## **David Powell**

## List of Publications by Year in descending order

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214721 186209 2,521 61 28 47 citations h-index g-index papers 65 65 65 4802 all docs docs citations times ranked 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. Cell Reports, 2018, 23, 3512-3524.	2.9	194
2	Glucose Homeostasis Is Important for Immune Cell Viability during Candida Challenge and Host Survival of Systemic Fungal Infection. Cell Metabolism, 2018, 27, 988-1006.e7.	7.2	162
3	Construction and analysis of chromosomal Clostridium difficile mutants. Molecular Microbiology, 2006, 61, 1335-1351.	1.2	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. Journal of Bacteriology, 2005, 187, 6300-6308.	1.0	133
5	ReprogrammingÂroadmap reveals route toÂhuman induced trophoblast stem cells. Nature, 2020, 586, 101-107.	13.7	131
6	Effects of Temperature on Gene Expression Patterns in Leptospira interrogans Serovar Lai as Assessed by Whole-Genome Microarrays. Infection and Immunity, 2006, 74, 5848-5859.	1.0	128
7	Mesenchymal stromal cell apoptosis is required for their therapeutic function. Nature Communications, 2021, 12, 6495.	5.8	91
8	Identification of Novel Acinetobacter baumannii Type VI Secretion System Antibacterial Effector and Immunity Pairs. Infection and Immunity, 2018, 86, .	1.0	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. Journal of Antimicrobial Chemotherapy, 2015, 70, 1303-1313.	1.3	85
10	Global Gene Expression in Skeletal Muscle from Well-Trained Strength and Endurance Athletes. Medicine and Science in Sports and Exercise, 2009, 41, 546-565.	0.2	82
11	Mesenchymal Niche-Derived Neuregulin-1 Drives Intestinal Stem Cell Proliferation and Regeneration of Damaged Epithelium. Cell Stem Cell, 2020, 27, 646-662.e7.	5.2	82
12	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant Staphylococcus aureus. MBio, 2015, 6, e00080.	1.8	81
13	PAT-seq: a method to study the integration of 3′-UTR dynamics with gene expression in the eukaryotic transcriptome. Rna, 2015, 21, 1502-1510.	1.6	78
14	Cell Type of Origin Dictates the Route to Pluripotency. Cell Reports, 2017, 21, 2649-2660.	2.9	49
15	Translation complex profile sequencing to study the in vivo dynamics of mRNA–ribosome interactions during translation initiation, elongation and termination. Nature Protocols, 2017, 12, 697-731.	5 <b>.</b> 5	43
16	Topconfects: a package for confident effect sizes in differential expression analysis provides a more biologically useful ranked gene list. Genome Biology, 2019, 20, 67.	3.8	43
17	Community-driven development for computational biology at Sprints, Hackathons and Codefests. BMC Bioinformatics, 2014, 15, S7.	1.2	42
18	RNAsik: A Pipeline for complete and reproducible RNA-seq analysis that runs anywhere with speed and ease. Journal of Open Source Software, 2018, 3, 583.	2.0	41

#	Article	lF	CITATIONS
19	The RNA-Binding Chaperone Hfq Is an Important Global Regulator of Gene Expression in Pasteurella multocida and Plays a Crucial Role in Production of a Number of Virulence Factors, Including Hyaluronic Acid Capsule. Infection and Immunity, 2016, 84, 1361-1370.	1.0	40
20	Comparison of the RpoH-Dependent Regulon and General Stress Response in Neisseria gonorrhoeae. Journal of Bacteriology, 2006, 188, 4769-4776.	1.0	38
21	Global Gene Expression Profile of Acinetobacter baumannii During Bacteremia. Journal of Infectious Diseases, 2017, 215, S52-S57.	1.9	38
22	Concurrent Host-Pathogen Transcriptional Responses in a <i>Clostridium perfringens</i> Murine Myonecrosis Infection. MBio, 2018, 9, .	1.8	38
23	De novo transcriptome assembly for the spiny mouse (Acomys cahirinus). Scientific Reports, 2017, 7, 8996.	1.6	37
24	A Metabolic Checkpoint for the Yeast-to-Hyphae Developmental Switch Regulated by Endogenous Nitric Oxide Signaling. Cell Reports, 2018, 25, 2244-2258.e7.	2.9	37
25	Genomic Evidence for a Globally Distributed, Bimodal Population in the Ovine Footrot Pathogen Dichelobacter nodosus. MBio, 2014, 5, e01821-14.	1.8	36
26	Emergence of High-Level Colistin Resistance in an Acinetobacter baumannii Clinical Isolate Mediated by Inactivation of the Global Regulator H-NS. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	36
27	<i>Wolbachia</i> enhances insectâ€specific flavivirus infection in <i>Aedes aegypti</i> mosquitoes. Ecology and Evolution, 2018, 8, 5441-5454.	0.8	35
28	Natural Variation Identifies ICARUS1, a Universal Gene Required for Cell Proliferation and Growth at High Temperatures in Arabidopsis thaliana. PLoS Genetics, 2015, 11, e1005085.	1.5	34
29	Integration of Posttranscriptional Gene Networks into Metabolic Adaptation and Biofilm Maturation in Candida albicans. PLoS Genetics, 2015, 11, e1005590.	1.5	31
30	Comparative analysis of long DNA sequences by per element information content using different contexts. BMC Bioinformatics, 2007, 8, S10.	1.2	30
31	The role of antigen presenting cells in the induction of HIV-1 latency in resting CD4+ T-cells. Retrovirology, 2015, 12, 76.	0.9	29
32	A Versatile Strategy for Isolating a Highly Enriched Population of Intestinal Stem Cells. Stem Cell Reports, 2016, 6, 321-329.	2.3	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. Rna, 2018, 24, 704-720.	1.6	26
34	Functional and genomic characterization of a xenograft model system for the study of metastasis in triple-negative breast cancer. DMM Disease Models and Mechanisms, $2018,11,1$	1.2	23
35	POS-1 Promotes Endo-mesoderm Development by Inhibiting the Cytoplasmic Polyadenylation of neg-1 mRNA. Developmental Cell, 2015, 34, 108-118.	3.1	22
36	Impact of endurance exercise training on adipocyte microRNA expression in overweight men. FASEB Journal, 2017, 31, 161-171.	0.2	21

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37	Segregation of Naturally Occurring Mitochondrial DNA Variants in a Mini-Pig Model. Genetics, 2016, 202, 931-944.	1.2	20
38	VAGUE: a graphical user interface for the Velvet assembler. Bioinformatics, 2013, 29, 264-265.	1.8	19
39	The YEATS Domain Histone Crotonylation Readers Control Virulence-Related Biology of a Major Human Pathogen. Cell Reports, 2020, 31, 107528.	2.9	19
40	Requirement for cleavage factor II <sub>m</sub> in the control of alternative polyadenylation in breast cancer cells. Rna, 2020, 26, 969-981.	1.6	18
41	Fast, Optimal Alignment of Three Sequences Using Linear Gap Costs. Journal of Theoretical Biology, 2000, 207, 325-336.	0.8	17
42	PUMA promotes apoptosis of hematopoietic progenitors driving leukemic progression in a mouse model of myelodysplasia. Cell Death and Differentiation, 2016, 23, 1049-1059.	5.0	15
43	A novel role for $\langle i \rangle$ Lyl $1 \langle  i \rangle$ in primitive erythropoiesis. Development (Cambridge), 2018, 145, .	1.2	14
44	Compression and approximate matching. Computer Journal, 1999, 42, 1-10.	1.5	13
45	Restricted cell cycle is essential for clonal evolution and therapeutic resistance of pre-leukemic stem cells. Nature Communications, 2018, 9, 3535.	5.8	13
46	Bionitio: demonstrating and facilitating best practices for bioinformatics command-line software. GigaScience, 2019, 8, .	3.3	13
47	A versatile divide and conquer technique for optimal string alignment. Information Processing Letters, 1999, 70, 127-139.	0.4	11
48	EST-PAC a web package for EST annotation and protein sequence prediction. Source Code for Biology and Medicine, 2006, $\hat{1}$ , 2.	1.7	9
49	Modelling-Alignment for Non-random Sequences. Lecture Notes in Computer Science, 2004, , 203-214.	1.0	8
50	Quantifying splice-site usage: a simple yet powerful approach to analyze splicing. NAR Genomics and Bioinformatics, 2021, 3, lqab041.	1.5	7
51	câ€Rel employs multiple mechanisms to promote the thymic development and peripheral function of regulatory T cells in mice. European Journal of Immunology, 2021, 51, 2006-2026.	1.6	7
52	Pan-transcriptomic analysis identified common differentially expressed genes of <i>Acinetobacter baumannii </i> in response to polymyxin treatments. Molecular Omics, 2020, 16, 327-338.	1.4	7
53	Haplotyping the human leukocyte antigen system from single chromosomes. Scientific Reports, 2016, 6, 30381.	1.6	6
54	The Detection and Bioinformatic Analysis of Alternative 3′ UTR Isoforms as Potential Cancer Biomarkers. International Journal of Molecular Sciences, 2021, 22, 5322.	1.8	5

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55	Genetic and pharmacological evidence for kinetic competition between alternative poly(A) sites in yeast. ELife, $2021,10,$	2.8	5
56	The Role and Targets of the RNA-Binding Protein ProQ in the Gram-Negative Bacterial Pathogen Pasteurella multocida. Journal of Bacteriology, 2022, 204, e0059221.	1.0	4
57	Transcriptional profile in afferent lymph cells following vaccination with liposomes incorporating CpG. Immunology, 2015, 144, 518-529.	2.0	3
58	Transcriptomic analysis of preovipositional embryonic arrest in a nonsquamate reptile (Chelonia) Tj ETQq0 0 0 rgt	BT/Overlo 2.0	ck <sub>3</sub> 10 Tf 50 6
59	A novel cause of DKC1 â€related bone marrow failure: Partial deletion of the 3′ untranslated region. EJHaem, 2021, 2, 157-166.	0.4	1
60	Maintenance of primitive haematopoiesis is shared by SCL and LYL1. Experimental Hematology, 2017, 53, S115.	0.2	0
61	Unsupervised Learning in Metagame. Lecture Notes in Computer Science, 1999, , 24-35.	1.0	O