21, 1502-1510.	3.5	78
14	Cell Type of Origin Dictates the Route to Pluripotency. <i>Cell Reports</i> , 2017, 21, 2649-2660.	6.4	49
15	Translation complex profile sequencing to study the <i>in vivo</i> dynamics of mRNA-ribosome interactions during translation initiation, elongation and termination. <i>Nature Protocols</i> , 2017, 12, 697-731.	12.0	43
16	Topconfects: a package for confident effect sizes in differential expression analysis provides a more biologically useful ranked gene list. <i>Genome Biology</i> , 2019, 20, 67.	8.8	43
17	Community-driven development for computational biology at Sprints, Hackathons and Codefests. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	42
18	RNAseq: A Pipeline for complete and reproducible RNA-seq analysis that runs anywhere with speed and ease. <i>Journal of Open Source Software</i> , 2018, 3, 583.	4.6	41

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19	The RNA-Binding Chaperone Hfq Is an Important Global Regulator of Gene Expression in <i>Pasteurella multocida</i> and Plays a Crucial Role in Production of a Number of Virulence Factors, Including Hyaluronic Acid Capsule. <i>Infection and Immunity</i> , 2016, 84, 1361-1370.	2.2	40
20	Comparison of the RpoH-Dependent Regulon and General Stress Response in <i>Neisseria gonorrhoeae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4769-4776.	2.2	38
21	Global Gene Expression Profile of <i>Acinetobacter baumannii</i> During Bacteremia. <i>Journal of Infectious Diseases</i> , 2017, 215, S52-S57.	4.0	38
22	Concurrent Host-Pathogen Transcriptional Responses in a <i>Clostridium perfringens</i> Murine Myonecrosis Infection. <i>MBio</i> , 2018, 9, .	4.1	38
23	De novo transcriptome assembly for the spiny mouse ( <i>Acomys cahirinus</i> ). <i>Scientific Reports</i> , 2017, 7, 8996.	3.3	37
24	A Metabolic Checkpoint for the Yeast-to-Hyphae Developmental Switch Regulated by Endogenous Nitric Oxide Signaling. <i>Cell Reports</i> , 2018, 25, 2244-2258.e7.	6.4	37
25	Genomic Evidence for a Globally Distributed, Bimodal Population in the Ovine Footrot Pathogen <i>Dichelobacter nodosus</i> . <i>MBio</i> , 2014, 5, e01821-14.	4.1	36
26	Emergence of High-Level Colistin Resistance in an <i>Acinetobacter baumannii</i> Clinical Isolate Mediated by Inactivation of the Global Regulator H-NS. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	36
27	<i>Wolbachia</i> enhances insect-specific flavivirus infection in <i>Aedes aegypti</i> mosquitoes. <i>Ecology and Evolution</i> , 2018, 8, 5441-5454.	1.9	35
28	Natural Variation Identifies ICARUS1, a Universal Gene Required for Cell Proliferation and Growth at High Temperatures in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2015, 11, e1005085.	3.5	34
29	Integration of Posttranscriptional Gene Networks into Metabolic Adaptation and Biofilm Maturation in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2015, 11, e1005590.	3.5	31
30	Comparative analysis of long DNA sequences by per element information content using different contexts. <i>BMC Bioinformatics</i> , 2007, 8, S10.	2.6	30
31	The role of antigen presenting cells in the induction of HIV-1 latency in resting CD4+ T-cells. <i>Retrovirology</i> , 2015, 12, 76.	2.0	29
32	A Versatile Strategy for Isolating a Highly Enriched Population of Intestinal Stem Cells. <i>Stem Cell Reports</i> , 2016, 6, 321-329.	4.8	27
33	Determination of the small RNA GcvB regulon in the Gram-negative bacterial pathogen <i>Pasteurella multocida</i> and identification of the GcvB seed binding region. <i>Rna</i> , 2018, 24, 704-720.	3.5	26
34	Functional and genomic characterization of a xenograft model system for the study of metastasis in triple-negative breast cancer. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	2.4	23
35	POS-1 Promotes Endo-mesoderm Development by Inhibiting the Cytoplasmic Polyadenylation of neg-1 mRNA. <i>Developmental Cell</i> , 2015, 34, 108-118.	7.0	22
36	Impact of endurance exercise training on adipocyte microRNA expression in overweight men. <i>FASEB Journal</i> , 2017, 31, 161-171.	0.5	21

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37	Segregation of Naturally Occurring Mitochondrial DNA Variants in a Mini-Pig Model. <i>Genetics</i> , 2016, 202, 931-944.	2.9	20
38	VAGUE: a graphical user interface for the Velvet assembler. <i>Bioinformatics</i> , 2013, 29, 264-265.	4.1	19
39	The YEATS Domain Histone Crotonylation Readers Control Virulence-Related Biology of a Major Human Pathogen. <i>Cell Reports</i> , 2020, 31, 107528.	6.4	19
40	Requirement for cleavage factor IIm in the control of alternative polyadenylation in breast cancer cells. <i>Rna</i> , 2020, 26, 969-981.	3.5	18
41	Fast, Optimal Alignment of Three Sequences Using Linear Gap Costs. <i>Journal of Theoretical Biology</i> , 2000, 207, 325-336.	1.7	17
42	PUMA promotes apoptosis of hematopoietic progenitors driving leukemic progression in a mouse model of myelodysplasia. <i>Cell Death and Differentiation</i> , 2016, 23, 1049-1059.	11.2	15
43	A novel role for <i>Lyl1</i> in primitive erythropoiesis. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	14
44	Compression and approximate matching. <i>Computer Journal</i> , 1999, 42, 1-10.	2.4	13
45	Restricted cell cycle is essential for clonal evolution and therapeutic resistance of pre-leukemic stem cells. <i>Nature Communications</i> , 2018, 9, 3535.	12.8	13
46	Bionitio: demonstrating and facilitating best practices for bioinformatics command-line software. <i>GigaScience</i> , 2019, 8, .	6.4	13
47	A versatile divide and conquer technique for optimal string alignment. <i>Information Processing Letters</i> , 1999, 70, 127-139.	0.6	11
48	EST-PAC a web package for EST annotation and protein sequence prediction. <i>Source Code for Biology and Medicine</i> , 2006, 1, 2.	1.7	9
49	Modelling-Alignment for Non-random Sequences. <i>Lecture Notes in Computer Science</i> , 2004, , 203-214.	1.3	8
50	Quantifying splice-site usage: a simple yet powerful approach to analyze splicing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab041.	3.2	7
51	câ€Rel employs multiple mechanisms to promote the thymic development and peripheral function of regulatory T cells in mice. <i>European Journal of Immunology</i> , 2021, 51, 2006-2026.	2.9	7
52	Pan-transcriptomic analysis identified common differentially expressed genes of <i>Acinetobacter baumannii</i> in response to polymyxin treatments. <i>Molecular Omics</i> , 2020, 16, 327-338.	2.8	7
53	Haplotyping the human leukocyte antigen system from single chromosomes. <i>Scientific Reports</i> , 2016, 6, 30381.	3.3	6
54	The Detection and Bioinformatic Analysis of Alternative 3' UTR Isoforms as Potential Cancer Biomarkers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5322.	4.1	5

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55	Genetic and pharmacological evidence for kinetic competition between alternative poly(A) sites in yeast. <i>ELife</i> , 2021, 10, .	6.0	5
56	The Role and Targets of the RNA-Binding Protein ProQ in the Gram-Negative Bacterial Pathogen <i>Pasteurella multocida</i> . <i>Journal of Bacteriology</i> , 2022, 204, e0059221.	2.2	4
57	Transcriptional profile in afferent lymph cells following vaccination with liposomes incorporating CpG. <i>Immunology</i> , 2015, 144, 518-529.	4.4	3
58	Transcriptomic analysis of preovipositional embryonic arrest in a nonsquamate reptile ( <i>Chelonia</i> ) Tj ETQq0 0 0 rgBT/Overlock <sub>3</sub> 10 Tf 50 6	3.9	3
59	A novel cause of DKC1 -related bone marrow failure: Partial deletion of the 3' untranslated region. <i>EJHaem</i> , 2021, 2, 157-166.	1.0	1
60	Maintenance of primitive haematopoiesis is shared by SCL and LYL1. <i>Experimental Hematology</i> , 2017, 53, S115.	0.4	0
61	Unsupervised Learning in Metagame. <i>Lecture Notes in Computer Science</i> , 1999, , 24-35.	1.3	0