Marco Pagni

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77 6,563 32 81 g-index

83 7,582 8.7 5.29 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
77	The PROSITE database, its status in 2002. <i>Nucleic Acids Research</i> , 2002 , 30, 235-8	20.1	787
76	PROSITE: a documented database using patterns and profiles as motif descriptors. <i>Briefings in Bioinformatics</i> , 2002 , 3, 265-74	13.4	676
75	The PROSITE database. <i>Nucleic Acids Research</i> , 2006 , 34, D227-30	20.1	649
74	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
73	Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20117-22	11.5	499
72	A downstream mediator in the growth repression limb of the jasmonate pathway. <i>Plant Cell</i> , 2007 , 19, 2470-83	11.6	491
71	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5	20.1	426
70	Methylobacterium genome sequences: a reference blueprint to investigate microbial metabolism of C1 compounds from natural and industrial sources. <i>PLoS ONE</i> , 2009 , 4, e5584	3.7	172
69	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. <i>Journal of Applied Crystallography</i> , 2009 , 42, 376-384	3.8	157
68	MyHits: improvements to an interactive resource for analyzing protein sequences. <i>Nucleic Acids Research</i> , 2007 , 35, W433-7	20.1	153
67	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002 , 3, 225-35	13.4	137
66	MetaNetX/MNXrefreconciliation of metabolites and biochemical reactions to bring together genome-scale metabolic networks. <i>Nucleic Acids Research</i> , 2016 , 44, D523-6	20.1	116
65	The elusive roles of bacterial glutathione S-transferases: new lessons from genomes. <i>Applied Microbiology and Biotechnology</i> , 2002 , 58, 138-46	5.7	114
64	Automated annotation of microbial proteomes in SWISS-PROT. <i>Computational Biology and Chemistry</i> , 2003 , 27, 49-58	3.6	112
63	Bacillus subtilis 168 gene lytF encodes a gamma-D-glutamate-meso-diaminopimelate muropeptidase expressed by the alternative vegetative sigma factor, sigmaD. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 1), 57-65	2.9	99
62	Soil fungal communities of grasslands are environmentally structured at a regional scale in the Alps. <i>Molecular Ecology</i> , 2014 , 23, 4274-90	5.7	85
61	De novo assembly of the Pneumocystis jirovecii genome from a single bronchoalveolar lavage fluid specimen from a patient. <i>MBio</i> , 2012 , 4, e00428-12	7.8	76

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60	MyHits: a new interactive resource for protein annotation and domain identification. <i>Nucleic Acids Research</i> , 2004 , 32, W332-5	20.1	76
59	Low number of fixed somatic mutations in a long-lived oak tree. <i>Nature Plants</i> , 2017 , 3, 926-929	11.5	74
58	MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. <i>Bioinformatics</i> , 2013 , 29, 815-6	7.2	73
57	Teichuronic acid operon of Bacillus subtilis 168. <i>Molecular Microbiology</i> , 1999 , 31, 795-805	4.1	66
56	Genome sequencing of the plant pathogen Taphrina deformans, the causal agent of peach leaf curl. <i>MBio</i> , 2013 , 4, e00055-13	7.8	58
55	The salivary microbiome for differentiating individuals: proof of principle. <i>Microbes and Infection</i> , 2016 , 18, 399-405	9.3	52
54	Reconciliation of metabolites and biochemical reactions for metabolic networks. <i>Briefings in Bioinformatics</i> , 2014 , 15, 123-35	13.4	49
53	Organic substrate diffusibility governs microbial community composition, nutrient removal performance and kinetics of granulation of aerobic granular sludge. <i>Water Research X</i> , 2019 , 4, 100033	8.1	46
52	Updates in Rhea - an expert curated resource of biochemical reactions. <i>Nucleic Acids Research</i> , 2017 , 45, D415-D418	20.1	46
51	RNA Enrichment Method for Quantitative Transcriptional Analysis of Pathogens In Vivo Applied to the Fungus Candida albicans. <i>MBio</i> , 2015 , 6, e00942-15	7.8	43
50	Population genomics reveals that within-fungus polymorphism is common and maintained in populations of the mycorrhizal fungus Rhizophagus irregularis. <i>ISME Journal</i> , 2016 , 10, 2514-26	11.9	41
49	The SIB Swiss Institute of BioinformaticsSresources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
48	Comparative genomics suggests that the human pathogenic fungus Pneumocystis jirovecii acquired obligate biotrophy through gene loss. <i>Genome Biology and Evolution</i> , 2014 , 6, 1938-48	3.9	38
47	Comparative genomics suggests that the fungal pathogen pneumocystis is an obligate parasite scavenging amino acids from its host's lungs. <i>PLoS ONE</i> , 2010 , 5, e15152	3.7	38
46	Comparative genomics suggests primary homothallism of Pneumocystis species. <i>MBio</i> , 2015 , 6,	7.8	32
45	Making sense of score statistics for sequence alignments. <i>Briefings in Bioinformatics</i> , 2001 , 2, 51-67	13.4	32
44	Microbiota present in cystic fibrosis lungs as revealed by whole genome sequencing. <i>PLoS ONE</i> , 2014 , 9, e90934	3.7	31
43	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. <i>Frontiers in Plant Science</i> , 2013 , 4, 500	6.2	29

42	A systems genetics resource and analysis of sleep regulation in the mouse. <i>PLoS Biology</i> , 2018 , 16, e200	557.50	26
41	MetaNetX/MNXref: unified namespace for metabolites and biochemical reactions in the context of metabolic models. <i>Nucleic Acids Research</i> , 2021 , 49, D570-D574	20.1	26
40	Persistence of in the Oral Mucosa Induces a Curbed Inflammatory Host Response That Is Independent of Immunosuppression. <i>Frontiers in Immunology</i> , 2019 , 10, 330	8.4	25
39	Vps13F links bacterial recognition and intracellular killing in Dictyostelium. <i>Cellular Microbiology</i> , 2017 , 19, e12722	3.9	23
38	RNA Sequencing-Based Genome Reannotation of the Dermatophyte and Characterization of Its Secretome and Whole Gene Expression Profile during Infection. <i>MSystems</i> , 2016 , 1,	7.6	23
37	Experience using web services for biological sequence analysis. <i>Briefings in Bioinformatics</i> , 2008 , 9, 493-	5054	22
36	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen. MBio, 2018, 9,	7.8	19
35	Mechanisms of Surface Antigenic Variation in the Human Pathogenic Fungus. MBio, 2017, 8,	7.8	19
34	JACOP: a simple and robust method for the automated classification of protein sequences with modular architecture. <i>BMC Bioinformatics</i> , 2005 , 6, 216	3.6	19
33	Complete genome sequence of the dog commensal and human pathogen Capnocytophaga canimorsus strain 5. <i>Journal of Bacteriology</i> , 2011 , 193, 5558-9	3.5	18
32	trome, trEST and trGEN: databases of predicted protein sequences. <i>Nucleic Acids Research</i> , 2004 , 32, D509-11	20.1	16
31	Density-based hierarchical clustering of pyro-sequences on a large scalethe case of fungal ITS1. <i>Bioinformatics</i> , 2013 , 29, 1268-74	7.2	14
30	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. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 5), 1049-1053	2.9	13
29	Anti-adipogenic signals at the onset of obesity-related inflammation in white adipose tissue. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 227-247	10.3	12
28	pfsearchV3: a code acceleration and heuristic to search PROSITE profiles. <i>Bioinformatics</i> , 2013 , 29, 1215	- 7 .2	10
27	Swiss EMBnet node web server. <i>Nucleic Acids Research</i> , 2003 , 31, 3782-3	20.1	10
26	HitKeeper, a generic software package for hit list management. <i>Source Code for Biology and Medicine</i> , 2007 , 2, 2	1.9	9
25	Grid Approach to Embarrassingly Parallel CPU-Intensive Bioinformatics Problems 2006,		9

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24	Inferring gene expression networks with hubs using a degree weighted Lasso approach. <i>Bioinformatics</i> , 2019 , 35, 987-994	7.2	8
23	Investigating unexplained genetic variation and its expression in the arbuscular mycorrhizal fungus Rhizophagus irregularis: A comparison of whole genome and RAD sequencing data. <i>PLoS ONE</i> , 2019 , 14, e0226497	3.7	7
22	Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis. <i>Bioinformatics</i> , 2019 , 35, 2258-2266	7.2	7
21	Transcriptional Responses of Exposed to Different Classes of Bacteria. <i>Frontiers in Microbiology</i> , 2020 , 11, 410	5.7	5
20	Identification and Functional Ascertainment of the Pneumocystis jirovecii Potential Drug Targets Gsc1 and Kre6 Involved in Glucan Synthesis. <i>Journal of Eukaryotic Microbiology</i> , 2017 , 64, 481-490	3.6	5
19	Low rate of somatic mutations in a long-lived oak tree 2017,		5
18	Identification of Anti- and Anti- Compounds With Potential Distinctive Structural Scaffolds From an HD-PBL Using Phenotypic Screens in Amoebae Host Models. <i>Frontiers in Microbiology</i> , 2020 , 11, 266	5.7	4
17	Functional characterization of the Pneumocystis jirovecii potential drug targets dhfs and abz2 involved in folate biosynthesis. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 2560-6	5.9	4
16	Predicting spatial patterns of soil bacteria under current and future environmental conditions. <i>ISME Journal</i> , 2021 , 15, 2547-2560	11.9	4
15	A new species of genus Eulimnadia Packard, 1874 (Branchiopoda: Spinicaudata: Limnadiidae) from India with an updated key for some Indian species. <i>Zootaxa</i> , 2018 , 4399, 341-350	0.5	4
14	The Microbe browser for comparative genomics. <i>Nucleic Acids Research</i> , 2009 , 37, W296-9	20.1	3
13	Specific labeling of diaminopimelate: a radioassay for the determination of the peptidoglycan cross-linking index. <i>Analytical Biochemistry</i> , 1994 , 223, 208-11	3.1	3
12	Dictyostelium discoideumflotillin homologues are essential for phagocytosis and participate in plasma membrane recycling and lysosome biogenesis		3
11	Time-resolved RNA-seq profiling of the infection of Dictyostelium discoideum by Mycobacterium marinum reveals an integrated host response to damage and stress		3
10	Genetic and physical maps of the Bacillus subtilis chromosome. <i>Genetics</i> , 1999 , 151, 1239-44	4	3
9	Greater topoclimatic control of above- versus below-ground communities. <i>Global Change Biology</i> , 2020 , 26, 6715-6728	11.4	3
8	The relationship between kinetics of substrate-limited transitions and steady-state growth in continuous cultures of Aquaspirillum autotrophicum limited by pyruvate. <i>Antonie Van Leeuwenhoek</i> , 1995 , 68, 181-9	2.1	2
7	Vacuolins and myosin VII are required for phagocytic uptake and phagosomal membrane recycling in. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	1

6	New genome assembly of the barn owl (). Ecology and Evolution, 2020, 10, 2284-2298	2.8	1
5	A Multi-protocol Bioinformatics Web Service: Use SOAP, Take a REST or Go with HTML 2008 ,		1
4	Investigating unexplained genetic variation and its expression in the arbuscular mycorrhizal fungus Rhizophagus irregularis		1
3	A Preliminary Study on the Prediction of Human Protein Functions. <i>Lecture Notes in Computer Science</i> , 2011 , 334-343	0.9	1
2	Expression Pattern of the Pneumocystis jirovecii Major Surface Glycoprotein Superfamily in Patients with Pneumonia. <i>Journal of Infectious Diseases</i> , 2021 , 223, 310-318	7	1
1	Candida albicans commensalism in the oral mucosa is favoured by limited virulence and metabolic adaptation <i>PLoS Pathogens</i> , 2022 , 18, e1010012	7.6	1