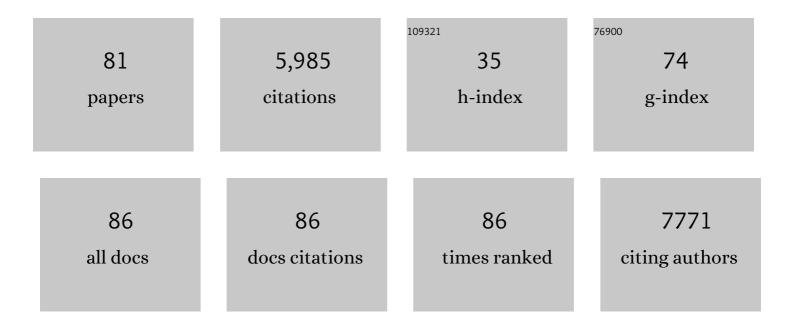
List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6594978/publications.pdf Version: 2024-02-01



CADI I VEOMAN

#	Article	IF	CITATIONS
1	Do gastrointestinal microbiomes play a role in bats' unique viral hosting capacity?. Trends in Microbiology, 2022, 30, 632-642.	7.7	9
2	Bacterial Vaginosis Monitoring with Carbon Nanotube Field-Effect Transistors. Analytical Chemistry, 2022, 94, 3849-3857.	6.5	5
3	Relationships among intramammary health, udder and teat characteristics, and productivity of extensively managed ewes. Journal of Animal Science, 2021, 99, .	0.5	7
4	Biogenic Amines Increase the Odds of Bacterial Vaginosis and Affect the Growth of and Lactic Acid Production by Vaginal <i>Lactobacillus</i> spp Applied and Environmental Microbiology, 2021, 87, .	3.1	24
5	<i>In Vivo</i> Competitions between Fibrobacter succinogenes, Ruminococcus flavefaciens, and Ruminoccus albus in a Gnotobiotic Sheep Model Revealed by Multi-Omic Analyses. MBio, 2021, 12, .	4.1	26
6	Perceived Stress and Molecular Bacterial Vaginosis in the National Institutes of Health Longitudinal Study of Vaginal Flora. American Journal of Epidemiology, 2021, 190, 2374-2383.	3.4	8
7	Temporal metabolic response yields a dynamic biosignature of inflammation. IScience, 2021, 24, 102817.	4.1	4
8	Determinants of the postprandial triglyceride response to a high-fat meal in healthy overweight and obese adults. Lipids in Health and Disease, 2021, 20, 107.	3.0	7
9	Vaginal microbiota of American Indian women and associations with measures of psychosocial stress. PLoS ONE, 2021, 16, e0260813.	2.5	8
10	Soil bacterial communities of wheat vary across the growing season and among dryland farming systems. Geoderma, 2020, 358, 113989.	5.1	30
11	The vaginal metabolome and microbiota of cervical HPVâ€positive and HPVâ€negative women: a crossâ€sectional analysis. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 182-192.	2.3	86
12	Investigating the relationship between vaginal microbiota and host genetics and their impact on immune response and farrowing traits in commercial gilts. Journal of Animal Breeding and Genetics, 2020, 137, 84-102.	2.0	16
13	Dryland Cropping Systems, Weed Communities, and Disease Status Modulate the Effect of Climate Conditions on Wheat Soil Bacterial Communities. MSphere, 2020, 5, .	2.9	3
14	Authors' reply re: The vaginal metabolome and microbiota of cervical HPVâ€positive and HPVâ€negative women: a crossâ€sectional analysis. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 773-774.	2.3	5
15	The association of Chlamydia trachomatis and Mycoplasma genitalium infection with the vaginal metabolome. Scientific Reports, 2020, 10, 3420.	3.3	23
16	Frequency And Mode Of Physical Activity Influence Gut Microbial Composition In Overweight And Obese Adults. Medicine and Science in Sports and Exercise, 2020, 52, 666-666.	0.4	0
17	20 Vaginal microbiome composition is associated with sow longevity. Journal of Animal Science, 2020, 98, 23-24.	0.5	0
18	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. MSphere, 2019, 4, .	2.9	40

#	Article	IF	CITATIONS
19	Pelleted-hay alfalfa feed increases sheep wether weight gain and rumen bacterial richness over loose-hay alfalfa feed. PLoS ONE, 2019, 14, e0215797.	2.5	19
20	Gut microbiome composition of wild western lowland gorillas is associated with individual age and sex factors. American Journal of Physical Anthropology, 2019, 169, 575-585.	2.1	15
21	Subclinical mastitis in sheep: etiology and association with milk somatic cell count and ewe productivity in three research flocks in the Western United States. Translational Animal Science, 2019, 3, 1739-1743.	1.1	8
22	Stress and smoking are major correlates of disparate rates of molecular bacterial vaginosis among American Indian women. American Journal of Obstetrics and Gynecology, 2019, 221, 698.	1.3	0
23	Complete Genome Sequence of Hypervirulent Streptococcus pyogenes emm 3 Strain 1838. Microbiology Resource Announcements, 2019, 8, .	0.6	1
24	Zinc AA supplementation alters yearling ram rumen bacterial communities but zinc sulfate supplementation does not1. Journal of Animal Science, 2019, 97, 687-697.	0.5	17
25	Genome-resolved insights into a novel <i>Spiroplasma</i> symbiont of the Wheat Stem Sawfly (<i>Cephus cinctus)</i> . PeerJ, 2019, 7, e7548.	2.0	11
26	Biogeographical Differences in the Influence of Maternal Microbial Sources on the Early Successional Development of the Bovine Neonatal Gastrointestinal tract. Scientific Reports, 2018, 8, 3197.	3.3	133
27	Cigarette smoking is associated with an altered vaginal tract metabolomic profile. Scientific Reports, 2018, 8, 852.	3.3	84
28	Differences in amino acid catabolism by gut microbes with/without prebiotics inclusion in GDDY-based diet affect feed utilization in rainbow trout. Aquaculture, 2018, 490, 108-119.	3.5	18
29	Water system is a controlling variable modulating bacterial diversity of gastrointestinal tract and performance in rainbow trout. PLoS ONE, 2018, 13, e0195967.	2.5	20
30	Relationships Between Gastrointestinal Parasite Infections and the Fecal Microbiome in Free-Ranging Western Lowland Gorillas. Frontiers in Microbiology, 2018, 9, 1202.	3.5	21
31	Postprandial Serum Concentrations of Trimethylamine N-oxide in Metabolically Healthy Adults with Low and High Inflammation. Medicine and Science in Sports and Exercise, 2018, 50, 217.	0.4	0
32	Physical Activity and Glycemic Control in Low Versus High Inflammation Phenotypes in Metabolically Healthy Adults. Medicine and Science in Sports and Exercise, 2018, 50, 220.	0.4	0
33	Increase In Beta-hydroxybutyrate After High-fat Meal In Metabolically Healthy Overweight/obese Adults. Medicine and Science in Sports and Exercise, 2018, 50, 216-217.	0.4	0
34	P1.27â€Hpv is associated with an altered metabolomic profile in the vaginal tract. , 2017, , .		0
35	Null Mutations of Group A Streptococcus Orphan Kinase RocA: Selection in Mouse Infection and Comparison with CovS Mutations in Alteration of <i>In Vitro</i> and <i>In Vivo</i> Protease SpeB Expression and Virulence. Infection and Immunity, 2017, 85, .	2.2	16
36	Impact of Cropping Systems, Soil Inoculum, and Plant Species Identity on Soil Bacterial Community Structure. Microbial Ecology, 2017, 73, 417-434.	2.8	46

3

#	Article	IF	CITATIONS
37	Ground Juniperus pinchotii and urea in supplements fed to Rambouillet ewe lambs Part 2: Ewe lamb rumen microbial communities1. Journal of Animal Science, 2017, 95, 4587-4599.	0.5	15
38	The Application of Molecular Methods Towards an Understanding of the Role of the Vaginal Microbiome in Health and Disease. Methods in Microbiology, 2017, 44, 37-91.	0.8	7
39	3: Cigarette smoking is associated with an altered metabolomic profile of the vaginal environment. American Journal of Obstetrics and Gynecology, 2016, 215, S815.	1.3	1
40	Microbiomes, metagenomics, and primate conservation: New strategies, tools, and applications. Biological Conservation, 2016, 199, 56-66.	4.1	73
41	Effect of Antibiotic Treatment on the Gastrointestinal Microbiome of Free-Ranging Western Lowland Gorillas (Gorilla g. gorilla). Microbial Ecology, 2016, 72, 943-954.	2.8	19
42	Xylan degradation by the human gut Bacteroides xylanisolvens XB1AT involves two distinct gene clusters that are linked at the transcriptional level. BMC Genomics, 2016, 17, 326.	2.8	81
43	Unraveling the pectinolytic function of Bacteroides xylanisolvens using a RNA-seq approach and mutagenesis. BMC Genomics, 2016, 17, 147.	2.8	33
44	Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. Cell Reports, 2016, 14, 2142-2153.	6.4	231
45	Temporal variation selects for diet–microbe co-metabolic traits in the gut of <i>Gorilla</i> spp. ISME Journal, 2016, 10, 514-526.	9.8	84
46	Variable responses of human and non-human primate gut microbiomes to a Western diet. Microbiome, 2015, 3, 53.	11.1	108
47	Vaginal biogenic amines: biomarkers of bacterial vaginosis or precursors to vaginal dysbiosis?. Frontiers in Physiology, 2015, 6, 253.	2.8	114
48	The Gut Microbiota Appears to Compensate for Seasonal Diet Variation in the Wild Black Howler Monkey (Alouatta pigra). Microbial Ecology, 2015, 69, 434-443.	2.8	254
49	Functional phylotyping approach for assessing intraspecific diversity of Ruminococcus albus within the rumen microbiome. FEMS Microbiology Letters, 2015, 362, 1-10.	1.8	12
50	Evaluation of Dietary Soy Sensitivity in Snake River Cutthroat Trout. North American Journal of Aquaculture, 2015, 77, 195-205.	1.4	3
51	Gut microbiome composition and metabolomic profiles of wild western lowland gorillas (<i>Gorilla) Tj ETQq1 1 (</i>).784314	rgBT_/Overlo
52	Caste-Specific Differences in Hindgut Microbial Communities of Honey Bees (Apis mellifera). PLoS ONE, 2015, 10, e0123911.	2.5	108
53	Feed Characteristics Alter Growth Efficiency of Cutthroat Trout. Journal of Fish and Wildlife Management, 2015, 6, 83-91.	0.9	2
54	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. PLoS ONE, 2014, 9, e99221.	2.5	73

#	Article	IF	CITATIONS
55	Characterization of the Vaginal Microbiota of Ewes and Cows Reveals a Unique Microbiota with Low Levels of Lactobacilli and Near-Neutral pH. Frontiers in Veterinary Science, 2014, 1, 19.	2.2	108
56	Temporal dynamics of fibrolytic and methanogenic rumen microorganisms during in situ incubation of switchgrass determined by 16S rRNA gene profiling. Frontiers in Microbiology, 2014, 5, 307.	3.5	78
57	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. ISME Journal, 2014, 8, 2431-2444.	9.8	149
58	The role of gut microbes in satisfying the nutritional demands of adult and juvenile wild, black howler monkeys (<scp><i>A</i></scp> <i>louatta pigra</i>). American Journal of Physical Anthropology, 2014, 155, 652-664.	2.1	103
59	Gastrointestinal Tract Microbiota and Probiotics in Production Animals. Annual Review of Animal Biosciences, 2014, 2, 469-486.	7.4	158
60	Pregnancy's Stronghold on the Vaginal Microbiome. PLoS ONE, 2014, 9, e98514.	2.5	146
61	Terrestrial Vertebrate Animal Metagenomics, Non-domesticated Primates, Simians. , 2014, , 1-5.		0
62	Habitat degradation impacts black howler monkey (<i>Alouatta pigra</i>) gastrointestinal microbiomes. ISME Journal, 2013, 7, 1344-1353.	9.8	1,031
63	Modulation of Systemic Immune Responses through Commensal Gastrointestinal Microbiota. PLoS ONE, 2013, 8, e53969.	2.5	42
64	The primate vaginal microbiome: Comparative context and implications for human health and disease. American Journal of Physical Anthropology, 2013, 152, 119-134.	2.1	115
65	Alteration of digestive tract microbiome in neonatal Holstein bull calves by bacitracin methylene disalicylate treatment and scours1. Journal of Animal Science, 2013, 91, 4984-4990.	0.5	17
66	A Multi-Omic Systems-Based Approach Reveals Metabolic Markers of Bacterial Vaginosis and Insight into the Disease. PLoS ONE, 2013, 8, e56111.	2.5	122
67	Expression of Cellulosome Components and Type IV Pili within the Extracellular Proteome of Ruminococcus flavefaciens 007. PLoS ONE, 2013, 8, e65333.	2.5	25
68	Low Incidence of Spontaneous Type 1 Diabetes in Non-Obese Diabetic Mice Raised on Gluten-Free Diets Is Associated with Changes in the Intestinal Microbiome. PLoS ONE, 2013, 8, e78687.	2.5	117
69	The microbiome of the chicken gastrointestinal tract. Animal Health Research Reviews, 2012, 13, 89-99.	3.1	239
70	Loss of Sex and Age Driven Differences in the Gut Microbiome Characterize Arthritis-Susceptible *0401 Mice but Not Arthritis-Resistant *0402 Mice. PLoS ONE, 2012, 7, e36095.	2.5	195
71	Phage–bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. Environmental Microbiology, 2012, 14, 207-227.	3.8	128
72	Comparative analysis of the vaginal microbiome in health and disease. Genome Biology, 2011, 12, .	9.6	0

#	Article	IF	CITATIONS
73	The large episomes of Butyrivibrio proteoclasticus B316T have arisen through intragenomic gene shuttling from the chromosome to smaller Butyrivibrio-specific plasmids. Plasmid, 2011, 66, 67-78.	1.4	6
74	Biochemical Characterization and Relative Expression Levels of Multiple Carbohydrate Esterases of the Xylanolytic Rumen Bacterium Prevotella ruminicola 23 Grown on an Ester-Enriched Substrate. Applied and Environmental Microbiology, 2011, 77, 5671-5681.	3.1	76
75	Towards an Evolutionary Model of Animal-Associated Microbiomes. Entropy, 2011, 13, 570-594.	2.2	48
76	Cellulosomics, a Gene-Centric Approach to Investigating the Intraspecific Diversity and Adaptation of Ruminococcus flavefaciens within the Rumen. PLoS ONE, 2011, 6, e25329.	2.5	28
77	The Glycobiome of the Rumen Bacterium Butyrivibrio proteoclasticus B316T Highlights Adaptation to a Polysaccharide-Rich Environment. PLoS ONE, 2010, 5, e11942.	2.5	102
78	Characterization of the Fecal Microbiome from Non-Human Wild Primates Reveals Species Specific Microbial Communities. PLoS ONE, 2010, 5, e13963.	2.5	225
79	The Genome Sequence of the Rumen Methanogen Methanobrevibacter ruminantium Reveals New Possibilities for Controlling Ruminant Methane Emissions. PLoS ONE, 2010, 5, e8926.	2.5	256
80	Thermostable Enzymes as Biocatalysts in the Biofuel Industry. Advances in Applied Microbiology, 2010, 70, 1-55.	2.4	235
81	Comparative Genomics of Gardnerella vaginalis Strains Reveals Substantial Differences in Metabolic and Virulence Potential. PLoS ONE, 2010, 5, e12411.	2.5	124