

Luis Pedro Coelho

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56
papers

7,407
citations

28
h-index

66
g-index

66
ext. papers

11,158
ext. citations

19.5
avg, IF

5.56
L-index

#	Paper	IF	Citations
56	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 ,	19.2	5
55	Microbiome and metabolome features of the cardiometabolic disease spectrum.. <i>Nature Medicine</i> , 2022 ,	50.5	4
54	A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments.. <i>Nature Communications</i> , 2022 , 13, 2326	17.4	4
53	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021 ,	50.4	11
52	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , 2021 ,	50.4	8
51	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021 , 22, 178	18.3	16
50	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021 , 23, 316-326	5.2	9
49	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020 , 581, 310-315	50.4	100
48	Voices of the new generation: science in a state of benign confusion. <i>Nature Reviews Molecular Cell Biology</i> , 2020 , 21, 560	48.7	
47	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020 , 14, 1247-1259	11.9	23
46	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	20.1	21
45	Macrel: antimicrobial peptide screening in genomes and metagenomes. <i>PeerJ</i> , 2020 , 8, e10555	3.1	8
44	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. <i>Microbiome</i> , 2019 , 7, 84	16.6	15
43	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019 , 33, 391-419	5.9	42
42	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
41	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019 , 25, 679-689	50.5	353
40	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019 , 179, 1068-1083.e21	56.2	113

39	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019 , 179, 1084-1097.e21	56.2	108
38	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019 , 8,	8.9	158
37	Selective maternal seeding and environment shape the human gut microbiome. <i>Genome Research</i> , 2018 , 28, 561-568	9.7	148
36	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018 , 560, 233-237	50.4	654
35	Similarity of the dog and human gut microbiomes in gene content and response to diet. <i>Microbiome</i> , 2018 , 6, 72	16.6	117
34	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018 , 3, 1255-1265	26.6	246
33	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2115-2122	8.3	966
32	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	14.4	274
31	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355
30	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , 2017 , 12, e0182392	3.7	64
29	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017 , 13, 960	12.2	69
28	Jug: Software for Parallel Reproducible Computation in Python. <i>Journal of Open Research Software</i> , 2017 , 5,	2.3	14
27	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. <i>ELife</i> , 2017 , 6,	8.9	20
26	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016 , 532, 465-470	50.4	392
25	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016 , 32, 2520-3.2	3.2	117
24	Automatic determination of NET (neutrophil extracellular traps) coverage in fluorescent microscopy images. <i>Bioinformatics</i> , 2015 , 31, 2364-70	7.2	13
23	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	4	13
22	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359	33.3	1261

21	Metagenomic insights into the human gut resistome and the forces that shape it. <i>BioEssays</i> , 2014 , 36, 316-29	4.1	57
20	Host-cell sensors for Plasmodium activate innate immunity against liver-stage infection. <i>Nature Medicine</i> , 2014 , 20, 47-53	50.5	186
19	A community computational challenge to predict the activity of pairs of compounds. <i>Nature Biotechnology</i> , 2014 , 32, 1213-22	44.5	184
18	A community effort to assess and improve drug sensitivity prediction algorithms. <i>Nature Biotechnology</i> , 2014 , 32, 1202-12	44.5	447
17	Trypanosoma brucei histone H1 inhibits RNA polymerase I transcription and is important for parasite fitness in vivo. <i>Molecular Microbiology</i> , 2014 , 93, 645-63	4.1	21
16	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
15	Determining the subcellular location of new proteins from microscope images using local features. <i>Bioinformatics</i> , 2013 , 29, 2343-9	7.2	44
14	Quantifying the distribution of probes between subcellular locations using unsupervised pattern unmixing. <i>Bioinformatics</i> , 2010 , 26, i7-12	7.2	35
13	Principles of Bioimage Informatics: Focus on Machine Learning of Cell Patterns. <i>Lecture Notes in Computer Science</i> , 2010 , 8-18	0.9	6
12	Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature. <i>Lecture Notes in Computer Science</i> , 2010 , 23-32	0.9	19
11	Automated image analysis for high-content screening and analysis. <i>Journal of Biomolecular Screening</i> , 2010 , 15, 726-34		85
10	Structured Literature Image Finder: Parsing Text and Figures in Biomedical Literature. <i>Web Semantics</i> , 2010 , 8, 151-154	2.9	12
9	NUCLEAR SEGMENTATION IN MICROSCOPE CELL IMAGES: A HAND-SEGMENTED DATASET AND COMPARISON OF ALGORITHMS 2009 , 5193098, 518-521	1.5	97
8	Cell cycle dependence of protein subcellular location inferred from static, asynchronous images. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2009 , 2009, 1016-9	0.9	3
7	Identifying Subcellular Locations from Images of Unknown Resolution. <i>Communications in Computer and Information Science</i> , 2008 , 235-242	0.3	1
6	. <i>Proceedings International Conference on Image Processing</i> , 2007 ,	1.6	6
5	Structured Literature Image Finder: Parsing Text and Figures in Biomedical Literature. <i>SSRN Electronic Journal</i> ,	1	1
4	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language		1

3	GUNC: Detection of Chimerism and Contamination in Prokaryotic Genomes	3
2	metaMIC: reference-free Misassembly Identification and Correction of de novo metagenomic assemblies	1
1	SemiBin: Incorporating information from reference genomes with semi-supervised deep learning leads to better metagenomic assembled genomes (MAGs)	1