Alex J Mccarthy

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4361482/publications.pdf

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38 papers 1,926 citations

346980 22 h-index 388640 36 g-index

40 all docs

40 docs citations

times ranked

40

2819 citing authors

#	Article	IF	Citations
1	Analysis of Escherichia coli K1 Virulence Genes by Transposon-Directed Sequencing. Methods in Molecular Biology, 2022, 2377, 199-213.	0.4	1
2	Group B Streptococcus Surface Protein β: Structural Characterization of a Complement Factor H–Binding Motif and Its Contribution to Immune Evasion. Journal of Immunology, 2022, , ji2101078.	0.4	O
3	Bacterial protein domains with a novel Igâ€like fold target human CEACAM receptors. EMBO Journal, 2021, 40, e106103.	3.5	16
4	Chemical Emissions from Cured and Uncured 3D-Printed Ventilator Patient Circuit Medical Parts. ACS Omega, 2021, 6, 30726-30733.	1.6	11
5	Increase in COVID-19 inpatient survival following detection of Thromboembolic and Cytokine storm risk from the point of admission to hospital by a near real time Traffic-light System (TraCe-Tic). Brazilian Journal of Infectious Diseases, 2020, 24, 412-421.	0.3	11
6	Genes on the Move: In Vitro Transduction of Antimicrobial Resistance Genes between Human and Canine Staphylococcal Pathogens. Microorganisms, 2020, 8, 2031.	1.6	19
7	Leukocyte Immunoglobulin-Like Receptors (LILRs) on Human Neutrophils: Modulators of Infection and Immunity. Frontiers in Immunology, 2020, 11, 857.	2.2	36
8	The Orphan Immune Receptor LILRB3 Modulates Fc Receptor–Mediated Functions of Neutrophils. Journal of Immunology, 2020, 204, 954-966.	0.4	21
9	Loss of Trefoil Factor 2 Sensitizes Rat Pups to Systemic Infection with the Neonatal Pathogen <i>Escherichia coli</i> K1. Infection and Immunity, 2019, 87, .	1.0	6
10	Genome-Wide Identification by Transposon Insertion Sequencing of Escherichia coli K1 Genes Essential for <i>In Vitro</i> Growth, Gastrointestinal Colonizing Capacity, and Survival in Serum. Journal of Bacteriology, 2018, 200, .	1.0	32
11	Molecular basis determining species specificity for TLR2 inhibition by staphylococcal superantigen-like protein 3 (SSL3). Veterinary Research, 2018, 49, 115.	1.1	5
12	Postnatal development of the small intestinal mucosa drives age-dependent, regio-selective susceptibility to Escherichia coli K1 infection. Scientific Reports, 2017, 7, 83.	1.6	24
13	Immune evasion by a staphylococcal inhibitor of myeloperoxidase. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9439-9444.	3.3	76
14	Pathoadaptive Mutations of Escherichia coli K1 in Experimental Neonatal Systemic Infection. PLoS ONE, 2016, 11, e0166793.	1.1	8
15	The Bacterial Stress-Responsive Hsp90 Chaperone (HtpG) Is Required for the Production of the Genotoxin Colibactin and the Siderophore Yersiniabactin in <i>Escherichia coli</i> Infectious Diseases, 2016, 214, 916-924.	1.9	51
16	Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i> . Journal of Antimicrobial Chemotherapy, 2015, 70, 997-1007.	1.3	77
17	The Genotoxin Colibactin Is a Determinant of Virulence in Escherichia coli K1 Experimental Neonatal Systemic Infection. Infection and Immunity, 2015, 83, 3704-3711.	1.0	69
18	Bioluminescent Imaging Reveals Novel Patterns of Colonization and Invasion in Systemic Escherichia coli K1 Experimental Infection in the Neonatal Rat. Infection and Immunity, 2015, 83, 4528-4540.	1.0	31

#	Article	lF	CITATIONS
19	Extensive Horizontal Gene Transfer during Staphylococcus aureus Co-colonization In Vivo. Genome Biology and Evolution, 2014, 6, 2697-2708.	1.1	119
20	Fructose transport-deficient Staphylococcus aureus reveals important role of epithelial glucose transporters in limiting sugar-driven bacterial growth in airway surface liquid. Cellular and Molecular Life Sciences, 2014, 71, 4665-4673.	2.4	33
21	Non-Invasive Model of Neuropathogenic Escherichia coli Infection in the Neonatal Rat. Journal of Visualized Experiments, 2014, , e52018.	0.2	17
22	Wholeâ€genome comparison of meticillinâ€resistant <i>Staphylococcus aureus</i> CC22 SCC <i>mec</i> IV from people and their inâ€contact pets. Veterinary Dermatology, 2013, 24, 538.	0.4	27
23	Staphylococcus aureus innate immune evasion is lineage-specific: A bioinfomatics study. Infection, Genetics and Evolution, 2013, 19, 7-14.	1.0	95
24	Shuffling of mobile genetic elements (MGEs) in successful healthcare-associated MRSA (HA-MRSA). Mobile Genetic Elements, 2012, 2, 239-243.	1.8	22
25	Detection of Mobile-Genetic-Element Variation between Colonizing and Infecting Hospital-Associated Methicillin-Resistant Staphylococcus aureus Isolates. Journal of Clinical Microbiology, 2012, 50, 1073-1075.	1.8	43
26	Identification of a Highly Transmissible Animal-Independent Staphylococcus aureus ST398 Clone with Distinct Genomic and Cell Adhesion Properties. MBio, 2012, 3, .	1.8	180
27	Staphylococcus aureus CC398 Clade Associated with Human-to-Human Transmission. Applied and Environmental Microbiology, 2012, 78, 8845-8848.	1.4	75
28	The distribution of plasmids that carry virulence and resistance genes in Staphylococcus aureus is lineage associated. BMC Microbiology, 2012, 12, 104.	1.3	138
29	Comparative Host Specificity of Human- and Pig- Associated Staphylococcus aureus Clonal Lineages. PLoS ONE, 2012, 7, e49344.	1.1	17
30	Staphylococcus aureus Temperate Bacteriophage: Carriage and Horizontal Gene Transfer is Lineage Associated. Frontiers in Cellular and Infection Microbiology, 2012, 2, 6.	1.8	85
31	Are all meticillinâ€resistant <i>Staphylococcus aureus</i> (MRSA) equal in all hosts? Epidemiological and genetic comparison between animal and human MRSA. Veterinary Dermatology, 2012, 23, 267.	0.4	58
32	Survival of Staphylococcus aureus ST398 in the Human Nose after Artificial Inoculation. PLoS ONE, 2012, 7, e48896.	1.1	23
33	Novel polymorphisms in ovine immune response genes and their association with abortion. Animal Genetics, 2011, 42, 535-543.	0.6	19
34	Variation in European harbour seal immune response genes and susceptibility to phocine distemper virus (PDV). Infection, Genetics and Evolution, 2011, 11, 1616-1623.	1.0	18
35	The Distribution of Mobile Genetic Elements (MGEs) in MRSA CC398 Is Associated with Both Host and Country. Genome Biology and Evolution, 2011, 3, 1164-1174.	1.1	82
36	Genetic variation in Staphylococcus aureus surface and immune evasion genes is lineage associated: implications for vaccine design and host-pathogen interactions. BMC Microbiology, 2010, 10, 173.	1.3	194

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#	Article	IF	CITATIONS
37	Reassessing conflicting evolutionary histories of the Paramyxoviridae and the origins of respiroviruses with Bayesian multigene phylogenies. Infection, Genetics and Evolution, 2010, 10, 97-107.	1.0	28
38	Pathogen evolution and disease emergence in carnivores. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 3165-3174.	1.2	148