## Philip Butcher

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7766802/publications.pdf

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78 papers 6,911 citations

34 h-index 71532 76 g-index

78 all docs 78 docs citations

times ranked

78

7570 citing authors

#	Article	IF	CITATIONS
1	Transcriptional Adaptation of Mycobacterium tuberculosis within Macrophages. Journal of Experimental Medicine, 2003, 198, 693-704.	4.2	1,311
2	Benzothiazinones Kill <i>Mycobacterium tuberculosis</i> by Blocking Arabinan Synthesis. Science, 2009, 324, 801-804.	6.0	660
3	Cytological and Transcript Analyses Reveal Fat and Lazy Persister-Like Bacilli in Tuberculous Sputum. PLoS Medicine, 2008, 5, e75.	3.9	383
4	High-Dose Rifapentine with Moxifloxacin for Pulmonary Tuberculosis. New England Journal of Medicine, 2014, 371, 1599-1608.	13.9	383
5	Mycobacterial P1-Type ATPases Mediate Resistance to Zinc Poisoning in Human Macrophages. Cell Host and Microbe, 2011, 10, 248-259.	5.1	304
6	Microarrays Reveal that Each of the Ten Dominant Lineages of Staphylococcus aureus Has a Unique Combination of Surface-Associated and Regulatory Genes. Journal of Bacteriology, 2006, 188, 669-676.	1.0	303
7	Dissection of ESAT-6 System 1 of Mycobacterium tuberculosis and Impact on Immunogenicity and Virulence. Infection and Immunity, 2006, 74, 88-98.	1.0	279
8	Whole Genome Comparison of Campylobacter jejuni Human Isolates Using a Low-Cost Microarray Reveals Extensive Genetic Diversity. Genome Research, 2001, 11, 1706-1715.	2.4	278
9	Stationary phase gene expression of Mycobacterium tuberculosis following a progressive nutrient depletion: a model for persistent organisms?. Tuberculosis, 2004, 84, 228-238.	0.8	185
10	Probing Host Pathogen Cross-Talk by Transcriptional Profiling of Both Mycobacterium tuberculosis and Infected Human Dendritic Cells and Macrophages. PLoS ONE, 2008, 3, e1403.	1.1	172
11	Detection of mRNA Transcripts and Active Transcription in Persistent Mycobacterium tuberculosisInduced by Exposure to Rifampin or Pyrazinamide. Journal of Bacteriology, 2000, 182, 6358-6365.	1.0	168
12	High Prevalence of Antibiotic-Resistant Mycoplasma genitalium in Nongonococcal Urethritis: The Need for Routine Testing and the Inadequacy of Current Treatment Options. Clinical Infectious Diseases, 2014, 58, 631-637.	2.9	142
13	Mycobacterium tuberculosis expresses two chaperonin-60 homologs Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 2608-2612.	3.3	134
14	Mycobacterium tuberculosis Expresses a Novel Ph-Dependent Divalent Cation Transporter Belonging to the Nramp Family. Journal of Experimental Medicine, 1999, 190, 717-724.	4.2	131
15	The influence of reduced oxygen availability on pathogenicity and gene expression in Mycobacterium tuberculosis. Tuberculosis, 2004, 84, 205-217.	0.8	127
16	Molecular epidemiology of tuberculosis in London 1995-7 showing low rate of active transmission. Thorax, 2002, 57, 617-622.	2.7	111
17	The use of DNA probes identifying restriction-fragment-length polymorphisms to examine the Mycobacterium avium complex. Molecular Microbiology, 1987, 1, 283-291.	1.2	110
18	Clinical Application of Whole-Genome Sequencing To Inform Treatment for Multidrug-Resistant Tuberculosis Cases. Journal of Clinical Microbiology, 2015, 53, 1473-1483.	1.8	89

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19	DNA Microarrays for Virus Detection in Cases of Central Nervous System Infection. Journal of Clinical Microbiology, 2004, 42, 5811-5818.	1.8	88
20	Variation in <i>Salmonella enterica</i> Serovar Typhi IncHI1 Plasmids during the Global Spread of Resistant Typhoid Fever. Antimicrobial Agents and Chemotherapy, 2009, 53, 716-727.	1,4	81
21	An effective method of RNA extraction from bacteria refractory to disruption, including mycobacteria. Nucleic Acids Research, 1997, 25, 675-676.	6.5	80
22	Design, Validation, and Application of a Seven-Strain Staphylococcus aureus PCR Product Microarray for Comparative Genomics. Applied and Environmental Microbiology, 2005, 71, 7504-7514.	1.4	77
23	Application of the polymerase chain reaction to the diagnosis of human toxoplasmosis. Journal of Infection, 1993, 26, 147-158.	1.7	66
24	Determination of Mycobacterium leprae Viability by Polymerase Chain Reaction Amplification of 71-kDa Heat-Shock Protein mRNA. Journal of Infectious Diseases, 1993, 168, 799-800.	1.9	61
25	Genome sequencing and characterization of an extensively drug-resistant sequence type 111 serotype O12 hospital outbreak strain of Pseudomonas aeruginosa. Clinical Microbiology and Infection, 2014, 20, O609-O618.	2.8	57
26	Mycobacterium tuberculosis DNA repair in response to subinhibitory concentrations of ciprofloxacin. Journal of Antimicrobial Chemotherapy, 2008, 62, 1199-1202.	1.3	47
27	Prevalence and clinical correlations of genetic subtypes of <i>Giardia lamblia</i> in an urban setting. Epidemiology and Infection, 2010, 138, 1459-1467.	1.0	45
28	Inactivation of polyketide synthase and related genes results in the loss of complex lipids in Mycobacterium tuberculosis H37Rv. Letters in Applied Microbiology, 2005, 40, 201-206.	1.0	43
29	Contrasting Transcriptional Responses of a Virulent and an Attenuated Strain of Mycobacterium tuberculosis Infecting Macrophages. PLoS ONE, 2010, 5, e11066.	1.1	42
30	Accurate detection of i> Neisseria gonorrhoeae  ciprofloxacin susceptibility directly from genital and extragenital clinical samples: towards genotype-guided antimicrobial therapy. Journal of Antimicrobial Chemotherapy, 2016, 71, 897-902.	1.3	41
31	Evidence for a Role for Interleukin-17, Th17 Cells and Iron Homeostasis in Protective Immunity against Tuberculosis in Cynomolgus Macaques. PLoS ONE, 2014, 9, e88149.	1.1	40
32	Evolutionary Relationships among Strains of Mycobacterium tuberculosis with Few Copies of IS 6110. Journal of Bacteriology, 2003, 185, 2555-2562.	1.0	38
33	Estimation of the Rate of Unrecognized Cross-Contamination with Mycobacterium tuberculosis in London Microbiology Laboratories. Journal of Clinical Microbiology, 2002, 40, 4100-4104.	1.8	37
34	Microarray Analysis of Whole Genome Expression of Intracellular Mycobacterium tuberculosis. Current Molecular Medicine, 2007, 7, 287-296.	0.6	36
35	Microarrays for Mycobacterium tuberculosis. Tuberculosis, 2004, 84, 131-137.	0.8	35
36	Gene expression during hostâ€"pathogen interactions: Approaches to bacterial mRNA extraction and labelling for microarray analysis. Methods in Microbiology, 2002, 33, 137-151.	0.4	34

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37	Investigation of mycobacteria in Crohn's disease tissue by Southern blotting and DNA hybridisation with cloned mycobacterial genomic DNA probes from a Crohn's disease isolated mycobacteria. Gut, 1988, 29, 1222-1228.	6.1	31
38	Diagnosis of Pneumocystis carinii pneumonia: Immunofluorescence staining, simple PCR or nPCR. Journal of Infection, 1999, 39, 77-80.	1.7	31
39	RNA profiling in host–pathogen interactions. Current Opinion in Microbiology, 2007, 10, 297-302.	2.3	31
40	Characterization of the heat shock response in Mycobacterium bovis BCG. Journal of Bacteriology, 1991, 173, 7982-7987.	1.0	30
41	Development of an in vitro model ofToxoplasma gondiicyst formation. FEMS Microbiology Letters, 1993, 114, 325-332.	0.7	30
42	Quantification of cytomegalovirus DNA in blood specimens from bone marrow transplant recipients by the polymerase chain reaction. Journal of Virological Methods, 1994, 47, 189-202.	1.0	29
43	A polymerase chain reaction to detect a spliced late transcript of human cytomegalovirus in the blood of bone marrow transplant recipients. Journal of Virological Methods, 1996, 56, 139-148.	1.0	29
44	Examining the basis of isoniazid tolerance in nonreplicating <i>Mycobacterium tuberculosis</i> using transcriptional profiling. Future Medicinal Chemistry, 2010, 2, 1371-1383.	1.1	29
45	Association of cytomegalovirus infection with post-transplantation cardiac rejection as studied using the polymerase chain reaction. Journal of Medical Virology, 1994, 42, 396-404.	2.5	28
46	Cytokine mRNA Expression in Mycobacteriam ulcerans-Infected Human Skin and Correlation with Local Inflammatory Response. Infection and Immunity, 2006, 74, 2917-2924.	1.0	28
47	XDR-TB transmission in London: Case management and contact tracing investigation assisted by early whole genome sequencing. Journal of Infection, 2016, 73, 210-218.	1.7	28
48	Whole-genome sequencing illuminates the evolution and spread of multidrug-resistant tuberculosis in Southwest Nigeria. PLoS ONE, 2017, 12, e0184510.	1.1	27
49	DNA probes for the faecal diagnosis of Giardia lamblia infections in man. Biochemical Society Transactions, 1989, 17, 363-364.	1.6	24
50	Use of Genome Level-Informed PCR as a New Investigational Approach for Analysis of Outbreak-Associated Mycobacterium tuberculosis Isolates. Journal of Clinical Microbiology, 2004, 42, 1890-1896.	1.8	24
51	Genetic Composition of Mycobacterium bovis BCG Substrain Sofia. Journal of Clinical Microbiology, 2003, 41, 5349-5349.	1.8	23
52	Characterisation of Bovine Leukocyte Ig-like Receptors. PLoS ONE, 2012, 7, e34291.	1.1	22
53	Extraction and characterization of mRNA from mycobacteria: implication for virulence gene identification. Journal of Microbiological Methods, 1991, 13, 99-111.	0.7	21
54	Early detection of cytomegalovirus (CMV) infection in bone marrow transplant patients by reverse transcription-PCR for CMV spliced late gene UL21.5: a two site evaluation. Journal of Clinical Virology, 2002, 24, 13-23.	1.6	20

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55	Point-of-care antibiotic susceptibility testing for gonorrhoea: improving therapeutic options and sparing the use of cephalosporins. Sexually Transmitted Infections, 2010, 86, 445-446.	0.8	20
56	The Heat Shock Response of Mycobacterium tuberculosis: Linking Gene Expression, Immunology and Pathogenesis. Comparative and Functional Genomics, 2002, 3, 348-351.	2.0	19
57	Genomic Diversity among Beijing and non-Beijing Mycobacterium tuberculosis Isolates from Myanmar. PLoS ONE, 2008, 3, e1973.	1.1	18
58	Genomic Analysis of Mycobacterium tuberculosis Complex Strains Used for Production of Purified Protein Derivative. Journal of Clinical Microbiology, 2003, 41, 3929-3932.	1.8	16
59	Efficient translation and polyribosome binding of 125 I-labelled rabbit globin messenger ribonucleoprotein. FEBS Letters, 1983, 153, 119-124.	1.3	15
60	Drug resistant TB: UK multicentre study (DRUMS): Treatment, management and outcomes in London and West Midlands 2008–2014. Journal of Infection, 2017, 74, 260-271.	1.7	15
61	Performance evaluation of automated urine microscopy as a rapid, non-invasive approach for the diagnosis of non-gonococcal urethritis. Sexually Transmitted Infections, 2015, 91, 165-170.	0.8	12
62	Recognition of tissue cyst-specific antigens in reactivating toxoplasmosis. Journal of Medical Microbiology, 1997, 46, 587-595.	0.7	11
63	Antimicrobial Treatment Improves Mycobacterial Survival in Nonpermissive Growth Conditions. Antimicrobial Agents and Chemotherapy, 2014, 58, 2798-2806.	1.4	11
64	Methionine Sulfoximine Resistance in Mycobacterium tuberculosis Is Due to a Single Nucleotide Deletion Resulting in Increased Expression of the Major Glutamine Synthetase, GlnA1. Microbial Drug Resistance, 2011, 17, 351-355.	0.9	10
65	Advanced significance analysis of microarray data based on weighted resampling: a comparative study and application to gene deletions in Mycobacterium bovis. Bioinformatics, 2004, 20, 357-363.	1.8	9
66	Serodiagnosis of giardiasis. Serodiagnosis and Immunotherapy in Infectious Disease, 1987, 1, 233-235.	0.2	8
67	Oleoyl Coenzyme A Regulates Interaction of Transcriptional Regulator RaaS (Rv1219c) with DNA in Mycobacteria. Journal of Biological Chemistry, 2014, 289, 25241-25249.	1.6	8
68	Minisatellites corresponding to the human polycore probes 33.6 and 33.15 in the genome of the most â€~primitive' known eukaryote Giardia lamblia. Gene, 1995, 166, 167-172.	1.0	7
69	Fidelity and reproducibility of antisense RNA amplification for the study of gene expression in human CD34+ haemopoietic stem and progenitor cells. British Journal of Haematology, 2003, 122, 498-505.	1.2	7
70	Increased transcription of a potential sigma factor regulatory gene Rv1364c in Mycobacterium bovis BCG while residing in macrophages indicates use of alternative promoters. FEMS Microbiology Letters, 2004, 233, 333-339.	0.7	7
71	Human cytomegalovirus genome sequences in lymph nodes. Microbes and Infection, 1999, 1, 279-283.	1.0	5
72	Microarrays for Microbes: the Bî½G@S Approach. Comparative and Functional Genomics, 2002, 3, 333-337.	2.0	3

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73	BÂG@Sbasea microbial gene expression and comparative genomic database. Nucleic Acids Research, 2012, 40, D605-D609.	6.5	3
74	Microarray-Based Comparative Genomics: Genome Plasticity in Mycobacterium bovis. Comparative and Functional Genomics, 2002, 3, 342-344.	2.0	2
75	The electrophoretic analysis of low molecular weight nucleic acids from Crohn's disease tissues in the search for an unconventional small infections agent. Archives of Virology, 1986, 88, 113-120.	0.9	1
76	The 1st Symposium of the Wellcome Trust-Funded Multi-Collaborative Microbial Pathogen Microarray Facility—Bl¾G@S 2002: â€⁻Bacterial Pathogens, Microarrays and Functional Genomics'. Comparative and Functional Genomics, 2002, 3, 326-329.	2.0	1
77	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.	1.6	0
78	Antibodies to gut protozoa in commercial immunoglobulin preparations. Transactions of the Royal Society of Tropical Medicine and Hygiene, 1991, 85, 74-76.	0.7	0