

Philip D Butcher

List of Publications by Year in descending order

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56
papers

6,194
citations

136950

32
h-index

168389

53
g-index

57
all docs

57
docs citations

57
times ranked

6528
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional Adaptation of <i>Mycobacterium tuberculosis</i> within Macrophages. <i>Journal of Experimental Medicine</i> , 2003, 198, 693-704.	8.5	1,311
2	Cytological and Transcript Analyses Reveal Fat and Lazy Persister-Like Bacilli in Tuberculous Sputum. <i>PLoS Medicine</i> , 2008, 5, e75.	8.4	383
3	High-Dose Rifapentine with Moxifloxacin for Pulmonary Tuberculosis. <i>New England Journal of Medicine</i> , 2014, 371, 1599-1608.	27.0	383
4	Dissection of the heat-shock response in <i>Mycobacterium tuberculosis</i> using mutants and microarrays a list of the 100 ORFs most highly induced by heat shock is provided as supplementary data with the online version of this paper (http://mic.sgmjournals.org). <i>Microbiology (United Kingdom)</i> , 2002, 148, 3129-3138.	1.8	318
5	<i>Mycobacterial P1-Type ATPases Mediate Resistance to Zinc Poisoning in Human Macrophages. Cell Host and Microbe</i> , 2011, 10, 248-259.	11.0	304
6	Microarrays Reveal that Each of the Ten Dominant Lineages of <i>Staphylococcus aureus</i> Has a Unique Combination of Surface-Associated and Regulatory Genes. <i>Journal of Bacteriology</i> , 2006, 188, 669-676.	2.2	303
7	Dissection of ESAT-6 System 1 of <i>Mycobacterium tuberculosis</i> and Impact on Immunogenicity and Virulence. <i>Infection and Immunity</i> , 2006, 74, 88-98.	2.2	279
8	Whole Genome Comparison of <i>Campylobacter jejuni</i> Human Isolates Using a Low-Cost Microarray Reveals Extensive Genetic Diversity. <i>Genome Research</i> , 2001, 11, 1706-1715.	5.5	278
9	Stationary phase gene expression of <i>Mycobacterium tuberculosis</i> following a progressive nutrient depletion: a model for persistent organisms?. <i>Tuberculosis</i> , 2004, 84, 228-238.	1.9	185
10	Probing Host Pathogen Cross-Talk by Transcriptional Profiling of Both <i>Mycobacterium tuberculosis</i> and Infected Human Dendritic Cells and Macrophages. <i>PLoS ONE</i> , 2008, 3, e1403.	2.5	172
11	Detection of mRNA Transcripts and Active Transcription in Persistent <i>Mycobacterium tuberculosis</i> Induced by Exposure to Rifampin or Pyrazinamide. <i>Journal of Bacteriology</i> , 2000, 182, 6358-6365.	2.2	168
12	Differential expression of mycobacterial proteins following phagocytosis by macrophages. <i>Microbiology (United Kingdom)</i> , 2001, 147, 459-471.	1.8	157
13	High Prevalence of Antibiotic-Resistant <i>Mycoplasma genitalium</i> in Nongonococcal Urethritis: The Need for Routine Testing and the Inadequacy of Current Treatment Options. <i>Clinical Infectious Diseases</i> , 2014, 58, 631-637.	5.8	142
14	<i>Mycobacterium tuberculosis</i> Expresses a Novel Ph-Dependent Divalent Cation Transporter Belonging to the Nramp Family. <i>Journal of Experimental Medicine</i> , 1999, 190, 717-724.	8.5	131
15	The influence of reduced oxygen availability on pathogenicity and gene expression in <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2004, 84, 205-217.	1.9	127
16	Protein synthesis is shutdown in dormant <i>Mycobacterium tuberculosis</i> and is reversed by oxygen or heat shock. <i>FEMS Microbiology Letters</i> , 1998, 158, 139-145.	1.8	98
17	Clinical use of whole genome sequencing for <i>Mycobacterium tuberculosis</i> . <i>BMC Medicine</i> , 2016, 14, 46.	5.5	91
18	Clinical Application of Whole-Genome Sequencing To Inform Treatment for Multidrug-Resistant Tuberculosis Cases. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1473-1483.	3.9	89

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19	DNA Microarrays for Virus Detection in Cases of Central Nervous System Infection. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5811-5818.	3.9	88
20	Lipid composition and transcriptional response of <i>Mycobacterium tuberculosis</i> grown under iron-limitation in continuous culture: identification of a novel wax ester. <i>Microbiology (United Kingdom)</i> , 2007, 161, 1051-1059.	1.5	69
21	Analysis of whole-genome microarray replicates using mixed models. <i>Bioinformatics</i> , 2003, 19, 53-61.	4.1	82
22	Regulation of <i>hmp</i> Gene Transcription in <i>Mycobacterium tuberculosis</i> : Effects of Oxygen Limitation and Nitrosative and Oxidative Stress. <i>Journal of Bacteriology</i> , 1999, 181, 3486-3493.	2.2	79
23	Design, Validation, and Application of a Seven-Strain <i>Staphylococcus aureus</i> PCR Product Microarray for Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7504-7514.	3.1	77
24	Potassium availability triggers <i>Mycobacterium tuberculosis</i> transition to, and resuscitation from, non-culturable (dormant) states. <i>Open Biology</i> , 2014, 4, 140106.	3.6	73
25	Characterization of a haemolysin from <i>Mycobacterium tuberculosis</i> with homology to a virulence factor of <i>Serpulina hyodysenteriae</i> . <i>Microbiology (United Kingdom)</i> , 1998, 144, 1205-1211.	1.8	68
26	Use of whole-genome sequencing to distinguish relapse from reinfection in a completed tuberculosis clinical trial. <i>BMC Medicine</i> , 2017, 15, 71.	5.5	57
27	Profiling persistent tubercle bacilli from patient sputa during therapy predicts early drug efficacy. <i>BMC Medicine</i> , 2016, 14, 68.	5.5	55
28	Contrasting Transcriptional Responses of a Virulent and an Attenuated Strain of <i>Mycobacterium tuberculosis</i> Infecting Macrophages. <i>PLoS ONE</i> , 2010, 5, e11066.	2.5	42
29	Evidence for a Role for Interleukin-17, Th17 Cells and Iron Homeostasis in Protective Immunity against Tuberculosis in <i>Cynomolgus</i> Macaques. <i>PLoS ONE</i> , 2014, 9, e88149.	2.5	40
30	Microarray Analysis of Whole Genome Expression of Intracellular <i>Mycobacterium tuberculosis</i> . <i>Current Molecular Medicine</i> , 2007, 7, 287-296.	1.3	36
31	Microarrays for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2004, 84, 131-137.	1.9	35
32	Gene expression during host-pathogen interactions: Approaches to bacterial mRNA extraction and labelling for microarray analysis. <i>Methods in Microbiology</i> , 2002, 33, 137-151.	0.8	34
33	RNA profiling in host-pathogen interactions. <i>Current Opinion in Microbiology</i> , 2007, 10, 297-302.	5.1	31
34	Intracellular Gene Expression: Analysis of RNA from <i>Mycobacteria</i> in Macrophages Using RT-PCR. , 1998, 101, 285-306.		30
35	Examining the basis of isoniazid tolerance in nonreplicating <i>Mycobacterium tuberculosis</i> using transcriptional profiling. <i>Future Medicinal Chemistry</i> , 2010, 2, 1371-1383.	2.3	29
36	cDNA-RNA subtractive hybridization reveals increased expression of mycocerosic acid synthase in intracellular <i>Mycobacterium bovis</i> BCG. <i>Microbiology (United Kingdom)</i> , 2001, 147, 2293-2305.	1.8	29

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37	XDR-TB transmission in London: Case management and contact tracing investigation assisted by early whole genome sequencing. <i>Journal of Infection</i> , 2016, 73, 210-218.	3.3	28
38	Microarray analysis of defined <i>Mycobacterium tuberculosis</i> populations using RNA amplification strategies. <i>BMC Genomics</i> , 2008, 9, 94.	2.8	25
39	DNA probes for the faecal diagnosis of <i>Giardia lamblia</i> infections in man. <i>Biochemical Society Transactions</i> , 1989, 17, 363-364.	3.4	24
40	Use of Genome Level-Informed PCR as a New Investigational Approach for Analysis of Outbreak-Associated <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1890-1896.	3.9	24
41	Genetic Composition of <i>Mycobacterium bovis</i> BCG Substrain Sofia. <i>Journal of Clinical Microbiology</i> , 2003, 41, 5349-5349.	3.9	23
42	Extraction and characterization of mRNA from mycobacteria: implication for virulence gene identification. <i>Journal of Microbiological Methods</i> , 1991, 13, 99-111.	1.6	21
43	The Heat Shock Response of <i>Mycobacterium tuberculosis</i> : Linking Gene Expression, Immunology and Pathogenesis. <i>Comparative and Functional Genomics</i> , 2002, 3, 348-351.	2.0	19
44	Genomic Diversity among Beijing and non-Beijing <i>Mycobacterium tuberculosis</i> Isolates from Myanmar. <i>PLoS ONE</i> , 2008, 3, e1973.	2.5	18
45	Use of DNA Arrays to Study Transcriptional Responses to Antimycobacterial Compounds. <i>Methods in Molecular Biology</i> , 2010, 642, 75-91.	0.9	18
46	Glass slide microarrays for bacterial genomes. <i>Methods in Microbiology</i> , 2002, , 83-99.	0.8	17
47	Genomic Analysis of <i>Mycobacterium tuberculosis</i> Complex Strains Used for Production of Purified Protein Derivative. <i>Journal of Clinical Microbiology</i> , 2003, 41, 3929-3932.	3.9	16
48	Increased transcription of a potential sigma factor regulatory gene Rv1364c in <i>Mycobacterium bovis</i> BCG while residing in macrophages indicates use of alternative promoters. <i>FEMS Microbiology Letters</i> , 2004, 233, 333-339.	1.8	15
49	Performance evaluation of automated urine microscopy as a rapid, non-invasive approach for the diagnosis of non-gonococcal urethritis. <i>Sexually Transmitted Infections</i> , 2015, 91, 165-170.	1.9	12
50	Antimicrobial Treatment Improves Mycobacterial Survival in Nonpermissive Growth Conditions. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2798-2806.	3.2	11
51	Methionine Sulfoximine Resistance in <i>Mycobacterium tuberculosis</i> Is Due to a Single Nucleotide Deletion Resulting in Increased Expression of the Major Glutamine Synthetase, GlnA1. <i>Microbial Drug Resistance</i> , 2011, 17, 351-355.	2.0	10
52	Extraction of RNA from Intracellular <i>Mycobacterium tuberculosis</i> : Methods, Considerations, and Applications. , 2001, 54, 031-042.		8
53	Oleoyl Coenzyme A Regulates Interaction of Transcriptional Regulator RaaS (Rv1219c) with DNA in <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 25241-25249.	3.4	8
54	Increased transcription of a potential sigma factor regulatory gene Rv1364c in <i>Mycobacterium bovis</i> BCG while residing in macrophages indicates use of alternative promoters. <i>FEMS Microbiology Letters</i> , 2004, 233, 333-339.	1.8	7

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55	The 1st Symposium of the Wellcome Trust-Funded Multi-Collaborative Microbial Pathogen Microarray Facilityâ€™s 2002: â€™Bacterial Pathogens, Microarrays and Functional Genomicsâ€™™. Comparative and Functional Genomics, 2002, 3, 326-329.	2.0	1
56	Comparison of human low-molecular-weight RNA from normal and Crohn's disease derived blood and mesenteric, lymph node leucocytes. Biochemical Society Transactions, 1984, 12, 1112-1113.	3.4	0