

Luis Pedro Coelho

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

13,938
citations

109321

35
h-index

189892

50
g-index

66
all docs

66
docs citations

66
times ranked

20816
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	8.9	2,156
2	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	12.6	2,137
3	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	27.8	1,370
4	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. Nature Medicine, 2019, 25, 679-689.	30.7	734
5	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	27.8	670
6	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
7	Towards standards for human fecal sample processing in metagenomic studies. Nature Biotechnology, 2017, 35, 1069-1076.	17.5	581
8	Recovery of gut microbiota of healthy adults following antibiotic exposure. Nature Microbiology, 2018, 3, 1255-1265.	13.3	483
9	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	19.0	442
10	Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. Genome Medicine, 2017, 9, 39.	8.2	420
11	Extensive transmission of microbes along the gastrointestinal tract. ELife, 2019, 8, .	6.0	313
12	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	12.8	298
13	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	27.8	283
14	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	28.9	271
15	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	28.9	268
16	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
17	Host-cell sensors for Plasmodium activate innate immunity against liver-stage infection. Nature Medicine, 2014, 20, 47-53.	30.7	256
18	Selective maternal seeding and environment shape the human gut microbiome. Genome Research, 2018, 28, 561-568.	5.5	247

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19	Similarity of the dog and human gut microbiomes in gene content and response to diet. Microbiome, 2018, 6, 72.	11.1	211
20	MOCAT2: a metagenomic assembly, annotation and profiling framework. Bioinformatics, 2016, 32, 2520-2523.	4.1	172
21	Nuclear segmentation in microscope cell images: A hand-segmented dataset and comparison of algorithms. , 2009, 5193098, 518-521.		138
22	Automated Image Analysis for High-Content Screening and Analysis. Journal of Biomolecular Screening, 2010, 15, 726-734.	2.6	117
23	Subspecies in the global human gut microbiome. Molecular Systems Biology, 2017, 13, 960.	7.2	115
24	Combinatorial, additive and dose-dependent drug-microbiome associations. Nature, 2021, 600, 500-505.	27.8	102
25	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	30.7	102
26	GUNC: detection of chimerism and contamination in prokaryotic genomes. Genome Biology, 2021, 22, 178.	8.8	94
27	metaSNV: A tool for metagenomic strain level analysis. PLoS ONE, 2017, 12, e0182392.	2.5	92
28	Towards the biogeography of prokaryotic genes. Nature, 2022, 601, 252-256.	27.8	85
29	Metagenomic insights into the human gut resistome and the forces that shape it. BioEssays, 2014, 36, 316-329.	2.5	76
30	Community-level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	4.9	76
31	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. ISME Journal, 2020, 14, 1247-1259.	9.8	74
32	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	14.5	60
33	Determining the subcellular location of new proteins from microscope images using local features. Bioinformatics, 2013, 29, 2343-2349.	4.1	59
34	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. Gut, 2022, 71, 2463-2480.	12.1	53
35	A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments. Nature Communications, 2022, 13, 2326.	12.8	47
36	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. ELife, 2017, 6, .	6.0	45

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37	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. Microbiome, 2019, 7, 84.	11.1	42
38	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. Environmental Microbiology, 2021, 23, 316-326.	3.8	42
39	Quantifying the distribution of probes between subcellular locations using unsupervised pattern unmixing. Bioinformatics, 2010, 26, i7-i12.	4.1	39
40	Macrel: antimicrobial peptide screening in genomes and metagenomes. PeerJ, 2020, 8, e10555.	2.0	37
41	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. Nucleic Acids Research, 2022, 50, 3155-3168.	14.5	34
42	Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature. Lecture Notes in Computer Science, 2010, , 23-32.	1.3	26
43	Automatic determination of NET (neutrophil extracellular traps) coverage in fluorescent microscopy images. Bioinformatics, 2015, 31, 2364-2370.	4.1	26
44	Jug: Software for Parallel Reproducible Computation in Python. Journal of Open Research Software, 2017, 5, 30.	5.9	24
45	T rypanosoma brucei histone H 1 inhibits RNA polymerase I transcription and is important for parasite fitness in vivo. Molecular Microbiology, 2014, 93, 645-663.	2.5	23
46	Gene expression changes in the salivary glands of Anopheles coluzzii elicited by Plasmodium berghei infection. Parasites and Vectors, 2015, 8, 485.	2.5	17
47	Structured literature image finder: Parsing text and figures in biomedical literature. Web Semantics, 2010, 8, 151-154.	2.9	14
48	An Adaptive Multiresolution Approach to Fingerprint Recognition. Proceedings International Conference on Image Processing, 2007, , .	0.0	11
49	Principles of Bioimage Informatics: Focus on Machine Learning of Cell Patterns. Lecture Notes in Computer Science, 2010, , 8-18.	1.3	8
50	Cell cycle dependence of protein subcellular location inferred from static, asynchronous images. , 2009, 2009, 1016-9.		4
51	Structured Literature Image Finder: Parsing Text and Figures in Biomedical Literature. SSRN Electronic Journal, 0, , .	0.4	1
52	Identifying Subcellular Locations from Images of Unknown Resolution. Communications in Computer and Information Science, 2008, , 235-242.	0.5	1
53	Software testing in microbial bioinformatics: a call to action. Microbial Genomics, 2022, 8, .	2.0	1
54	Voices of the new generation: science in a state of benign confusion. Nature Reviews Molecular Cell Biology, 2020, 21, 560-560.	37.0	0