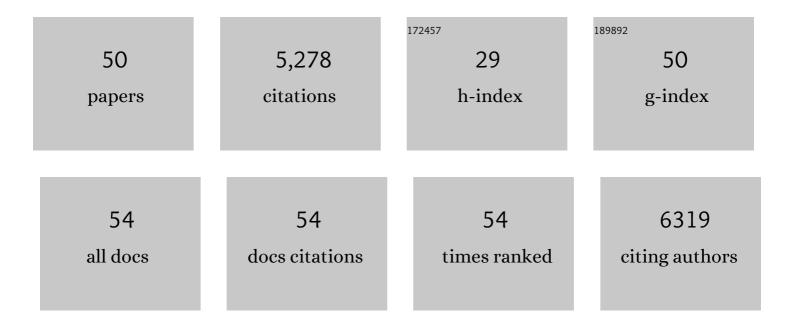
Gregory A Buck

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Complete Genome Sequence of the Apicomplexan, Cryptosporidium parvum. Science, 2004, 304, 441-445.	12.6	877
2	The vaginal microbiome and preterm birth. Nature Medicine, 2019, 25, 1012-1021.	30.7	600
3	The genome of Cryptosporidium hominis. Nature, 2004, 431, 1107-1112.	27.8	506
4	Differences in vaginal microbiome in African American women versus women of European ancestry. Microbiology (United Kingdom), 2014, 160, 2272-2282.	1.8	390
5	The truth about metagenomics: quantifying and counteracting bias in 16S rRNA studies. BMC Microbiology, 2015, 15, 66.	3.3	388
6	Racioethnic diversity in the dynamics of the vaginal microbiome during pregnancy. Nature Medicine, 2019, 25, 1001-1011.	30.7	204
7	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
8	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
9	The Changing Landscape of the Vaginal Microbiome. Clinics in Laboratory Medicine, 2014, 34, 747-761.	1.4	166
10	Species-level classification of the vaginal microbiome. BMC Genomics, 2012, 13, S17.	2.8	145
11	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
12	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
13	Genomic sequence analysis and characterization of Sneathia amnii sp. nov. BMC Genomics, 2012, 13, S4.	2.8	108
14	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
15	IL-13 is a driver of COVID-19 severity. JCI Insight, 2021, 6, .	5.0	80
16	MeFiT: merging and filtering tool for illumina paired-end reads for 16S rRNA amplicon sequencing. BMC Bioinformatics, 2016, 17, 491.	2.6	79
17	CryptoDB: the Cryptosporidium genome resource. Nucleic Acids Research, 2004, 32, 329D-331.	14.5	78
18	A New Era of the Vaginal Microbiome: Advances Using Nextâ€Generation Sequencing. Chemistry and Biodiversity, 2012, 9, 965-976.	2.1	74

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19	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
20	Changes in vaginal community state types reflect major shifts in the microbiome. Microbial Ecology in Health and Disease, 2017, 28, 1303265.	3.5	66
21	An Emerging Mycoplasma Associated with Trichomoniasis, Vaginal Infection and Disease. PLoS ONE, 2014, 9, e110943.	2.5	64
22	Identification of a gene in Mycoplasma hominis associated with preterm birth and microbial burden in in intraamniotic infection. American Journal of Obstetrics and Gynecology, 2015, 212, 779.e1-779.e13.	1.3	64
23	Skin-to-Skin Care and the Development of the Preterm Infant Oral Microbiome. American Journal of Perinatology, 2015, 32, 1205-1216.	1.4	50
24	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
25	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
26	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
27	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
28	Relationship between vitamin D status and the vaginal microbiome during pregnancy. Journal of Perinatology, 2019, 39, 824-836.	2.0	40
29	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
30	Comparative Genomics of <i>Cryptosporidium </i> . International Journal of Genomics, 2013, 2013, 1-8.	1.6	28
31	Automated System for Gene Annotation and Metabolic Pathway Reconstruction Using General Sequence Databases. Chemistry and Biodiversity, 2007, 4, 2593-2602.	2.1	27
32	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
33	Race, the Vaginal Microbiome, and Spontaneous Preterm Birth. MSystems, 2022, 7, e0001722.	3.8	24
34	Association between statin use, the vaginal microbiome, and Gardnerella vaginalis vaginolysin-mediated cytotoxicity. PLoS ONE, 2017, 12, e0183765.	2.5	21
35	The HSP70 Gene Family inPneumocystis carinii: Molecular and Phylogenetic Characterization of Cytoplasmic Members. Journal of Eukaryotic Microbiology, 1998, 45, 589-599.	1.7	18
36	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

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37	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
38	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
39	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
40	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
41	Sequence Comparison of Vaginolysin from Different Gardnerella Species. Pathogens, 2021, 10, 86.	2.8	14
42	Genome-wide identification of evolutionarily conserved Small Heat-Shock and eight other proteins bearing α-crystallin domain-like in kinetoplastid protists. PLoS ONE, 2018, 13, e0206012.	2.5	13
43	The vaginal microbiome in women of reproductive age with healthy weight versus overweight/obesity. Obesity, 2022, 30, 142-152.	3.0	12
44	Multi-omic Microbiome Profiles in the Female Reproductive Tract in Early Pregnancy. Infectious Microbes & Diseases, 2019, 1, 49-60.	1.3	9
45	Vaginal microbiome Lactobacillus crispatus is heritable among European American women. Communications Biology, 2021, 4, 872.	4.4	7
46	Unique roles of vaginal Megasphaera phylotypes in reproductive health. Microbial Genomics, 2021, 7, .	2.0	6
47	An Arrayed Bacteriophage P1 Genomic Library of Pneumocystis carinii. Journal of Eukaryotic Microbiology, 1996, 43, 171-176.	1.7	3
48	Airway microbiome dynamics and relationship to ventilatorâ€associated infection in intubated pediatric patients. Pediatric Pulmonology, 2022, 57, 508-518.	2.0	3
49	Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids Angomonas spp Pathogens, 2021, 10, 702.	2.8	2
50	Tâ€bet is required for survival and immunity to the intracellular pathogen Trypanosoma cruzi (T. cruzi). FASEB Journal, 2008, 22, .	0.5	0