Gregory A Buck

List of Publications by Year
in descending order

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		172457	189892
50	5,278	29	50
papers	citations	h-index	g-index
54	54	54	6319
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The vaginal microbiome in women of reproductive age with healthy weight versus overweight/obesity. Obesity, 2022, 30, 142-152.	3.0	12
2	Airway microbiome dynamics and relationship to ventilatorâ€associated infection in intubated pediatric patients. Pediatric Pulmonology, 2022, 57, 508-518.	2.0	3
3	Race, the Vaginal Microbiome, and Spontaneous Preterm Birth. MSystems, 2022, 7, e0001722.	3.8	24
4	Sequence Comparison of Vaginolysin from Different Gardnerella Species. Pathogens, 2021, 10, 86.	2.8	14
5	Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids Angomonas spp.. Pathogens, 2021, 10, 702.	2.8	2
6	IL-13 is a driver of COVID-19 severity. JCI Insight, 2021, 6, .	5.0	80
7	Vaginal microbiome Lactobacillus crispatus is heritable among European American women. Communications Biology, 2021, 4, 872.	4.4	7
8	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
9	Unique roles of vaginal Megasphaera phylotypes in reproductive health. Microbial Genomics, 2021, 7, .	2.0	6
10	Proteomic Analysis Reveals a Predominant NFE2L2 (NRF2) Signature in Canonical Pathway and Upstream Regulator Analysis of Leishmania-Infected Macrophages. Frontiers in Immunology, 2019, 10, 1362.	4.8	14
11	The vaginal microbiome and preterm birth. Nature Medicine, 2019, 25, 1012-1021.	30.7	600
12	Racioethnic diversity in the dynamics of the vaginal microbiome during pregnancy. Nature Medicine, 2019, 25, 1001-1011.	30.7	204
13	Impact of Herpes Simplex Virus Type 2 and Human Immunodeficiency Virus Dual Infection on Female Genital Tract Mucosal Immunity and the Vaginal Microbiome. Journal of Infectious Diseases, 2019, 220, 852-861.	4.0	14
14	Does the human placenta delivered at term have a microbiota? Results of cultivation, quantitative real-time PCR, 16S rRNA gene sequencing, and metagenomics. American Journal of Obstetrics and Gynecology, 2019, 220, 267.e1-267.e39.	1.3	196
15	Relationship between vitamin D status and the vaginal microbiome during pregnancy. Journal of Perinatology, 2019, 39, 824-836.	2.0	40
16	Multi-omic Microbiome Profiles in the Female Reproductive Tract in Early Pregnancy. Infectious Microbes & Diseases, 2019, 1, 49-60.	1.3	9
17	Genomic comparison of Trypanosoma conorhini and Trypanosoma rangeli to Trypanosoma cruzi strains of high and low virulence. BMC Genomics, 2018, 19, 770.	2.8	14
18	Genome-wide identification of evolutionarily conserved Small Heat-Shock and eight other proteins bearing Î±-crystallin domain-like in kinetoplastid protists. PLoS ONE, 2018, 13, e0206012.	2.5	13

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19	The Evolutionary Loss of RNAi Key Determinants in Kinetoplastids as a Multiple Sporadic Phenomenon. Journal of Molecular Evolution, 2017, 84, 104-115.	1.8	15
20	Effects of combined oral contraceptives, depot medroxyprogesterone acetate and the levonorgestrel-releasing intrauterine system on the vaginal microbiome. Contraception, 2017, 95, 405-413.	1.5	95
21	Changes in vaginal community state types reflect major shifts in the microbiome. Microbial Ecology in Health and Disease, 2017, 28, 1303265.	3.5	66
22	Association between statin use, the vaginal microbiome, and Gardnerella vaginalis vaginolysin-mediated cytotoxicity. PLoS ONE, 2017, 12, e0183765.	2.5	21
23	MeFiT: merging and filtering tool for illumina paired-end reads for 16S rRNA amplicon sequencing. BMC Bioinformatics, 2016, 17, 491.	2.6	79
24	Comparison of Lactobacillus crispatus isolates from Lactobacillus-dominated vaginal microbiomes with isolates from microbiomes containing bacterial vaginosis-associated bacteria. Microbiology (United Kingdom), 2016, 162, 466-475.	1.8	46
25	Revisiting the reference genomes of human pathogenic Cryptosporidium species: reannotation of C. parvum Iowa and a new C. hominis reference. Scientific Reports, 2015, 5, 16324.	3.3	44
26	The truth about metagenomics: quantifying and counteracting bias in 16S rRNA studies. BMC Microbiology, 2015, 15, 66.	3.3	388
27	Identification of a gene in Mycoplasma hominis associated with preterm birth and microbial burden in intraamniotic infection. American Journal of Obstetrics and Gynecology, 2015, 212, 779.e1-779.e13.	1.3	64
28	Genetic diversity of Trypanosoma cruzi in bats, and multilocus phylogenetic and phylogeographical analyses supporting Tcbat as an independent DTU (discrete typing unit). Acta Tropica, 2015, 151, 166-177.	2.0	112
29	Phylogenetic and syntenic data support a single horizontal transference to a Trypanosoma ancestor of a prokaryotic proline racemase implicated in parasite evasion from host defences. Parasites and Vectors, 2015, 8, 222.	2.5	25
30	Skin-to-Skin Care and the Development of the Preterm Infant Oral Microbiome. American Journal of Perinatology, 2015, 32, 1205-1216.	1.4	50
31	An Emerging Mycoplasma Associated with Trichomoniasis, Vaginal Infection and Disease. PLoS ONE, 2014, 9, e110943.	2.5	64
32	The Changing Landscape of the Vaginal Microbiome. Clinics in Laboratory Medicine, 2014, 34, 747-761.	1.4	166
33	Differences in vaginal microbiome in African American women versus women of European ancestry. Microbiology (United Kingdom), 2014, 160, 2272-2282.	1.8	390
34	Comparative Genomics of<i>Cryptosporidium</i>. International Journal of Genomics, 2013, 2013, 1-8.	1.6	28
35	Genome Evolution and Phylogenomic Analysis of Candidatus Kinetoplastibacterium, the Betaproteobacterial Endosymbionts of Strigomonas and Angomonas. Genome Biology and Evolution, 2013, 5, 338-350.	2.5	47
36	Genomic sequence analysis and characterization of Sneathia amnii sp. nov. BMC Genomics, 2012, 13, S4.	2.8	108

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37	Species-level classification of the vaginal microbiome. BMC Genomics, 2012, 13, S17.	2.8	145
38	Repertoire, Genealogy and Genomic Organization of Cruzipain and Homologous Genes in Trypanosoma cruzi, T. cruzi-Like and Other Trypanosome Species. PLoS ONE, 2012, 7, e38385.	2.5	31
39	A New Era of the Vaginal Microbiome: Advances Using Nextâ€Generation Sequencing. Chemistry and Biodiversity, 2012, 9, 965-976.	2.1	74
40	Tâ€bet is required for survival and immunity to the intracellular pathogen Trypanosoma cruzi (T. cruzi). FASEB Journal, 2008, 22, .	0.5	0
41	Automated System for Gene Annotation and Metabolic Pathway Reconstruction Using General Sequence Databases. Chemistry and Biodiversity, 2007, 4, 2593-2602.	2.1	27
42	CryptoDB: the Cryptosporidium genome resource. Nucleic Acids Research, 2004, 32, 329D-331.	14.5	78
43	The genome of Cryptosporidium hominis. Nature, 2004, 431, 1107-1112.	27.8	506
44	Complete Genome Sequence of the Apicomplexan, Cryptosporidium parvum. Science, 2004, 304, 441-445.	12.6	877
45	Evidence for genetic exchange and hybridization in Trypanosoma cruzi based on nucleotide sequences and molecular karyotype. Infection, Genetics and Evolution, 2003, 2, 173-183.	2.3	138
46	Polymorphisms at the Topoisomerase II Gene Locus Provide More Evidence for the Partition of Trypanosoma cruzi into Two Major Groups. Journal of Eukaryotic Microbiology, 1999, 46, 17-23.	1.7	44
47	High Prevalence of GB Virus C in Brazil and Molecular Evidence for Intrafamilial Transmission. Journal of Clinical Microbiology, 1999, 37, 1634-1637.	3.9	18
48	The HSP70 Gene Family inPneumocystis carinii: Molecular and Phylogenetic Characterization of Cytoplasmic Members. Journal of Eukaryotic Microbiology, 1998, 45, 589-599.	1.7	18
49	Mutations in the Human Biotinidase Gene That Cause Profound Biotinidase Deficiency in Symptomatic Children: Molecular, Biochemical, and Clinical Analysis. Pediatric Research, 1997, 42, 840-848.	2.3	73
50	An Arrayed Bacteriophage P1 Genomic Library of Pneumocystis carinii. Journal of Eukaryotic Microbiology, 1996, 43, 171-176.	1.7	3