

David Powell

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5573194/publications.pdf>

Version: 2024-02-01

61
papers

2,521
citations

186209

28
h-index

214721

47
g-index

65
all docs

65
docs citations

65
times ranked

4802
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.0	4
2	Transcriptomic analysis of preovipositional embryonic arrest in a nonsquamate reptile (<i>Chelonia</i>) Tj ETQq0 0 0 rgBT ₂ Overlock ₃ 10 Tf 50 7	2.0	3
3	Quantifying splice-site usage: a simple yet powerful approach to analyze splicing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab041.	1.5	7
4	The Detection and Bioinformatic Analysis of Alternative 3' UTR Isoforms as Potential Cancer Biomarkers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5322.	1.8	5
5	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.	1.6	7
6	Genetic and pharmacological evidence for kinetic competition between alternative poly(A) sites in yeast. <i>ELife</i> , 2021, 10, .	2.8	5
7	A novel cause of DKC1 related bone marrow failure: Partial deletion of the 5' untranslated region. <i>EJHaem</i> , 2021, 2, 157-166.	0.4	1
8	Mesenchymal stromal cell apoptosis is required for their therapeutic function. <i>Nature Communications</i> , 2021, 12, 6495.	5.8	91
9	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.	5.2	82
10	Reprogramming roadmap reveals route to human induced trophoblast stem cells. <i>Nature</i> , 2020, 586, 101-107.	13.7	131
11	The YEATS Domain Histone Crotonylation Readers Control Virulence-Related Biology of a Major Human Pathogen. <i>Cell Reports</i> , 2020, 31, 107528.	2.9	19
12	Requirement for cleavage factor Im in the control of alternative polyadenylation in breast cancer cells. <i>Rna</i> , 2020, 26, 969-981.	1.6	18
13	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.	1.4	7
14	Bionitio: demonstrating and facilitating best practices for bioinformatics command-line software. <i>GigaScience</i> , 2019, 8, .	3.3	13
15	Topconfacts: 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.	3.8	43
16	Concurrent Host-Pathogen Transcriptional Responses in a <i>Clostridium perfringens</i> Murine Myonecrosis Infection. <i>MBio</i> , 2018, 9, .	1.8	38
17	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.	1.6	26
18	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, .	1.2	23

#	ARTICLE	IF	CITATIONS
19	Glucose Homeostasis Is Important for Immune Cell Viability during Candida Challenge and Host Survival of Systemic Fungal Infection. <i>Cell Metabolism</i> , 2018, 27, 988-1006.e7.	7.2	162
20	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, .	1.4	36
21	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.	2.9	37
22	A novel role for <i>Lyl1</i> in primitive erythropoiesis. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	14
23	Restricted cell cycle is essential for clonal evolution and therapeutic resistance of pre-leukemic stem cells. <i>Nature Communications</i> , 2018, 9, 3535.	5.8	13
24	<i>Wolbachia</i> enhances insect-specific flavivirus infection in <i>Aedes aegypti</i> mosquitoes. <i>Ecology and Evolution</i> , 2018, 8, 5441-5454.	0.8	35
25	Identification of Novel <i>Acinetobacter baumannii</i> Type VI Secretion System Antibacterial Effector and Immunity Pairs. <i>Infection and Immunity</i> , 2018, 86, .	1.0	88
26	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.	2.9	194
27	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.	2.0	41
28	Translation complex profile sequencing to study the in vivo dynamics of mRNA-ribosome interactions during translation initiation, elongation and termination. <i>Nature Protocols</i> , 2017, 12, 697-731.	5.5	43
29	Global Gene Expression Profile of <i>Acinetobacter baumannii</i> During Bacteremia. <i>Journal of Infectious Diseases</i> , 2017, 215, S52-S57.	1.9	38
30	Maintenance of primitive haematopoiesis is shared by SCL and LYL1. <i>Experimental Hematology</i> , 2017, 53, S115.	0.2	0
31	De novo transcriptome assembly for the spiny mouse (<i>Acomys cahirinus</i>). <i>Scientific Reports</i> , 2017, 7, 8996.	1.6	37
32	Cell Type of Origin Dictates the Route to Pluripotency. <i>Cell Reports</i> , 2017, 21, 2649-2660.	2.9	49
33	Impact of endurance exercise training on adipocyte microRNA expression in overweight men. <i>FASEB Journal</i> , 2017, 31, 161-171.	0.2	21
34	Haplotyping the human leukocyte antigen system from single chromosomes. <i>Scientific Reports</i> , 2016, 6, 30381.	1.6	6
35	A Versatile Strategy for Isolating a Highly Enriched Population of Intestinal Stem Cells. <i>Stem Cell Reports</i> , 2016, 6, 321-329.	2.3	27
36	Segregation of Naturally Occurring Mitochondrial DNA Variants in a Mini-Pig Model. <i>Genetics</i> , 2016, 202, 931-944.	1.2	20

#	ARTICLE	IF	CITATIONS
37	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.	1.0	40
38	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.	5.0	15
39	The role of antigen presenting cells in the induction of HIV-1 latency in resting CD4+ T-cells. <i>Retrovirology</i> , 2015, 12, 76.	0.9	29
40	Integration of Posttranscriptional Gene Networks into Metabolic Adaptation and Biofilm Maturation in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2015, 11, e1005590.	1.5	31
41	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.	1.6	78
42	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.	1.3	85
43	POS-1 Promotes Endo-mesoderm Development by Inhibiting the Cytoplasmic Polyadenylation of <i>neg-1</i> mRNA. <i>Developmental Cell</i> , 2015, 34, 108-118.	3.1	22
44	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.	1.5	34
45	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015, 6, e00080.	1.8	81
46	Transcriptional profile in afferent lymph cells following vaccination with liposomes incorporating CpG. <i>Immunology</i> , 2015, 144, 518-529.	2.0	3
47	Genomic Evidence for a Globally Distributed, Bimodal Population in the Ovine Footrot Pathogen <i>Dichelobacter nodosus</i> . <i>MBio</i> , 2014, 5, e01821-14.	1.8	36
48	Community-driven development for computational biology at Sprints, Hackathons and Codefests. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	42
49	VAGUE: a graphical user interface for the Velvet assembler. <i>Bioinformatics</i> , 2013, 29, 264-265.	1.8	19
50	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.	0.2	82
51	Comparative analysis of long DNA sequences by per element information content using different contexts. <i>BMC Bioinformatics</i> , 2007, 8, S10.	1.2	30
52	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
53	Construction and analysis of chromosomal <i>Clostridium difficile</i> mutants. <i>Molecular Microbiology</i> , 2006, 61, 1335-1351.	1.2	149
54	Comparison of the RpoH-Dependent Regulon and General Stress Response in <i>Neisseria gonorrhoeae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4769-4776.	1.0	38

#	ARTICLE	IF	CITATIONS
55	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.	1.0	128
56	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.	1.0	133
57	Modelling-Alignment for Non-random Sequences. <i>Lecture Notes in Computer Science</i> , 2004, , 203-214.	1.0	8
58	Fast, Optimal Alignment of Three Sequences Using Linear Gap Costs. <i>Journal of Theoretical Biology</i> , 2000, 207, 325-336.	0.8	17
59	Compression and approximate matching. <i>Computer Journal</i> , 1999, 42, 1-10.	1.5	13
60	A versatile divide and conquer technique for optimal string alignment. <i>Information Processing Letters</i> , 1999, 70, 127-139.	0.4	11
61	Unsupervised Learning in Metagame. <i>Lecture Notes in Computer Science</i> , 1999, , 24-35.	1.0	0