Guilherme Oliveira

List of Publications by Year in descending order

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210 papers 7,417 citations

76326 40 h-index 76900 74 g-index

219 all docs 219 docs citations

219 times ranked 9117 citing authors

#	Article	IF	CITATIONS
1	The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358.	27.8	945
2	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2012, 6, e1455.	3.0	400
3	Whole-genome sequence of Schistosoma haematobium. Nature Genetics, 2012, 44, 221-225.	21.4	383
4	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. Nature Communications, 2017, 8, 15451.	12.8	216
5	HDAC8: a multifaceted target for therapeutic interventions. Trends in Pharmacological Sciences, 2015, 36, 481-492.	8.7	210
6	Molecular Characterization of an Interleukin-4-inducing Factor from Schistosoma mansoni Eggs. Journal of Biological Chemistry, 2003, 278, 18384-18392.	3.4	160
7	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. Science Advances, 2017, 3, e1700299.	10.3	142
8	Structural Basis for the Inhibition of Histone Deacetylase 8 (HDAC8), a Key Epigenetic Player in the Blood Fluke Schistosoma mansoni. PLoS Pathogens, 2013, 9, e1003645.	4.7	136
9	Medicinal Plants Recommended by the World Health Organization: DNA Barcode Identification Associated with Chemical Analyses Guarantees Their Quality. PLoS ONE, 2015, 10, e0127866.	2.5	130
10	Effectiveness of ITS and sub-regions as DNA barcode markers for the identification of Basidiomycota (Fungi). BMC Microbiology, 2017, 17, 42.	3.3	126
11	PCR-RFLP to identify Leishmania (Viannia) braziliensis and L. (Leishmania) amazonensis causing American cutaneous leishmaniasis. Acta Tropica, 2004, 90, 31-37.	2.0	101
12	Genomic signatures and coâ€occurrence patterns of the ultraâ€small Saccharimonadia (phylum) Tj ETQq0 0 0 rg	gBT ₃ /9verlo	ock 10 Tf 50 3
13	Metagenome of a Microbial Community Inhabiting a Metal-Rich Tropical Stream Sediment. PLoS ONE, 2015, 10, e0119465.	2.5	95
14	A Comparative Chemogenomics Strategy to Predict Potential Drug Targets in the Metazoan Pathogen, Schistosoma mansoni. PLoS ONE, 2009, 4, e4413.	2.5	94
15	Vaginal Microbiome Characterization of Nellore Cattle Using Metagenomic Analysis. PLoS ONE, 2015, 10, e0143294.	2.5	92
16	Eukaryotic Protein Kinases (ePKs) of the Helminth Parasite Schistosoma mansoni. BMC Genomics, 2011, 12, 215.	2.8	90
17	Analysis of the cytokine profile in spleen cells from dogs naturally infected by Leishmania chagasi. Veterinary Immunology and Immunopathology, 2007, 115, 135-145.	1.2	89
18	Assessing the efficiency of multiple sequence alignment programs. Algorithms for Molecular Biology, 2014, 9, 4.	1.2	87

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19	Suppressing Glucose Transporter Gene Expression in Schistosomes Impairs Parasite Feeding and Decreases Survival in the Mammalian Host. PLoS Pathogens, 2010, 6, e1000932.	4.7	78
20	An Immunomics Approach to Schistosome Antigen Discovery: Antibody Signatures of Naturally Resistant and Chronically Infected Individuals from Endemic Areas. PLoS Pathogens, 2014, 10, e1004033.	4.7	78
21	Schistosoma mansoni Sirtuins: Characterization and Potential as Chemotherapeutic Targets. PLoS Neglected Tropical Diseases, 2013, 7, e2428.	3.0	77
22	Signal transduction regulates schistosome reproductive biology. Current Opinion in Microbiology, 2009, 12, 422-428.	5.1	75
23	Regulation of Schistosoma mansoni Development and Reproduction by the Mitogen-Activated Protein Kinase Signaling Pathway. PLoS Neglected Tropical Diseases, 2014, 8, e2949.	3.0	7 3
24	SchistoDB: a Schistosoma mansoni genome resource. Nucleic Acids Research, 2009, 37, D579-D582.	14.5	72
25	Identification of Schistosoma mansoni microRNAs. BMC Genomics, 2011, 12, 47.	2.8	62
26	New Frontiers in <i> Schistosoma < /i > Genomics and Transcriptomics. Journal of Parasitology Research, 2012, 2012, 1-11.</i>	1.2	61
27	The human immune response to defined immunogens of Schistosoma mansoni: elevated antibody levels to paramyosin in stool-negative individuals from two endemic areas in Brazil. Transactions of the Royal Society of Tropical Medicine and Hygiene, 1989, 83, 798-804.	1.8	53
28	Neurological disease in HIV-infected patients in the era of highly active antiretroviral treatment: a Brazilian experience. Revista Da Sociedade Brasileira De Medicina Tropical, 2006, 39, 146-151.	0.9	52
29	Helminth secretomes reflect different lifestyles and parasitized hosts. International Journal for Parasitology, 2017, 47, 529-544.	3.1	50
30	Serological Screening of the Schistosoma mansoni Adult Worm Proteome. PLoS Neglected Tropical Diseases, 2014, 8, e2745.	3.0	48
31	Landscape Genomic Conservation Assessment of a Narrow-Endemic and a Widespread Morning Glory From Amazonian Savannas. Frontiers in Plant Science, 2018, 9, 532.	3.6	48
32	Targeting schistosome histone modifying enzymes for drug development. Current Pharmaceutical Design, 2012, 18, 3567-78.	1.9	48
33	Praziquantel Treatment Decreases Schistosoma mansoni Genetic Diversity in Experimental Infections. PLoS Neglected Tropical Diseases, 2013, 7, e2596.	3.0	47
34	Cytokine and transcription factor profiles in the skin of dogs naturally infected by Leishmania (Leishmania) chagasi presenting distinct cutaneous parasite density and clinical status. Veterinary Parasitology, 2011, 177, 39-49.	1.8	46
35	Deep evolutionary origin of limb and fin regeneration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15106-15115.	7.1	46
36	SchistoDB: an updated genome resource for the three key schistosomes of humans. Nucleic Acids Research, 2012, 41, D728-D731.	14.5	45

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37	BMPOS: a Flexible and User-Friendly Tool Sets for Microbiome Studies. Microbial Ecology, 2016, 72, 443-447.	2.8	45
38	Bioleaching of electronic waste using bacteria isolated from the marine sponge Hymeniacidon heliophila (Porifera). Journal of Hazardous Materials, 2017, 329, 120-130.	12.4	45
39	Hepatitis C and hepatitis B virus infection in different hemodialysis units in Belo Horizonte, Minas Gerais, Brazil. Memorias Do Instituto Oswaldo Cruz, 2002, 97, 775-778.	1.6	44
40	Phred-Phrap package to analyses tools: a pipeline to facilitate population genetics re-sequencing studies. Investigative Genetics, 2011, 2, 3.	3.3	42
41	The Echinococcus canadensis (G7) genome: a key knowledge of parasitic platyhelminth human diseases. BMC Genomics, 2017, 18, 204.	2.8	42
42	A multiscale study of fungal endophyte communities of the foliar endosphere of native rubber trees in Eastern Amazon. Scientific Reports, 2018, 8, 16151.	3.3	42
43	Landscape genomics to the rescue of a tropical bee threatened by habitat loss and climate change. Evolutionary Applications, 2019, 12, 1164-1177.	3.1	41
44	Higher Expression of CCL2, CCL4, CCL5, CCL21, and CXCL8 Chemokines in the Skin Associated with Parasite Density in Canine Visceral Leishmaniasis. PLoS Neglected Tropical Diseases, 2012, 6, e1566.	3.0	39
45	Metagenomic signatures of a tropical mining-impacted stream reveal complex microbial and metabolic networks. Chemosphere, 2016, 161, 266-273.	8.2	39
46	Schistosoma mansoni: Germ-line transformation approaches and actin-promoter analysis. Experimental Parasitology, 2007, 117, 292-303.	1.2	37
47	Reconciling Mining with the Conservation of Cave Biodiversity: A Quantitative Baseline to Help Establish Conservation Priorities. PLoS ONE, 2016, 11, e0168348.	2.5	37
48	Sm14 gene expression in different stages of the Schistosoma mansoni life cycle and immunolocalization of the Sm14 protein within the adult worm. Brazilian Journal of Medical and Biological Research, 2002, 35, 377-381.	1.5	36
49	Biogeochemical processes in canga ecosystems: Armoring of iron ore against erosion and importance in iron duricrust restoration in Brazil. Ore Geology Reviews, 2019, 107, 573-586.	2.7	36
50	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. BMC Genomics, 2016, 17, 623.	2.8	35
51	A metagenomic survey of soil microbial communities along a rehabilitation chronosequence after iron ore mining. Scientific Data, 2019, 6, 190008.	5. 3	35
52	Epigenetic control of gene function in schistosomes: a source of therapeutic targets?. Frontiers in Genetics, 2014, 5, 317.	2.3	34
53	Recent Developments for Remediating Acidic Mine Waters Using Sulfidogenic Bacteria. BioMed Research International, 2017, 2017, 1-17.	1.9	34
54	Analysis of Predicted Host–Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. Frontiers in Immunology, 2019, 10, 212.	4.8	34

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55	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation. Nature Communications, 2022, 13, 1086.	12.8	34
56	Xerostomia, hyposalivation and sialadenitis in patients with chronic hepatitis C are not associated with the detection of HCV RNA in saliva or salivary glands. Journal of Clinical Pathology, 2010, 63, 1002-1007.	2.0	33
57	Complete genome sequence of Streptococcus agalactiae strain SA20-06, a fish pathogen associated to meningoencephalitis outbreaks. Standards in Genomic Sciences, 2013, 8, 188-197.	1.5	33
58	Adaptation and tolerance mechanisms developed by mycorrhizal Bipinnula fimbriata plantlets (Orchidaceae) in a heavy metal-polluted ecosystem. Mycorrhiza, 2018, 28, 651-663.	2.8	33
59	Isolation and characterisation of mineral-oxidising "Acidibacillus―spp. from mine sites and geothermal environments in different global locations. Research in Microbiology, 2016, 167, 613-623.	2.1	32
60	Habitat Loss Does Not Always Entail Negative Genetic Consequences. Frontiers in Genetics, 2019, 10, 1011.	2.3	32
61	Cancer and parasitic infections: similarities and opportunities for the development of new control tools. Revista Da Sociedade Brasileira De Medicina Tropical, 2014, 47, 1-2.	0.9	32
62	Mining the schistosome DNA sequence database. Trends in Parasitology, 2001, 17, 501-503.	3.3	31
63	Independent origins of loss-of-function mutations conferring oxamniquine resistance in a Brazilian schistosome population. International Journal for Parasitology, 2016, 46, 417-424.	3.1	31
64	Going out for dinnerâ€"The consumption of agriculture pests by bats in urban areas. PLoS ONE, 2021, 16, e0258066.	2.5	31
65	Antibodies from dogs with canine visceral leishmaniasis recognise two proteins from the saliva of Lutzomyia longipalpis. Parasitology Research, 2006, 100, 449-454.	1.6	30
66	Spatial distribution of Biomphalaria mollusks at São Francisco River Basin, Minas Gerais, Brazil, using geostatistical procedures. Acta Tropica, 2009, 109, 181-186.	2.0	30
67	Biomphalaria tenagophila/Schistosoma mansoni interaction: premises for a new approach to biological control of schistosomiasis. Memorias Do Instituto Oswaldo Cruz, 2004, 99, 109-111.	1.6	30
68	Smp38 MAP Kinase Regulation in Schistosoma mansoni: Roles in Survival, Oviposition, and Protection Against Oxidative Stress. Frontiers in Immunology, 2019, 10, 21.	4.8	29
69	Schistosoma mansoni: Expression of Fes-like tyrosine kinase SmFes in the tegument and terebratorium suggests its involvement in host penetration. Experimental Parasitology, 2007, 116, 225-232.	1.2	28
70	The Schistosoma mansoni phylome: using evolutionary genomics to gain insight into a parasite's biology. BMC Genomics, 2012, 13, 617.	2.8	28
71	Natural history of the narrow endemics Ipomoea cavalcantei and I. marabaensis from Amazon Canga savannahs. Scientific Reports, 2017, 7, 7493.	3.3	28
72	The distribution of motor proteins in the muscles and flame cells of the Schistosoma mansoni miracidium and primary sporocyst. Parasitology, 2006, 133, 321-329.	1.5	27

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73	Developmental Regulation of Genes Encoding Universal Stress Proteins in <i>Schistosoma mansoni</i> . Gene Regulation and Systems Biology, 2011, 5, GRSB.S7491.	2.3	27
74	Vertebrate diversity revealed by metabarcoding of bulk arthropod samples from tropical forests. Environmental DNA, 2019, 1, 329-341.	5.8	27
75	Significant variance in genetic diversity among populations of Schistosoma haematobium detected using microsatellite DNA loci from a genome-wide database. Parasites and Vectors, 2013, 6, 300.	2.5	26
76	Characterization of new Schistosoma mansoni microsatellite loci in sequences obtained from public DNA databases and microsatellite enriched genomic libraries. Memorias Do Instituto Oswaldo Cruz, 2002, 97, 71-75.	1.6	25
77	Protein tyrosine kinases in Schistosoma mansoni. Memorias Do Instituto Oswaldo Cruz, 2006, 101, 137-143.	1.6	25
78	Infection with Schistosoma mansoni correlates with altered immune responses to Ascaris lumbricoides and hookworm. Acta Tropica, 2002, 83, 123-132.	2.0	24
79	Genetic filtering and optimal sampling of Schistosoma mansoni populations. Parasitology, 2006, 133, 443-451.	1.5	24
80	A geoprocessing approach for studying and controlling schistosomiasis in the state of Minas Gerais, Brazil. Memorias Do Instituto Oswaldo Cruz, 2010, 105, 524-531.	1.6	24
81	Identification of paramyosin T cell epitopes associated with human resistance to Schistosoma mansoni reinfection. Clinical and Experimental Immunology, 2005, 142, 050927060953001.	2.6	23
82	The Schistosoma mansoni transcriptome: An update. Experimental Parasitology, 2007, 117, 229-235.	1.2	23
83	Single nucleotide polymorphisms identification in expressed genes of Schistosoma mansoni. Molecular and Biochemical Parasitology, 2007, 154, 134-140.	1.1	22
84	Drugging the schistosome zinc-dependent HDACs: current progress and future perspectives. Future Medicinal Chemistry, 2015, 7, 783-800.	2.3	22
85	A next-generation proteome array for Schistosoma mansoni. International Journal for Parasitology, 2016, 46, 411-415.	3.1	22
86	USING Next-Generation Sequencing (NGS) TO UNCOVER DIVERSITY OF WOOD-DECAYING FUNGI IN NEOTROPICAL ATLANTIC FORESTS. Phytotaxa, 2017, 295, 1.	0.3	22
87	Genome and genomics of schistosomes. Canadian Journal of Zoology, 2004, 82, 375-390.	1.0	21
88	Use of Humanised Rat Basophilic Leukaemia Cell Line RS-ATL8 for the Assessment of Allergenicity of Schistosoma mansoni Proteins. PLoS Neglected Tropical Diseases, 2014, 8, e3124.	3.0	21
89	The Leishmania metaphylome: a comprehensive survey of Leishmania protein phylogenetic relationships. BMC Genomics, 2015, 16, 887.	2.8	21
90	Whole genome analysis of codon usage in Echinococcus. Molecular and Biochemical Parasitology, 2018, 225, 54-66.	1.1	21

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91	Integrating environmental variables by multivariate ordination enables the reliable estimation of mineland rehabilitation status. Journal of Environmental Management, 2020, 256, 109894.	7.8	21
92	Evolutionary relationships among protein lysine deacetylases of parasites causing neglected diseases. Infection, Genetics and Evolution, 2017, 53, 175-188.	2.3	20
93	Illumina sequencing-based analysis of a microbial community enriched under anaerobic methane oxidation condition coupled to denitrification revealed coexistence of aerobic and anaerobic methanotrophs. Environmental Science and Pollution Research, 2017, 24, 16751-16764.	5.3	20
94	Quillworts from the Amazon: A multidisciplinary populational study on Isoetes serracarajensis and Isoetes cangae. PLoS ONE, 2018, 13, e0201417.	2.5	20
95	Microsatellite-enriched genomic libraries as a source of polymorphic loci forSchistosoma mansoni. Molecular Ecology Notes, 2007, 7, 263-265.	1.7	19
96	Functional Diversity of the <i>Schistosoma mansoni</i> Tyrosine Kinases. Journal of Signal Transduction, 2011, 2011, 1-11.	2.0	19
97	Plant growth and nutrient use efficiency of two native Fabaceae species for mineland revegetation in the eastern Amazon. Journal of Forestry Research, 2020, 31, 2287-2293.	3.6	19
98	Cloning of two actin genes from Schistosoma mansoni. Molecular and Biochemical Parasitology, 1995, 75, 119-122.	1.1	18
99	SmPKC1, a new protein kinase C identified in the platyhelminth parasite Schistosoma mansoni. Biochemical and Biophysical Research Communications, 2006, 345, 1138-1148.	2.1	18
100	Survey of genome organization and gene content of Corynebacterium pseudotuberculosis. Microbiological Research, 2010, 165, 312-320.	5. 3	17
101	Synergy of Omeprazole and Praziquantel In Vitro Treatment against Schistosoma mansoni Adult Worms. PLoS Neglected Tropical Diseases, 2015, 9, e0004086.	3.0	17
102	Pleiotropic alterations in gene expression in Latin American Fasciola hepatica isolates with different susceptibility to drugs. Parasites and Vectors, 2018, 11, 56.	2.5	17
103	A common vaginal microbiota composition among breeds of Bos taurus indicus (Gyr and Nellore). Brazilian Journal of Microbiology, 2019, 50, 1115-1124.	2.0	17
104	Brazilian studies on the genetics of Schistosoma mansoni. Acta Tropica, 2008, 108, 175-178.	2.0	16
105	Microarray analysis of tick-infested skin in resistant and susceptible cattle confirms the role of inflammatory pathways in immune activation and larval rejection. Veterinary Parasitology, 2014, 205, 307-317.	1.8	16
106	Host Resistance, Genomics and Population Dynamics in a Salmonella Enteritidis and Phage System. Viruses, 2019, 11, 188.	3.3	16
107	Detection of hepatitis C virus RNA in saliva samples from patients with seric anti-HCV antibodies. Brazilian Journal of Infectious Diseases, 2005, 9, 28-34.	0.6	16
108	Hepatitis C virus genotypes in hemophiliacs in the state of Minas Gerais, Brazil. Transfusion, 1999, 39, 1194-1199.	1.6	15

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109	Whole genome sequencing of GuzerÃ; cattle reveals genetic variants in candidate genes for production, disease resistance, and heat tolerance. Mammalian Genome, 2017, 28, 66-80.	2.2	15
110	Plastome-based phylogenomics elucidate relationships in rare Iso \tilde{A} «tes species groups from the Neotropics. Molecular Phylogenetics and Evolution, 2021, 161, 107177.	2.7	15
111	Population genetic structure of Biomphalaria glabrata in a schistosomiasis-endemic region in Brazil. Journal of Molluscan Studies, 2007, 73, 45-52.	1.2	14
112	MST (Molecular Serotyping Tool): a Program for Computer-Assisted Molecular Identification of <i>Escherichia coli</i> and <i>Shigella</i> O Antigens. Journal of Clinical Microbiology, 2010, 48, 1921-1923.	3.9	14
113	Recent advances in <i>Schistosoma</i> genomics. Parasite Immunology, 2012, 34, 151-162.	1.5	14
114	Machine learning meets genome assembly. Briefings in Bioinformatics, 2019, 20, 2116-2129.	6.5	14
115	The genetic diversity and population structure of two endemic Amazonian quillwort (<i>Isoetes</i>) Tj ETQq1	1 0.784314 2.0	rgBT /Overlo
116	Transmission control of schistosomiasis mansoni by introduction of a resistant strain of Biomphalaria tenagophila in areas where transmission is maintained by this species. Acta Tropica, 2008, 108, 245-248.	2.0	13
117	Utilizing environmental, socioeconomic data and GIS techniques to estimate the risk for ascariasis and trichuriasis in Minas Gerais, Brazil. Acta Tropica, 2012, 121, 112-117.	2.0	13
118	Evolutionary analysis of the cystatin family in three Schistosoma species. Frontiers in Genetics, 2014, 5, 206.	2.3	13
119	Comparative proteomics of cerebrospinal fluid reveals a predictive model for differential diagnosis of pneumococcal, meningococcal, and enteroviral meningitis, and novel putative therapeutic targets. BMC Genomics, 2015, 16, S11.	2.8	13
120	Computational and Experimental Approaches to Predict Host–Parasite Protein–Protein Interactions. Methods in Molecular Biology, 2018, 1819, 153-173.	0.9	13
121	Differential accumulation of proteins in oil palms affected by fatal yellowing disease. PLoS ONE, 2018, 13, e0195538.	2.5	13
122	Diversity of yeasts during fermentation of cocoa from two sites in the Brazilian Amazon. Acta Amazonica, 2019, 49, 64-70.	0.7	13
123	Coupling physiological analysis with proteomic profile to understand the photosynthetic responses of young Euterpe oleracea palms to drought. Photosynthesis Research, 2019, 140, 189-205.	2.9	13
124	Evolutionary histories of expanded peptidase families in Schistosoma mansoni. Memorias Do Instituto Oswaldo Cruz, 2011, 106, 864-877.	1.6	12
125	The use of an integrated molecular-, chemical- and biological-based approach for promoting the better use and conservation of medicinal species: A case study of Brazilian quinas. Journal of Ethnopharmacology, 2014, 155, 815-822.	4.1	12
126	Metagenomic analysis and performance of a mesophilic anaerobic reactor treating food waste at various load rates. Environmental Technology (United Kingdom), 2017, 38, 2153-2163.	2.2	12

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127	Revisiting the Phylogenetic History of Helminths Through Genomics, the Case of the New Echinococcus oligarthrus Genome. Frontiers in Genetics, 2019, 10, 708.	2.3	12
128	Biodiversity surrogates in Amazonian iron cave ecosystems. Ecological Indicators, 2019, 101, 813-820.	6.3	12
129	Non-Specific Interactions of Rhizospheric Microbial Communities Support the Establishment of Mimosa acutistipula var. ferrea in an Amazon Rehabilitating Mineland. Processes, 2021, 9, 2079.	2.8	12
130	Molecular analysis of SmFes, a tyrosine kinase of Schistosoma mansoni orthologous to the members of the Fes/Fps/Fer family. Biochemical and Biophysical Research Communications, 2007, 360, 163-172.	2.1	11
131	The Brazilian contribution to the study of the Schistosoma mansoni transcriptome. Acta Tropica, 2008, 108, 179-182.	2.0	11
132	The Estrada Real project and endemic diseases: the case of schistosomiasis, geoprocessing and tourism. Memorias Do Instituto Oswaldo Cruz, 2010, 105, 532-536.	1.6	11
133	Detection of HCV RNA in saliva does not correlate with salivary flow or xerostomia in patients with chronic hepatitis C. Oral Surgery Oral Medicine Oral Pathology Oral Radiology and Endodontics, 2010, 109, 851-856.	1.4	11
134	Molecular characterization of the hexose transporter gene in benznidazole resistant and susceptible populations of Trypanosoma cruzi. Parasites and Vectors, 2012, 5, 161.	2.5	11
135	Elucidating the temporal and spatial dynamics of <i><scp>B</scp>iomphalaria glabrata</i> genetic diversity in three <scp>B</scp> razilian villages. Tropical Medicine and International Health, 2013, 18, 1164-1173.	2.3	11
136	Metagenomic analysis of a desulphurisation system used to treat biogas from vinasse methanisation. Bioresource Technology, 2016, 205, 58-66.	9.6	11
137	Bioreductive Dissolution as a Pretreatment for Recalcitrant Rare-Earth Phosphate Minerals Associated with Lateritic Ores. Minerals (Basel, Switzerland), 2019, 9, 136.	2.0	11
138	Profiling Transcriptional Regulation and Functional Roles of Schistosoma mansoni c-Jun N-Terminal Kinase. Frontiers in Genetics, 2019, 10, 1036.	2.3	11
139	The potential for histone deacetylase (HDAC) inhibitors as cestocidal drugs. PLoS Neglected Tropical Diseases, 2021, 15, e0009226.	3.0	11
140	Genomic analysis of a parasite invasion: Colonization of the Americas by the blood fluke <i>Schistosoma mansoni</i> . Molecular Ecology, 2022, 31, 2242-2263.	3.9	11
141	PIPEBAR and OverlapPER: tools for a fast and accurate DNA barcoding analysis and paired-end assembly. BMC Bioinformatics, 2018, 19, 297.	2.6	10
142	Filamentous fungi diversity in the natural fermentation of Amazonian cocoa beans and the microbial enzyme activities. Annals of Microbiology, 2019, 69, 975-987.	2.6	10
143	Chloroplast genomes of key species shed light on the evolution of the ancient genus Isoetes. Journal of Systematics and Evolution, 2020, 59, 429.	3.1	10
144	Accelerating microbial iron cycling promotes reâ€cementation of surface crusts in iron ore regions. Microbial Biotechnology, 2020, 13, 1960-1971.	4.2	10

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145	Evaluation of a linear spectral mixture model and vegetation indices (NDVI and EVI) in a study of schistosomiasis mansoni and Biomphalaria glabrata distribution in the state of Minas Gerais, Brazil. Memorias Do Instituto Oswaldo Cruz, 2010, 105, 512-518.	1.6	9
146	Electropolymerization of hydroxyphenylacetic acid isomers and the development of a bioelectrode for the diagnosis of bacterial meningitis. Journal of Applied Electrochemistry, 2015, 45, 1277-1287.	2.9	9
147	New insights on the phylogenetic relationships among the traditional Philodendron subgenera and the other groups of the Homalomena clade (Araceae). Molecular Phylogenetics and Evolution, 2018, 127, 168-178.	2.7	9
148	Covellite (CuS) Production from a Real Acid Mine Drainage Treated with Biogenic H2S. Metals, 2019, 9, 206.	2.3	9
149	Conservation implications of genetic structure in the narrowest endemic quillwort from the Eastern Amazon. Ecology and Evolution, 2021, 11, 10119-10132.	1.9	9
150	Schistosoma gene discovery project update. Trends in Parasitology, 2001, 17, 108-109.	3.3	8
151	Mitochondrial Cardioencephalomyopathy Due to a Novel SCO2 Mutation in a Brazilian Patient. JAMA Neurology, 2013, 70, 258.	9.0	8
152	Taxonomic and functional diversity of microbial community from a mining environment. BMC Bioinformatics, $2015, 16, .$	2.6	8
153	Expression of myogenes in longissimus dorsi muscle during prenatal development in commercial and local Piau pigs. Genetics and Molecular Biology, 2016, 39, 589-599.	1.3	8
154	Draft Genome Sequence of " <i>Acidibacillus ferrooxidans</i> ―ITV01, a Novel Acidophilic Firmicute Isolated from a Chalcopyrite Mine Drainage Site in Brazil. Genome Announcements, 2016, 4, .	0.8	8
155	Schistosoma mansoni: Off-target analyses using nonspecific double-stranded RNAs as control for RNAi experiments in schistosomula. Experimental Parasitology, 2017, 177, 98-103.	1.2	8
156	Singleâ€cell sequencing unveils the lifestyle and CRISPRâ€based population history of <i>Hydrotalea</i> sp. in acid mine drainage. Molecular Ecology, 2017, 26, 5541-5551.	3.9	8
157	Use of Indicator Kriging to Investigate Schistosomiasis in Minas Gerais State, Brazil. Journal of Tropical Medicine, 2012, 2012, 1-10.	1.7	7
158	Preliminary Characterization of Mitochondrial Genome of <i>Melipona scutellaris </i> , a Brazilian Stingless Bee. BioMed Research International, 2014, 2014, 1-6.	1.9	7
159	Draft Genome Sequences of Staphylococcus aureus Strains Isolated from Subclinical Bovine Mastitis in Brazil. Genome Announcements, 2016, 4, .	0.8	7
160	Hybrid agent-based model for quantitative in-silico cell-free protein synthesis. BioSystems, 2016, 150, 22-34.	2.0	7
161	Blind Testing: DNA Barcoding Sheds Light Upon the Identity of Plant Fragments as a Subsidy for Cave Conservation. Frontiers in Plant Science, 2018, 9, 1052.	3.6	7
162	Metaproteomes reveal increased capacity for stress tolerance of soil microbes in ferruginous tropical rocky outcrops. Pedobiologia, 2020, 81-82, 150664.	1.2	7

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163	Distinct Reproductive Strategy of Two Endemic Amazonian Quillworts. Diversity, 2021, 13, 348.	1.7	7
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165	Proteomic Profiling and Rhizosphere-Associated Microbial Communities Reveal Adaptive Mechanisms of Dioclea apurensis Kunth in Eastern Amazon's Rehabilitating Minelands. Plants, 2022, 11, 712.	3.5	7
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