Juan S Escobar

List of Publications by Year in descending order

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LUAN S ESCORAD

#	Article	IF	CITATIONS
1	Identification and Removal of Potential Contaminants in 16S rRNA Gene Sequence Data Sets from Low-Microbial-Biomass Samples: an Example from Mosquito Tissues. MSphere, 2021, 6, e0050621.	2.9	5
2	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
3	Variants in genes of innate immunity, appetite control and energy metabolism are associated with host cardiometabolic health and gut microbiota composition. Gut Microbes, 2020, 11, 556-568.	9.8	7
4	Gut microbiota composition explains more variance in the host cardiometabolic risk than genetic ancestry. Gut Microbes, 2020, 11, 191-204.	9.8	11
5	Diet Quality, Food Groups and Nutrients Associated with the Gut Microbiota in a Nonwestern Population. Nutrients, 2020, 12, 2938.	4.1	24
6	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. MSystems, 2019, 4, .	3.8	214
7	Green Coffee Extract Improves Cardiometabolic Parameters and Modulates Gut Microbiota in High-Fat-Diet-Fed ApoE-/- Mice. Nutrients, 2019, 11, 497.	4.1	30
8	Higher Fecal Short-Chain Fatty Acid Levels Are Associated with Gut Microbiome Dysbiosis, Obesity, Hypertension and Cardiometabolic Disease Risk Factors. Nutrients, 2019, 11, 51.	4.1	312
9	Impact of DNA extraction, sample dilution, and reagent contamination on 16S rRNA gene sequencing of human feces. Applied Microbiology and Biotechnology, 2018, 102, 403-411.	3.6	43
10	Body size phenotypes comprehensively assess cardiometabolic risk and refine the association between obesity and gut microbiota. International Journal of Obesity, 2018, 42, 424-432.	3.4	48
11	Gut microbiota is associated with obesity and cardiometabolic disease in a population in the midst of Westernization. Scientific Reports, 2018, 8, 11356.	3.3	82
12	Selfâ€fertilization, longâ€distance flash invasion and biogeography shape the population structure of <i>Pseudosuccinea columella</i> at the worldwide scale. Molecular Ecology, 2017, 26, 887-903.	3.9	40
13	Metformin Is Associated With Higher Relative Abundance of Mucin-Degrading <i>Akkermansia muciniphila</i> and Several Short-Chain Fatty Acid–Producing Microbiota in the Gut. Diabetes Care, 2017, 40, 54-62.	8.6	521
14	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. Frontiers in Nutrition, 2016, 3, 26.	3.7	40
15	Molecular Evolution of Freshwater Snails with Contrasting Mating Systems. Molecular Biology and Evolution, 2015, 32, 2403-2416.	8.9	54
16	The gut microbiota of Colombians differs from that of Americans, Europeans and Asians. BMC Microbiology, 2014, 14, 311.	3.3	178
17	The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nature Genetics, 2013, 45, 831-835.	21.4	374
18	COMPARATIVE POPULATION GENOMICS INCOLLINSIASISTER SPECIES REVEALS EVIDENCE FOR REDUCED EFFECTIVE POPULATION SIZE, RELAXED SELECTION, AND EVOLUTION OF BIASED GENE CONVERSION WITH AN ONGOING MATING SYSTEM SHIFT. Evolution; International Journal of Organic Evolution, 2012, 67, no-no.	2.3	36

#	Article	IF	CITATIONS
19	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). BMC Evolutionary Biology, 2011, 11, 181.	3.2	72
20	PATTERNS OF MATINGâ€SYSTEM EVOLUTION IN HERMAPHRODITIC ANIMALS: CORRELATIONS AMONG SELFING RATE, INBREEDING DEPRESSION, AND THE TIMING OF REPRODUCTION. Evolution; International Journal of Organic Evolution, 2011, 65, 1233-1253.	2.3	123
21	Morphological and molecular characterization of Neotropic Lymnaeidae (Gastropoda: Lymnaeoidea), vectors of fasciolosis. Infection, Genetics and Evolution, 2011, 11, 1978-1988.	2.3	72
22	GC-Biased Gene Conversion Impacts Ribosomal DNA Evolution in Vertebrates, Angiosperms, and Other Eukaryotes. Molecular Biology and Evolution, 2011, 28, 2561-2575.	8.9	53
23	GC-Biased Gene Conversion and Selection Affect GC Content in the Oryza Genus (rice). Molecular Biology and Evolution, 2011, 28, 2695-2706.	8.9	83
24	Bridging gaps in the molecular phylogeny of the Lymnaeidae (Gastropoda: Pulmonata), vectors of Fascioliasis. BMC Evolutionary Biology, 2010, 10, 381.	3.2	123
25	AN INTEGRATIVE TEST OF THE DEAD-END HYPOTHESIS OF SELFING EVOLUTION IN TRITICEAE (POACEAE). Evolution; International Journal of Organic Evolution, 2010, 64, no-no.	2.3	69
26	CORRELATED EVOLUTION OF MATING STRATEGY AND INBREEDING DEPRESSION WITHIN AND AMONG POPULATIONS OF THE HERMAPHRODITIC SNAILPHYSA ACUTA. Evolution; International Journal of Organic Evolution, 2009, 63, 2790-2804.	2.3	27
27	Did life history evolve in response to parasites in invasive populations of Melanoides tuberculata?. Acta Oecologica, 2009, 35, 639-644.	1.1	3
28	Outbreeding Alleviates Senescence in Hermaphroditic Snails as Expected from the Mutation-Accumulation Theory. Current Biology, 2008, 18, 906-910.	3.9	59
29	The Different Sources of Variation in Inbreeding Depression, Heterosis and Outbreeding Depression in a Metapopulation of <i>Physa acuta</i> . Genetics, 2008, 180, 1593-1608.	2.9	115
30	NO CORRELATION BETWEEN INBREEDING DEPRESSION AND DELAYED SELFING IN THE FRESHWATER SNAIL PHYSA ACUTA. Evolution; International Journal of Organic Evolution, 2007, 61, 2655-2670.	2.3	33