

M Pilar Francino

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

5,422
citations

218677

26
h-index

214800

47
g-index

55
all docs

55
docs citations

55
times ranked

7744
citing authors

#	ARTICLE	IF	CITATIONS
1	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. <i>Science</i> , 2002, 298, 2157-2167.	12.6	1,539
2	Antibiotics and the Human Gut Microbiome: Dysbioses and Accumulation of Resistances. <i>Frontiers in Microbiology</i> , 2015, 6, 1543.	3.5	613
3	Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer. <i>Science</i> , 2007, 318, 1449-1452.	12.6	383
4	Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , 2006, 17, 7-15.	5.5	352
5	Meconium microbiota types dominated by lactic acid or enteric bacteria are differentially associated with maternal eczema and respiratory problems in infants. <i>Clinical and Experimental Allergy</i> , 2013, 43, 198-211.	2.9	297
6	Strand asymmetries in DNA evolution. <i>Trends in Genetics</i> , 1997, 13, 240-245.	6.7	228
7	Comparative Metagenomics and Population Dynamics of the Gut Microbiota in Mother and Infant. <i>Genome Biology and Evolution</i> , 2010, 2, 53-66.	2.5	202
8	Microbial Succession in the Gut: Directional Trends of Taxonomic and Functional Change in a Birth Cohort of Spanish Infants. <i>PLoS Genetics</i> , 2014, 10, e1004406.	3.5	164
9	An adaptive radiation model for the origin of new gene functions. <i>Nature Genetics</i> , 2005, 37, 573-578.	21.4	162
10	Early Development of the Gut Microbiota and Immune Health. <i>Pathogens</i> , 2014, 3, 769-790.	2.8	139
11	Asymmetries Generated by Transcription-Coupled Repair in Enterobacterial Genes. <i>Science</i> , 1996, 272, 107-109.	12.6	137
12	The Gut as Reservoir of Antibiotic Resistance: Microbial Diversity of Tetracycline Resistance in Mother and Infant. <i>PLoS ONE</i> , 2011, 6, e21644.	2.5	111
13	Isochores result from mutation not selection. <i>Nature</i> , 1999, 400, 30-31.	27.8	98
14	Deamination as the Basis of Strand-Asymmetric Evolution in Transcribed <i>Escherichia coli</i> Sequences. <i>Molecular Biology and Evolution</i> , 2001, 18, 1147-1150.	8.9	96
15	The Genome of the Obligately Intracellular Bacterium <i>Ehrlichia canis</i> Reveals Themes of Complex Membrane Structure and Immune Evasion Strategies. <i>Journal of Bacteriology</i> , 2006, 188, 4015-4023.	2.2	90
16	Birth Mode-Related Differences in Gut Microbiota Colonization and Immune System Development. <i>Annals of Nutrition and Metabolism</i> , 2018, 73, 12-16.	1.9	63
17	High frequencies of antibiotic resistance genes in infants' meconium and early fecal samples. <i>Journal of Developmental Origins of Health and Disease</i> , 2016, 7, 35-44.	1.4	61
18	Air Pollution, Early Life Microbiome, and Development. <i>Current Environmental Health Reports</i> , 2018, 5, 512-521.	6.7	59

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19	Metagenomics and development of the gut microbiota in infants. <i>Clinical Microbiology and Infection</i> , 2012, 18, 21-26.	6.0	54
20	Effect of Food Thermal Processing on the Composition of the Gut Microbiota. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 11500-11509.	5.2	50
21	Spent Coffee Grounds Extract, Rich in Mannoooligosaccharides, Promotes a Healthier Gut Microbial Community in a Dose-Dependent Manner. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2500-2509.	5.2	49
22	Selection for Unequal Densities of λ 70 Promoter-Like Signals in Different Regions of Large Bacterial Genomes. <i>PLoS Genetics</i> , 2006, 2, e185.	3.5	43
23	R1 and R2 retrotransposable elements of <i>Drosophila</i> evolve at rates similar to those of nuclear genes. <i>Genetics</i> , 1995, 139, 685-695.	2.9	42
24	Metabolic adaptation in the human gut microbiota during pregnancy and the first year of life. <i>EBioMedicine</i> , 2019, 39, 497-509.	6.1	37
25	Strand Symmetry Around the β -Globin Origin of Replication in Primates. <i>Molecular Biology and Evolution</i> , 2000, 17, 416-422.	8.9	35
26	The Ecology of Bacterial Genes and the Survival of the New. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-14.	1.0	33
27	Potential probiotic salami with dietary fiber modulates metabolism and gut microbiota in a human intervention study. <i>Journal of Functional Foods</i> , 2020, 66, 103790.	3.4	30
28	Enrichment of Food With Tannin Extracts Promotes Healthy Changes in the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 625782.	3.5	28
29	Selection against Spurious Promoter Motifs Correlates with Translational Efficiency across Bacteria. <i>PLoS ONE</i> , 2007, 2, e745.	2.5	24
30	Mastiha (<i>Pistacia lentiscus</i>) Improves Gut Microbiota Diversity, Hepatic Steatosis, and Disease Activity in a Biopsy-Confirmed Mouse Model of Advanced Non-Alcoholic Steatohepatitis and Fibrosis. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1900927.	3.3	22
31	Roles of Secretory Immunoglobulin A in Host-Microbiota Interactions in the Gut Ecosystem. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	21
32	Effect of Mastiha supplementation on NAFLD: The MAST4HEALTH Randomised, Controlled Trial. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2001178.	3.3	19
33	An extended reconstruction of human gut microbiota metabolism of dietary compounds. <i>Nature Communications</i> , 2021, 12, 4728.	12.8	19
34	Effect of roasting conditions on cocoa bioactivity and gut microbiota modulation. <i>Food and Function</i> , 2021, 12, 9680-9692.	4.6	17
35	A Comparative Genomics Approach to DNA Asymmetry. <i>Annals of the New York Academy of Sciences</i> , 1999, 870, 428-431.	3.8	13
36	Nutrigenetic Interactions Might Modulate the Antioxidant and Anti-Inflammatory Status in Mastiha-Supplemented Patients With NAFLD. <i>Frontiers in Immunology</i> , 2021, 12, 683028.	4.8	12

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37	Adaptation of the Human Gut Microbiota Metabolic Network During the First Year After Birth. <i>Frontiers in Microbiology</i> , 2019, 10, 848.	3.5	11
38	The Gut Microbiome and Metabolic Health. <i>Current Nutrition Reports</i> , 2017, 6, 16-23.	4.3	10
39	Evaluation of the Effects of a Short Supplementation With Tannins on the Gut Microbiota of Healthy Subjects. <i>Frontiers in Microbiology</i> , 2022, 13, 848611.	3.5	10
40	The Stance4Health Project: Evaluating a Smart Personalised Nutrition Service for Gut Microbiota Modulation in Normal- and Overweight Adults and Children with Obesity, Gluten-Related Disorders or Allergy/Intolerance to Cow's Milk. <i>Foods</i> , 2022, 11, 1480.	4.3	10
41	Phylogenetic Relationships of Bacteria with Special Reference to Endosymbionts and Enteric Species. , 2006, , 41-59.		9
42	Prediction of degradation pathways of phenolic compounds in the human gut microbiota through enzyme promiscuity methods. <i>Npj Systems Biology and Applications</i> , 2022, 8, .	3.0	8
43	Opportunities and Challenges to Microbial Symbiosis Research in the Microbiome Era. <i>Frontiers in Microbiology</i> , 2020, 11, 1150.	3.5	5
44	Positional Conservation of Clusters of Overlapping Promoter-Like Sequences in Enterobacterial Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 997-1010.	8.9	4
45	Human Microbiome and Diseases. , 2013, , 235-249.		4
46	Effect of Freezing on Gut Microbiota Composition and Functionality for In Vitro Fermentation Experiments. <i>Nutrients</i> , 2021, 13, 2207.	4.1	4
47	Editorial: Recent Advances in Symbiosis Research: Integrative Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 1331.	3.5	2
48	Association of Dietary Patterns with MRI Markers of Hepatic Inflammation and Fibrosis in the MAST4HEALTH Study. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 971.	2.6	2
49	SUN-PO055: The Effect of Mastiha Supplement in Microbiota Composition in Patients with IBD; Preliminary Results. <i>Clinical Nutrition</i> , 2019, 38, S79.	5.0	0
50	Gut microbiome characteristics at the crossroads of metabolic health and lifestyle patterns in an adult population. <i>Proceedings of the Nutrition Society</i> , 2020, 79, .	1.0	0
51	Editorial: Nutrition and Behavior as Determinants of Host-Associated Microbiomes. <i>Frontiers in Microbiology</i> , 2021, 12, 835394.	3.5	0
52	Living Large: Elucidation of the Frankia EAN1pec Genome Sequence Shows Gene Expansion and Metabolic Versatility. <i>Current Plant Science and Biotechnology in Agriculture</i> , 2008, , 255-255.	0.0	0