Vicente Perez Brocal

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3318824/publications.pdf

Version: 2024-02-01

71 papers

4,830 citations

30 h-index 61 g-index

73 all docs

73 docs citations

times ranked

73

6899 citing authors

#	Article	IF	CITATIONS
1	Intestinal mycobiota composition and changes in children with thalassemia who underwent allogeneic hematopoietic stem cell transplantation. Pediatric Blood and Cancer, 2022, 69, e29411.	0.8	5
2	Kin recognition in <i>Drosophila</i> : rearing environment and relatedness can modulate gut microbiota and cuticular hydrocarbon odour profiles. Oikos, 2022, 2022, .	1.2	3
3	Caudovirales bacteriophages are associated with improved executive function and memory in flies, mice, and humans. Cell Host and Microbe, 2022, 30, 340-356.e8.	5.1	50
4	Microbiota alterations in proline metabolism impact depression. Cell Metabolism, 2022, 34, 681-701.e10.	7.2	77
5	Presence of <i>Blastocystis</i> in gut microbiota is associated with cognitive traits and decreased executive function. ISME Journal, 2022, 16, 2181-2197.	4.4	10
6	Metagenomic analysis of formalin-fixed paraffin-embedded tumor and normal mucosa reveals differences in the microbiome of colorectal cancer patients. Scientific Reports, 2021, 11, 391.	1.6	21
7	The intestinal mycobiota and its relationship with overweight, obesity and nutritional aspects. Journal of Human Nutrition and Dietetics, 2021, 34, 645-655.	1.3	29
8	Human Milk Virome Analysis: Changing Pattern Regarding Mode of Delivery, Birth Weight, and Lactational Stage. Nutrients, 2021, 13, 1779.	1.7	18
9	Subjects with detectable <i>Saccharomyces cerevisiae</i> in the gut microbiota show deficits in attention and executive function. Journal of Internal Medicine, 2021, 290, 740-743.	2.7	4
10	Iron status influences non-alcoholic fatty liver disease in obesity through the gut microbiome. Microbiome, 2021, 9, 104.	4.9	70
11	Dysbiotic gut microbiota in patients with inflammatory rosacea: another clue towards the existence of a brain–gut–skin axis. British Journal of Dermatology, 2021, 185, 655-657.	1.4	9
12	Interkingdom Gut Microbiome and Resistome of the Cockroach <i>Blattella germanica</i> . MSystems, 2021, 6, .	1.7	13
13	Metagenomic Survey of the Highly Polyphagous Anastrepha ludens Developing in Ancestral and Exotic Hosts Reveals the Lack of a Stable Microbiota in Larvae and the Strong Influence of Metamorphosis on Adult Gut Microbiota. Frontiers in Microbiology, 2021, 12, 685937.	1.5	10
14	Obesity status and obesity-associated gut dysbiosis effects on hypothalamic structural covariance. International Journal of Obesity, 2021, , .	1.6	1
15	Obesity-associated deficits in inhibitory control are phenocopied to mice through gut microbiota changes in one-carbon and aromatic amino acids metabolic pathways. Gut, 2021, 70, 2283-2296.	6.1	31
16	Changes in glucagonâ€like peptide 1 and 2 levels in people with obesity after a dietâ€induced weightâ€loss intervention are related to a specific microbiota signature: A prospective cohort study. Clinical and Translational Medicine, 2021, 11, e575.	1.7	3
17	A Real-Time PCR Assay for Detection of Low Pneumocystis jirovecii Levels. Frontiers in Microbiology, 2021, 12, 787554.	1.5	1
18	Analysis of the gut microbiota in alopecia areata: identification of bacterial biomarkers. Journal of the European Academy of Dermatology and Venereology, 2020, 34, 400-405.	1.3	68

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19	Obesity Impairs Short-Term and Working Memory through Gut Microbial Metabolism of Aromatic Amino Acids. Cell Metabolism, 2020, 32, 548-560.e7.	7.2	88
20	Optimized DNA extraction and purification method for characterization of bacterial and fungal communities in lung tissue samples. Scientific Reports, 2020, 10, 17377.	1.6	15
21	Gut microbiota steroid sexual dimorphism and its impact on gonadal steroids: influences of obesity and menopausal status. Microbiome, 2020, 8, 136.	4.9	72
22	Gut bacterial ClpB-like gene function is associated with decreased body weight and a characteristic microbiota profile. Microbiome, 2020, 8, 59.	4.9	46
23	Advanced strategy to exploit wine-making waste by manufacturing antioxidant and prebiotic fibre-enriched vesicles for intestinal health. Colloids and Surfaces B: Biointerfaces, 2020, 193, 111146.	2.5	14
24	AB0492â€INTESTINAL MICROBIOTA COMPOSITION OF PATIENT'S WITH BEHCET'S DISEASE: DIFFERENC BETWEEN EYE, MUCOCUTANEOUS AND VASCULAR INVOLVEMENT (RHEUMA-BIOTA STUDY). Annals of the Rheumatic Diseases, 2020, 79, 1543.2-1544.	CES 0.5	2
25	Human milk mycobiota composition: relationship with gestational age, delivery mode, and birth weight. Beneficial Microbes, 2020, 11, 151-162.	1.0	18
26	AB1035â€INTESTINAL MICROBIOTA COMPOSITION OF ADULT PATIENTS WITH FAMILIAL MEDITERRANEAN FEVE AND HEALTHY CONTROLS (THE RHEUMA-BIOTA STUDY). Annals of the Rheumatic Diseases, 2020, 79, 1809.2-1809.	ER 0.5	0
27	Cross-Regional View of Functional and Taxonomic Microbiota Composition in Obesity and Post-obesity Treatment Shows Country Specific Microbial Contribution. Frontiers in Microbiology, 2019, 10, 2346.	1.5	17
28	OR40: Gut Bacterial ClpB Gene Function is Associated with Dietary Fiber Intake and Decreased Body Weight. Clinical Nutrition, 2019, 38, S19.	2.3	0
29	Glutamate interactions with obesity, insulin resistance, cognition and gut microbiota composition. Acta Diabetologica, 2019, 56, 569-579.	1.2	49
30	The Endobiota Study: Comparison of Vaginal, Cervical and Gut Microbiota Between Women with Stage 3/4 Endometriosis and Healthy Controls. Scientific Reports, 2019, 9, 2204.	1.6	125
31	Profiling of Protein Degraders in Cultures of Human Gut Microbiota. Frontiers in Microbiology, 2019, 10, 2614.	1.5	74
32	Beyond cells – The virome in the human holobiont. Microbial Cell, 2019, 6, 373-396.	1.4	17
33	New DNA Extraction Method for the Detection of Pneumocystis in Lung Tissue Samples of Colonized Individuals. OBM Genetics, 2019, 3, 1-1.	0.2	1
34	Elevated circulating levels of succinate in human obesity are linked to specific gut microbiota. ISME Journal, 2018, 12, 1642-1657.	4.4	260
35	Isolation in small populations of Wayampi Amerindians promotes endemicity and homogenisation of their faecal virome, but its distribution is not entirely random. FEMS Microbiology Ecology, 2018, 94, .	1.3	0
36	The endobiota study: comparison of vaginal, cervical and intestinal microbiota composition between women with histology proven endometriosis and healthy controls. Fertility and Sterility, 2018, 110, e391.	0.5	1

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37	The respiratory virome in chronic obstructive pulmonary disease. Future Virology, 2018, 13, 457-466.	0.9	2
38	The analysis of the oral DNA virome reveals which viruses are widespread and rare among healthy young adults in Valencia (Spain). PLoS ONE, 2018, 13, e0191867.	1.1	33
39	The respiratory microbiome in bronchial mucosa and secretions from severe IgE-mediated asthma patients. BMC Microbiology, 2017, 17, 20.	1.3	20
40	The microbiome in respiratory medicine: current challenges and future perspectives. European Respiratory Journal, 2017, 49, 1602086.	3.1	194
41	The Gut Metagenome Changes in Parallel to Waist Circumference, Brain Iron Deposition, and Cognitive Function. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2962-2973.	1.8	40
42	Bronchial microbiome, PA biofilm-forming capacity and exacerbation in severe COPD patients colonized by <i>P. aeruginosa </i> Future Microbiology, 2017, 12, 379-392.	1.0	24
43	Metagenomic Analysis of Crohn $\hat{E}^{1}\!\!/_{4}$ s Disease Patients Identifies Changes in the Virome and Microbiome Related to Disease Status and Therapy, and Detects Potential Interactions and Biomarkers. Inflammatory Bowel Diseases, 2015, 21, 2515-2532.	0.9	79
44	Reply to "Chronic Obstructive Pulmonary Disease Lung Microbiota Diversity May Be Mediated by Age or Inhaled Corticosteroid Use― Journal of Clinical Microbiology, 2015, 53, 1051-1051.	1.8	0
45	Influence of biofim on the bronchial microbiome in COPD patients colonized or infected bypseudomonas aeruginosa. , 2015, , .		1
46	Functional Metagenomics of the Bronchial Microbiome in COPD. PLoS ONE, 2015, 10, e0144448.	1.1	40
47	LSC Abstract – Functional metagenomics of respiratoy microbiome in exacerbated COPD. , 2015, , .		0
48	$ \begin{tabular}{l} LATE-BREAKING ABSTRACT: Bronchial microbiome in severe persistent oral corticosteroid-dependent as thm a.\ , 2015,\ ,\ . \end{tabular}$		0
49	Severity-Related Changes of Bronchial Microbiome in Chronic Obstructive Pulmonary Disease. Journal of Clinical Microbiology, 2014, 52, 4217-4223.	1.8	181
50	Bronchial microbiome of severe COPD patients colonised by Pseudomonas aeruginosa. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 1101-1111.	1.3	112
51	Comparison of different assembly and annotation tools on analysis of simulated viral metagenomic communities in the gut. BMC Genomics, 2014, 15, 37.	1.2	73
52	Retrospective case–control study of viral pathogen screening in proliferative verrucous leukoplakia lesions. Clinical Otolaryngology, 2014, 39, 272-280.	0.6	15
53	Study of the Viral and Microbial Communities Associated With Crohn's Disease: A Metagenomic Approach. Clinical and Translational Gastroenterology, 2013, 4, e36.	1.3	108
54	Gut Microbiota in Children Vaccinated With Rotavirus Vaccine. Pediatric Infectious Disease Journal, 2012, 31, 1300-1302.	1.1	16

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55	Symbionts and Pathogens: What is the Difference?. Current Topics in Microbiology and Immunology, 2011, 358, 215-243.	0.7	27
56	A Genomic Reappraisal of Symbiotic Function in the Aphid/Buchnera Symbiosis: Reduced Transporter Sets and Variable Membrane Organisations. PLoS ONE, 2011, 6, e29096.	1.1	44
57	New Insights on the Evolutionary History of Aphids and Their Primary Endosymbiont Buchnera aphidicola. International Journal of Evolutionary Biology, 2011, 2011, 1-9.	1.0	10
58	A Linear Molecule with Two Large Inverted Repeats: The Mitochondrial Genome of the Stramenopile Proteromonas lacertae. Genome Biology and Evolution, 2010, 2, 257-266.	1.1	31
59	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	2.6	913
60	Immunity and other defenses in pea aphids, Acyrthosiphon pisum. Genome Biology, 2010, 11, R21.	13.9	389
61	Identification of the Weevil immune genes and their expression in the bacteriome tissue. BMC Biology, 2008, 6, 43.	1.7	114
62	Organelles in Blastocystis that Blur the Distinction between Mitochondria and Hydrogenosomes. Current Biology, 2008, 18, 580-585.	1.8	167
63	Evolution of the Secondary Symbiont " <i>Candidatus</i> Serratia symbiotica―in Aphid Species of the Subfamily Lachninae. Applied and Environmental Microbiology, 2008, 74, 4236-4240.	1.4	77
64	Analysis of Two Genomes from the Mitochondrion-Like Organelle of the Intestinal Parasite Blastocystis: Complete Sequences, Gene Content, and Genome Organization. Molecular Biology and Evolution, 2008, 25, 2475-2482.	3.5	59
65	A Small Microbial Genome: The End of a Long Symbiotic Relationship?. Science, 2006, 314, 312-313.	6.0	309
66	Plasmids in the aphid endosymbiont Buchnera aphidicola with the smallest genomes. A puzzling evolutionary story. Gene, 2006, 370, 17-25.	1.0	50
67	Symbiosis. Current Biology, 2006, 16, R866-R871.	1.8	345
68	Comparative analysis of two genomic regions among four strains of Buchnera aphidicola, primary endosymbiont of aphids. Gene, 2005, 345, 73-80.	1.0	9
69	Coexistence of Wolbachia with Buchnera aphidicola and a Secondary Symbiont in the Aphid Cinara cedri. Journal of Bacteriology, 2004, 186, 6626-6633.	1.0	119
70	Minimal genomes required for life., 0,, 105-122.		2
71	Optimized DNA Extraction and Purification Method for Characterization of Bacterial and Fungal Communities in Lung Tissue Samples. SSRN Electronic Journal, 0, , .	0.4	0