Susana Fuentes

List of Publications by Year in descending order

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46 papers

8,913 citations

172207 29 h-index 243296 44 g-index

50 all docs

50 docs citations

50 times ranked

12086 citing authors

#	Article	IF	CITATIONS
1	Duodenal Infusion of Donor Feces for Recurrent <i>Clostridium difficile</i> . New England Journal of Medicine, 2013, 368, 407-415.	13.9	3,157
2	Findings From a Randomized Controlled Trial of Fecal Transplantation for Patients With Ulcerative Colitis. Gastroenterology, 2015, 149, 110-118.e4.	0.6	769
3	Insight into the prebiotic concept: lessons from an exploratory, double blind intervention study with inulin-type fructans in obese women. Gut, 2013, 62, 1112-1121.	6.1	632
4	Impact of oral vancomycin on gut microbiota, bile acid metabolism, and insulin sensitivity. Journal of Hepatology, 2014, 60, 824-831.	1.8	475
5	Human intestinal microbiota composition is associated with local and systemic inflammation in obesity. Obesity, 2013, 21, E607-15.	1.5	469
6	Bacterial Diversity in Meconium of Preterm Neonates and Evolution of Their Fecal Microbiota during the First Month of Life. PLoS ONE, 2013, 8, e66986.	1.1	315
7	Aberrant gut microbiota composition at the onset of type 1 diabetes in young children. Diabetologia, 2014, 57, 1569-1577.	2.9	274
8	Characterization of Romboutsia ilealis gen. nov., sp. nov., isolated from the gastro-intestinal tract of a rat, and proposal for the reclassification of five closely related members of the genus Clostridium into the genera Romboutsia gen. nov., Intestinibacter gen. nov., Terrisporobacter gen. nov. and Asaccharospora gen. nov International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 1600-1616.	0.8	259
9	Significant Correlation Between the Infant Gut Microbiome and Rotavirus Vaccine Response in Rural Ghana. Journal of Infectious Diseases, 2017, 215, 34-41.	1.9	227
10	Intestinal Microbiota of Infants With Colic: Development and Specific Signatures. Pediatrics, 2013, 131, e550-e558.	1.0	213
11	Impact of delivery mode-associated gut microbiota dynamics on health in the first year of life. Nature Communications, 2019, 10, 4997.	5 . 8	209
12	Reset of a critically disturbed microbial ecosystem: faecal transplant in recurrent <i>Clostridium difficile</i> infection. ISME Journal, 2014, 8, 1621-1633.	4.4	172
13	Effect of Vegan Fecal Microbiota Transplantation on Carnitine―and Cholineâ€Derived Trimethylamineâ€Nâ€Oxide Production and Vascular Inflammation in Patients With Metabolic Syndrome. Journal of the American Heart Association, 2018, 7, .	1.6	164
14	Microbial shifts and signatures of long-term remission in ulcerative colitis after faecal microbiota transplantation. ISME Journal, 2017, 11, 1877-1889.	4.4	157
15	Evaluation of microbial community reproducibility, stability and composition in a human distal gut chemostat model. Journal of Microbiological Methods, 2013, 95, 167-174.	0.7	144
16	Rotavirus vaccine response correlates with the infant gut microbiota composition in Pakistan. Gut Microbes, 2018, 9, 93-101.	4.3	142
17	Combating inflammaging through a Mediterranean whole diet approach: The NU-AGE project's conceptual framework and design. Mechanisms of Ageing and Development, 2014, 136-137, 3-13.	2.2	131
18	The Mucosa-associated Microbiota of PSC Patients is Characterized by Low Diversity and Low Abundance of Uncultured Clostridiales II. Journal of Crohn's and Colitis, 2015, 9, 342-348.	0.6	106

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19	Comparative gut microbiota and resistome profiling of intensive care patients receiving selective digestive tract decontamination and healthy subjects. Microbiome, 2017, 5, 88.	4.9	90
20	Phylogenetic and Metabolic Tracking of Gut Microbiota during Perinatal Development. PLoS ONE, 2015, 10, e0137347.	1.1	84
21	Novel Polyfermentor Intestinal Model (PolyFermS) for Controlled Ecological Studies: Validation and Effect of pH. PLoS ONE, 2013, 8, e77772.	1.1	82
22	Crying in infants. Gut Microbes, 2013, 4, 416-421.	4.3	78
23	Colonic metaproteomic signatures of active bacteria and the host in obesity. Proteomics, 2015, 15, 3544-3552.	1.3	70
24	Microbial signatures in post-infectious irritable bowel syndrome – toward patient stratification for improved diagnostics and treatment. Gut Microbes, 2015, 6, 364-369.	4.3	51
25	Simulating distal gut mucosal and luminal communities using packed-column biofilm reactors and an in vitro chemostat model. Journal of Microbiological Methods, 2015, 108, 36-44.	0.7	47
26	Administration of Lactobacillus casei and Lactobacillus plantarum affects the diversity of murine intestinal lactobacilli, but not the overall bacterial community structure. Research in Microbiology, 2008, 159, 237-243.	1.0	45
27	Associations between Pro- and Anti-Inflammatory Gastro-Intestinal Microbiota, Diet, and Cognitive Functioning in Dutch Healthy Older Adults: The NU-AGE Study. Nutrients, 2020, 12, 3471.	1.7	42
28	Fecal Transplantation Treatment of Antibiotic-Induced, Noninfectious Colitis and Long-Term Microbiota Follow-Up. Case Reports in Medicine, 2014, 2014, 1-7.	0.3	37
29	A strain of Lactobacillus plantarum affects segmented filamentous bacteria in the intestine of immunosuppressed mice. FEMS Microbiology Ecology, 2008, 63, 65-72.	1.3	35
30	Correlation between Protection against Sepsis by Probiotic Therapy and Stimulation of a Novel Bacterial Phylotype. Applied and Environmental Microbiology, 2011, 77, 7749-7756.	1.4	31
31	Halomonas indalinina sp. nov., a moderately halophilic bacterium isolated from a solar saltern in Cabo de Gata, AlmerÃa, southern Spain. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 376-380.	0.8	27
32	Effects of plant stanol ester consumption on fasting plasma oxy(phyto)sterol concentrations as related to fecal microbiota characteristics. Journal of Steroid Biochemistry and Molecular Biology, 2017, 169, 46-53.	1.2	27
33	Chromohalobacter salarius sp. nov., a moderately halophilic bacterium isolated from a solar saltern in Cabo de Gata, AlmerÃa, southern Spain. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 1238-1242.	0.8	25
34	How to Manipulate the Microbiota: Fecal Microbiota Transplantation. Advances in Experimental Medicine and Biology, 2016, 902, 143-153.	0.8	25
35	Bacteriological and Immunological Profiling of Meconium and Fecal Samples from Preterm Infants: A Two-Year Follow-Up Study. Nutrients, 2017, 9, 1293.	1.7	18
36	Associations of faecal microbiota with influenza-like illness in participants aged 60 years or older: an observational study. The Lancet Healthy Longevity, 2021, 2, e13-e23.	2.0	17

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37	Impact of long-term dietary habits on the human gut resistome in the Dutch population. Scientific Reports, 2022, 12, 1892.	1.6	12
38	Benchmarking laboratory processes to characterise low-biomass respiratory microbiota. Scientific Reports, 2021, 11, 17148.	1.6	10
39	An Explorative Biomarker Study for Vaccine Responsiveness after a Primary Meningococcal Vaccination in Middle-Aged Adults. Frontiers in Immunology, 2017, 8, 1962.	2.2	6
40	Some comments on certain statistical aspects of the study of the microbiome. Briefings in Bioinformatics, 2020, 21, 1487-1494.	3.2	5
41	Associations and recovery dynamics of the nasopharyngeal microbiota during influenza-like illness in the aging population. Scientific Reports, 2022, 12, 1915.	1.6	5
42	Su2046 Gut Microbiota Correlate With Psychological Distress and Intestinal Lymphocyte Composition in Post-Infectious Irritable Bowel Syndrome Patients. Gastroenterology, 2015, 148, S-584.	0.6	1
43	Reply. Gastroenterology, 2016, 150, 286-287.	0.6	1
44	Mo1804 Composition and Stability of the Mucosal-Associated Microbiota Compared With the Faecal-Associated Microbiota in Healthy Individuals and Irritable Bowel Syndrome Patients. Gastroenterology, 2015, 148, S-715.	0.6	0
45	Su2047 Fecal and Mucosal Intestinal Microbiota in Postinfectious Irritable Bowel Syndrome (IBS) Patients Differs From General IBS Patients As Well As Healthy Subjects. Gastroenterology, 2015, 148, S-584.	0.6	0
46	Chromohalobacter nigrandesensis sp. nov., a moderately halophilic, Gram-negative bacterium isolated from Lake Tebenquiche on the Atacama Saltern, Chile. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 2725-2725.	0.8	0