

Luis Pedro Coelho

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

13,938
citations

109137

35
h-index

189595

50
g-index

66
all docs

66
docs citations

66
times ranked

20816
citing authors

#	ARTICLE	IF	CITATIONS
1	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. <i>Gut</i> , 2022, 71, 2463-2480.	6.1	53
2	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
3	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	15.2	102
4	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	6.5	34
5	Software testing in microbial bioinformatics: a call to action. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
6	A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments. <i>Nature Communications</i> , 2022, 13, 2326.	5.8	47
7	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	1.8	42
8	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021, 22, 178.	3.8	94
9	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	13.7	102
10	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, D621-D625.	6.5	60
11	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
12	Voices of the new generation: science in a state of benign confusion. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 560-560.	16.1	0
13	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
14	Macrel: antimicrobial peptide screening in genomes and metagenomes. <i>PeerJ</i> , 2020, 8, e10555.	0.9	37
15	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
16	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
17	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. <i>Microbiome</i> , 2019, 7, 84.	4.9	42
18	Community-level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76

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19	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
20	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
21	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	2.8	313
22	Selective maternal seeding and environment shape the human gut microbiome. <i>Genome Research</i> , 2018, 28, 561-568.	2.4	247
23	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	5.9	483
24	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	13.7	1,370
25	Similarity of the dog and human gut microbiomes in gene content and response to diet. <i>Microbiome</i> , 2018, 6, 72.	4.9	211
26	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	3.5	2,156
27	Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. <i>Genome Medicine</i> , 2017, 9, 39.	3.6	420
28	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
29	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	3.2	115
30	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , 2017, 12, e0182392.	1.1	92
31	Jug: Software for Parallel Reproducible Computation in Python. <i>Journal of Open Research Software</i> , 2017, 5, 30.	2.7	24
32	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. <i>ELife</i> , 2017, 6, .	2.8	45
33	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	1.8	172
34	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
35	Gene expression changes in the salivary glands of <i>Anopheles coluzzii</i> elicited by <i>Plasmodium berghei</i> infection. <i>Parasites and Vectors</i> , 2015, 8, 485.	1.0	17
36	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137

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37	Automatic determination of NET (neutrophil extracellular traps) coverage in fluorescent microscopy images. <i>Bioinformatics</i> , 2015, 31, 2364-2370.	1.8	26
38	Metagenomic insights into the human gut resistome and the forces that shape it. <i>BioEssays</i> , 2014, 36, 316-329.	1.2	76
39	Host-cell sensors for <i>Plasmodium</i> activate innate immunity against liver-stage infection. <i>Nature Medicine</i> , 2014, 20, 47-53.	15.2	256
40	A community computational challenge to predict the activity of pairs of compounds. <i>Nature Biotechnology</i> , 2014, 32, 1213-1222.	9.4	264
41	A community effort to assess and improve drug sensitivity prediction algorithms. <i>Nature Biotechnology</i> , 2014, 32, 1202-1212.	9.4	653
42	T <i>trypanosoma brucei</i> histone H 1 inhibits RNA polymerase I transcription and is important for parasite fitness in vivo. <i>Molecular Microbiology</i> , 2014, 93, 645-663.	1.2	23
43	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
44	Determining the subcellular location of new proteins from microscope images using local features. <i>Bioinformatics</i> , 2013, 29, 2343-2349.	1.8	59
45	Structured literature image finder: Parsing text and figures in biomedical literature. <i>Web Semantics</i> , 2010, 8, 151-154.	2.2	14
46	Quantifying the distribution of probes between subcellular locations using unsupervised pattern unmixing. <i>Bioinformatics</i> , 2010, 26, i7-i12.	1.8	39
47	Principles of Bioimage Informatics: Focus on Machine Learning of Cell Patterns. <i>Lecture Notes in Computer Science</i> , 2010, , 8-18.	1.0	8
48	Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature. <i>Lecture Notes in Computer Science</i> , 2010, , 23-32.	1.0	26
49	Automated Image Analysis for High-Content Screening and Analysis. <i>Journal of Biomolecular Screening</i> , 2010, 15, 726-734.	2.6	117
50	Nuclear segmentation in microscope cell images: A hand-segmented dataset and comparison of algorithms. , 2009, 5193098, 518-521.		138
51	Cell cycle dependence of protein subcellular location inferred from static, asynchronous images. , 2009, 2009, 1016-9.		4
52	Identifying Subcellular Locations from Images of Unknown Resolution. <i>Communications in Computer and Information Science</i> , 2008, , 235-242.	0.4	1
53	An Adaptive Multiresolution Approach to Fingerprint Recognition. <i>Proceedings International Conference on Image Processing</i> , 2007, , .	0.0	11
54	Structured Literature Image Finder: Parsing Text and Figures in Biomedical Literature. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1