Marco Pagni

List of Publications by Year in Descending Order

77 papers	6,563 citations	32 h-index	81 g-index
83 ext. papers	7,582 ext. citations	8.7 avg, IF	5.29 L-index

#	Paper	IF	Citations
77	Candida albicans commensalism in the oral mucosa is favoured by limited virulence and metabolic adaptation.. *PLoS Pathogens*, **2022**, 18, e1010012	7.6	1
76	MetaNetX/MNXref: unified namespace for metabolites and biochemical reactions in the context of metabolic models. *Nucleic Acids Research*, **2021**, 49, D570-D574	20.1	26
75	Predicting spatial patterns of soil bacteria under current and future environmental conditions. *ISME Journal*, **2021**, 15, 2547-2560	11.9	4
74	Anti-adipogenic signals at the onset of obesity-related inflammation in white adipose tissue. *Cellular and Molecular Life Sciences*, **2021**, 78, 227-247	10.3	12
73	Expression Pattern of the Pneumocystis jirovecii Major Surface Glycoprotein Superfamily in Patients with Pneumonia. *Journal of Infectious Diseases*, **2021**, 223, 310-318	7	1
72	Vacuolins and myosin VII are required for phagocytic uptake and phagosomal membrane recycling in. *Journal of Cell Science*, **2020**, 133,	5.3	1
71	Identification of Anti- and Anti- Compounds With Potential Distinctive Structural Scaffolds From an HD-PBL Using Phenotypic Screens in Amoebae Host Models. *Frontiers in Microbiology*, **2020**, 11, 266	5.7	4
70	Transcriptional Responses of Exposed to Different Classes of Bacteria. *Frontiers in Microbiology*, **2020**, 11, 410	5.7	5
69	New genome assembly of the barn owl (). *Ecology and Evolution*, **2020**, 10, 2284-2298	2.8	1
68	Greater topoclimatic control of above- versus below-ground communities. *Global Change Biology*, **2020**, 26, 6715-6728	11.4	3
67	Organic substrate diffusibility governs microbial community composition, nutrient removal performance and kinetics of granulation of aerobic granular sludge. *Water Research X*, **2019**, 4, 100033	8.1	46
66	Persistence of in the Oral Mucosa Induces a Curbed Inflammatory Host Response That Is Independent of Immunosuppression. *Frontiers in Immunology*, **2019**, 10, 330	8.4	25
65	Investigating unexplained genetic variation and its expression in the arbuscular mycorrhizal fungus Rhizophagus irregularis: A comparison of whole genome and RAD sequencing data. *PLoS ONE*, **2019**, 14, e0226497	3.7	7
64	Inferring gene expression networks with hubs using a degree weighted Lasso approach. *Bioinformatics*, **2019**, 35, 987-994	7.2	8
63	Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis. *Bioinformatics*, **2019**, 35, 2258-2266	7.2	7
62	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen. *MBio*, **2018**, 9,	7.8	19
61	A systems genetics resource and analysis of sleep regulation in the mouse. *PLoS Biology*, **2018**, 16, e2005750	7.5	26

60	A new species of genus Eulimnadia Packard, 1874 (Branchiopoda: Spinicaudata: Limnadiidae) from India with an updated key for some Indian species. *Zootaxa*, **2018**, 4399, 341-350	0.5	4
59	Vps13F links bacterial recognition and intracellular killing in Dictyostelium. *Cellular Microbiology*, **2017**, 19, e12722	3.9	23
58	Mechanisms of Surface Antigenic Variation in the Human Pathogenic Fungus. *MBio*, **2017**, 8,	7.8	19
57	Low number of fixed somatic mutations in a long-lived oak tree. *Nature Plants*, **2017**, 3, 926-929	11.5	74
56	Identification and Functional Ascertainment of the Pneumocystis jirovecii Potential Drug Targets Gsc1 and Kre6 Involved in Glucan Synthesis. *Journal of Eukaryotic Microbiology*, **2017**, 64, 481-490	3.6	5
55	Low rate of somatic mutations in a long-lived oak tree **2017**,		5
54	Updates in Rhea - an expert curated resource of biochemical reactions. *Nucleic Acids Research*, **2017** , 45, D415-D418	20.1	46
53	Population genomics reveals that within-fungus polymorphism is common and maintained in populations of the mycorrhizal fungus Rhizophagus irregularis. *ISME Journal*, **2016**, 10, 2514-26	11.9	41
52	MetaNetX/MNXref--reconciliation of metabolites and biochemical reactions to bring together genome-scale metabolic networks. *Nucleic Acids Research*, **2016**, 44, D523-6	20.1	116
51	The SIB Swiss Institute of BioinformaticsSresources: focus on curated databases. *Nucleic Acids Research*, **2016**, 44, D27-37	20.1	41
50	The salivary microbiome for differentiating individuals: proof of principle. *Microbes and Infection*, **2016**, 18, 399-405	9.3	52
49	RNA Sequencing-Based Genome Reannotation of the Dermatophyte and Characterization of Its Secretome and Whole Gene Expression Profile during Infection. *MSystems*, **2016**, 1,	7.6	23
48	RNA Enrichment Method for Quantitative Transcriptional Analysis of Pathogens In Vivo Applied to the Fungus Candida albicans. *MBio*, **2015**, 6, e00942-15	7.8	43
47	Comparative genomics suggests primary homothallism of Pneumocystis species. *MBio*, **2015**, 6,	7.8	32
46	Functional characterization of the Pneumocystis jirovecii potential drug targets dhfs and abz2 involved in folate biosynthesis. *Antimicrobial Agents and Chemotherapy*, **2015**, 59, 2560-6	5.9	4
45	Soil fungal communities of grasslands are environmentally structured at a regional scale in the Alps. *Molecular Ecology*, **2014**, 23, 4274-90	5.7	85
44	Microbiota present in cystic fibrosis lungs as revealed by whole genome sequencing. *PLoS ONE*, **2014**, 9, e90934	3.7	31
43	Reconciliation of metabolites and biochemical reactions for metabolic networks. *Briefings in Bioinformatics*, **2014**, 15, 123-35	13.4	49

42	Comparative genomics suggests that the human pathogenic fungus Pneumocystis jirovecii acquired obligate biotrophy through gene loss. *Genome Biology and Evolution*, **2014**, 6, 1938-48	3.9	38
41	Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 20117-22	11.5	499
40	MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. *Bioinformatics*, **2013**, 29, 815-6	7.2	73
39	Genome sequencing of the plant pathogen Taphrina deformans, the causal agent of peach leaf curl. *MBio*, **2013**, 4, e00055-13	7.8	58
38	pfsearchV3: a code acceleration and heuristic to search PROSITE profiles. *Bioinformatics*, **2013**, 29, 1215-7	7.2	10
37	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. *Frontiers in Plant Science*, **2013**, 4, 500	6.2	29
36	Density-based hierarchical clustering of pyro-sequences on a large scale--the case of fungal ITS1. *Bioinformatics*, **2013**, 29, 1268-74	7.2	14
35	De novo assembly of the Pneumocystis jirovecii genome from a single bronchoalveolar lavage fluid specimen from a patient. *MBio*, **2012**, 4, e00428-12	7.8	76
34	Complete genome sequence of the dog commensal and human pathogen Capnocytophaga canimorsus strain 5. *Journal of Bacteriology*, **2011**, 193, 5558-9	3.5	18
33	A Preliminary Study on the Prediction of Human Protein Functions. *Lecture Notes in Computer Science*, **2011**, 334-343	0.9	1
32	Comparative genomics suggests that the fungal pathogen pneumocystis is an obligate parasite scavenging amino acids from its host's lungs. *PLoS ONE*, **2010**, 5, e15152	3.7	38
31	Methylobacterium genome sequences: a reference blueprint to investigate microbial metabolism of C1 compounds from natural and industrial sources. *PLoS ONE*, **2009**, 4, e5584	3.7	172
30	The Microbe browser for comparative genomics. *Nucleic Acids Research*, **2009**, 37, W296-9	20.1	3
29	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. *Journal of Applied Crystallography*, **2009**, 42, 376-384	3.8	157
28	A Multi-protocol Bioinformatics Web Service: Use SOAP, Take a REST or Go with HTML **2008**,		1
27	Experience using web services for biological sequence analysis. *Briefings in Bioinformatics*, **2008**, 9, 493-505	9.4	22
26	HitKeeper, a generic software package for hit list management. *Source Code for Biology and Medicine*, **2007**, 2, 2	1.9	9
25	MyHits: improvements to an interactive resource for analyzing protein sequences. *Nucleic Acids Research*, **2007**, 35, W433-7	20.1	153

24	A downstream mediator in the growth repression limb of the jasmonate pathway. *Plant Cell*, **2007**, 19, 2470-83	11.6	491
23	Grid Approach to Embarrassingly Parallel CPU-Intensive Bioinformatics Problems **2006**,		9
22	The PROSITE database. *Nucleic Acids Research*, **2006**, 34, D227-30	20.1	649
21	InterPro, progress and status in 2005. *Nucleic Acids Research*, **2005**, 33, D201-5	20.1	426
20	JACOP: a simple and robust method for the automated classification of protein sequences with modular architecture. *BMC Bioinformatics*, **2005**, 6, 216	3.6	19
19	trome, trEST and trGEN: databases of predicted protein sequences. *Nucleic Acids Research*, **2004**, 32, D509-11	20.1	16
18	MyHits: a new interactive resource for protein annotation and domain identification. *Nucleic Acids Research*, **2004**, 32, W332-5	20.1	76
17	Automated annotation of microbial proteomes in SWISS-PROT. *Computational Biology and Chemistry*, **2003**, 27, 49-58	3.6	112
16	Swiss EMBnet node web server. *Nucleic Acids Research*, **2003**, 31, 3782-3	20.1	10
15	The InterPro Database, 2003 brings increased coverage and new features. *Nucleic Acids Research*, **2003**, 31, 315-8	20.1	556
14	The elusive roles of bacterial glutathione S-transferases: new lessons from genomes. *Applied Microbiology and Biotechnology*, **2002**, 58, 138-46	5.7	114
13	PROSITE: a documented database using patterns and profiles as motif descriptors. *Briefings in Bioinformatics*, **2002**, 3, 265-74	13.4	676
12	The PROSITE database, its status in 2002. *Nucleic Acids Research*, **2002**, 30, 235-8	20.1	787
11	InterPro: an integrated documentation resource for protein families, domains and functional sites. *Briefings in Bioinformatics*, **2002**, 3, 225-35	13.4	137
10	Making sense of score statistics for sequence alignments. *Briefings in Bioinformatics*, **2001**, 2, 51-67	13.4	32
9	Teichuronic acid operon of Bacillus subtilis 168. *Molecular Microbiology*, **1999**, 31, 795-805	4.1	66
8	Bacillus subtilis 168 gene lytF encodes a gamma-D-glutamate-meso-diaminopimelate muropeptidase expressed by the alternative vegetative sigma factor, sigmaD. *Microbiology (United Kingdom)*, **1999**, 145 (Pt 1), 57-65	2.9	99
7	Assay for UDPglucose 6-dehydrogenase in phosphate-starved cells: gene tuaD of Bacillus subtilis 168 encodes the UDPglucose 6-dehydrogenase involved in teichuronic acid synthesis. *Microbiology (United Kingdom)*, **1999**, 145 (Pt 5), 1049-1053	2.9	13

6	Genetic and physical maps of the Bacillus subtilis chromosome. *Genetics*, **1999**, 151, 1239-44	4	3
5	The relationship between kinetics of substrate-limited transitions and steady-state growth in continuous cultures of Aquaspirillum autotrophicum limited by pyruvate. *Antonie Van Leeuwenhoek*, **1995**, 68, 181-9	2.1	2
4	Specific labeling of diaminopimelate: a radioassay for the determination of the peptidoglycan cross-linking index. *Analytical Biochemistry*, **1994**, 223, 208-11	3.1	3
3	Investigating unexplained genetic variation and its expression in the arbuscular mycorrhizal fungus Rhizophagus irregularis		1
2	Dictyostelium discoideumflotillin homologues are essential for phagocytosis and participate in plasma membrane recycling and lysosome biogenesis		3
1	Time-resolved RNA-seq profiling of the infection of Dictyostelium discoideum by Mycobacterium marinum reveals an integrated host response to damage and stress		3