

Guilherme Oliveira

List of Publications by Year in descending order

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Version: 2024-02-01

210
papers

7,417
citations

76294

40
h-index

76872

74
g-index

219
all docs

219
docs citations

219
times ranked

9117
citing authors

#	ARTICLE	IF	CITATIONS
1	Spectral and Soil Quality Index for Monitoring Environmental Rehabilitation and Soil Carbon Stock in an Amazonian Sandstone Mine. <i>Sustainability</i> , 2022, 14, 597.	1.6	7
2	Genomic analysis of a parasite invasion: Colonization of the Americas by the blood fluke <i>Schistosoma mansoni</i> . <i>Molecular Ecology</i> , 2022, 31, 2242-2263.	2.0	11
3	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation. <i>Nature Communications</i> , 2022, 13, 1086.	5.8	34
4	Proteomic Profiling and Rhizosphere-Associated Microbial Communities Reveal Adaptive Mechanisms of <i>Dioclea apurensis</i> Kunth in Eastern Amazon's Rehabilitating Minelands. <i>Plants</i> , 2022, 11, 712.	1.6	7
5	New plastomes of eight <i>Ipomoea</i> species and four putative hybrids from Eastern Amazon. <i>PLoS ONE</i> , 2022, 17, e0265449.	1.1	2
6	An Integrative View of the Phyllosphere Mycobiome of Native Rubber Trees in the Brazilian Amazon. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 373.	1.5	7
7	Cross-species transcriptomes reveal species-specific and shared molecular adaptations for plants development on iron-rich rocky outcrops soils. <i>BMC Genomics</i> , 2022, 23, 313.	1.2	2
8	PipeCoV: a pipeline for SARS-CoV-2 genome assembly, annotation and variant identification. <i>PeerJ</i> , 2022, 10, e13300.	0.9	7
9	Draft Genome Sequence of the Novel, Moderately Thermophilic, Iron- and Sulfur-Oxidizing Firmicute Strain Y002, Isolated from an Extremely Acidic Geothermal Environment. <i>Microbiology Resource Announcements</i> , 2022, , e0014922.	0.3	1
10	Yeast isolation and identification during on-farm cocoa natural fermentation in a highly producer region in northern Brazil. <i>Scientia Plena</i> , 2021, 16, .	0.1	5
11	Complete mitochondrial genome of a cave dwelling <i>Desmopachria</i> (Insecta: Coleoptera: Tj ETQq1 1 0.784314 rgBT /Qverlock 10.2		
12	The potential for histone deacetylase (HDAC) inhibitors as cestocidal drugs. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009226.	1.3	11
13	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	1.5	2
14	Conservation implications of genetic structure in the narrowest endemic quillwort from the Eastern Amazon. <i>Ecology and Evolution</i> , 2021, 11, 10119-10132.	0.8	9
15	Distinct Reproductive Strategy of Two Endemic Amazonian Quillworts. <i>Diversity</i> , 2021, 13, 348.	0.7	7
16	Plastome-based phylogenomics elucidate relationships in rare Isoetes species groups from the Neotropics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107177.	1.2	15
17	Unraveling the plant diversity of the Amazonian <i>canga</i> through DNA barcoding. <i>Ecology and Evolution</i> , 2021, 11, 13348-13362.	0.8	6
18	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. <i>PLoS Computational Biology</i> , 2021, 17, e1009218.	1.5	4

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19	Soil Metaproteomics as a Tool for Environmental Monitoring of Minelands. <i>Forests</i> , 2021, 12, 1158.	0.9	3
20	Identification and in silico characterization of structural and functional impacts of genetic variants in milk protein genes in the Zebu breeds Guzerat and Gyr. <i>Tropical Animal Health and Production</i> , 2021, 53, 524.	0.5	2
21	Going out for dinner—The consumption of agriculture pests by bats in urban areas. <i>PLoS ONE</i> , 2021, 16, e0258066.	1.1	31
22	Non-Specific Interactions of Rhizospheric Microbial Communities Support the Establishment of <i>Mimosa acutistipula</i> var. <i>ferrea</i> in an Amazon Rehabilitating Mineland. <i>Processes</i> , 2021, 9, 2079.	1.3	12
23	Plant growth and nutrient use efficiency of two native Fabaceae species for mineland revegetation in the eastern Amazon. <i>Journal of Forestry Research</i> , 2020, 31, 2287-2293.	1.7	19
24	Integrating environmental variables by multivariate ordination enables the reliable estimation of mineland rehabilitation status. <i>Journal of Environmental Management</i> , 2020, 256, 109894.	3.8	21
25	Genome size and chromosome number conservation contrasting with karyotype diversity in <i>Hohenbergia</i> (Bromelioideae, Bromeliaceae). <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 900-909.	0.8	1
26	Chloroplast genomes of key species shed light on the evolution of the ancient genus <i>Isoetes</i> . <i>Journal of Systematics and Evolution</i> , 2020, 59, 429.	1.6	10
27	Metaproteomes reveal increased capacity for stress tolerance of soil microbes in ferruginous tropical rocky outcrops. <i>Pedobiologia</i> , 2020, 81-82, 150664.	0.5	7
28	Complete mitochondrial genome of <i>Glomeridesmus spelaeus</i> (Diplopoda, Glomeridesmida), a troglobitic species from iron-ore caves in Eastern Amazon. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3272-3273.	0.2	5
29	Accelerating microbial iron cycling promotes re-ementation of surface crusts in iron ore regions. <i>Microbial Biotechnology</i> , 2020, 13, 1960-1971.	2.0	10
30	Climate-induced distribution dynamics of <i>Plebeia flavocincta</i> , a stingless bee from Brazilian tropical dry forests. <i>Ecology and Evolution</i> , 2020, 10, 10130-10138.	0.8	4
31	The phylogenetic placement of a new species of <i>Belemia</i> in Nyctaginaceae, and the first plastome description for the genus. <i>Systematics and Biodiversity</i> , 2020, 18, 328-337.	0.5	0
32	The genetic diversity and population structure of two endemic Amazonian quillwort (<i>Isoetes</i>)	0.9	14
33	Machine learning meets genome assembly. <i>Briefings in Bioinformatics</i> , 2019, 20, 2116-2129.	3.2	14
34	Revisiting the Phylogenetic History of Helminths Through Genomics, the Case of the New <i>Echinococcus oligarthrus</i> Genome. <i>Frontiers in Genetics</i> , 2019, 10, 708.	1.1	12
35	Deep evolutionary origin of limb and fin regeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15106-15115.	3.3	46
36	A metagenomic survey of soil microbial communities along a rehabilitation chronosequence after iron ore mining. <i>Scientific Data</i> , 2019, 6, 190008.	2.4	35

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37	Vertebrate diversity revealed by metabarcoding of bulk arthropod samples from tropical forests. <i>Environmental DNA</i> , 2019, 1, 329-341.	3.1	27
38	Genomic signatures and co-occurrence patterns of the ultra-small <i>Saccharimonadia</i> (phylum) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7	2.0	101
39	A common vaginal microbiota composition among breeds of <i>Bos taurus indicus</i> (Gyr and Nellore). <i>Brazilian Journal of Microbiology</i> , 2019, 50, 1115-1124.	0.8	17
40	Smp38 MAP Kinase Regulation in <i>Schistosoma mansoni</i> : Roles in Survival, Oviposition, and Protection Against Oxidative Stress. <i>Frontiers in Immunology</i> , 2019, 10, 21.	2.2	29
41	Filamentous fungi diversity in the natural fermentation of Amazonian cocoa beans and the microbial enzyme activities. <i>Annals of Microbiology</i> , 2019, 69, 975-987.	1.1	10
42	Complete mitochondrial genomes of three troglophile cave spiders (<i>Mesabolivar</i> , pholcidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 251-252.	0.2	3
43	Bioreductive Dissolution as a Pretreatment for Recalcitrant Rare-Earth Phosphate Minerals Associated with Lateritic Ores. <i>Minerals (Basel, Switzerland)</i> , 2019, 9, 136.	0.8	11
44	Landscape genomics to the rescue of a tropical bee threatened by habitat loss and climate change. <i>Evolutionary Applications</i> , 2019, 12, 1164-1177.	1.5	41
45	Covellite (CuS) Production from a Real Acid Mine Drainage Treated with Biogenic H ₂ S. <i>Metals</i> , 2019, 9, 206.	1.0	9
46	Biogeochemical processes in canga ecosystems: Armoring of iron ore against erosion and importance in iron duricrust restoration in Brazil. <i>Ore Geology Reviews</i> , 2019, 107, 573-586.	1.1	36
47	Host Resistance, Genomics and Population Dynamics in a <i>Salmonella</i> Enteritidis and Phage System. <i>Viruses</i> , 2019, 11, 188.	1.5	16
48	Biodiversity surrogates in Amazonian iron cave ecosystems. <i>Ecological Indicators</i> , 2019, 101, 813-820.	2.6	12
49	Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. <i>Frontiers in Immunology</i> , 2019, 10, 212.	2.2	34
50	Complete mitochondrial genome of a troglophile Cydnidae (Hemiptera). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 420-422.	0.2	0
51	Habitat Loss Does Not Always Entail Negative Genetic Consequences. <i>Frontiers in Genetics</i> , 2019, 10, 1011.	1.1	32
52	Profiling Transcriptional Regulation and Functional Roles of <i>Schistosoma mansoni</i> c-Jun N-Terminal Kinase. <i>Frontiers in Genetics</i> , 2019, 10, 1036.	1.1	11
53	Diversity of yeasts during fermentation of cocoa from two sites in the Brazilian Amazon. <i>Acta Amazonica</i> , 2019, 49, 64-70.	0.3	13
54	Coupling physiological analysis with proteomic profile to understand the photosynthetic responses of young <i>Euterpe oleracea</i> palms to drought. <i>Photosynthesis Research</i> , 2019, 140, 189-205.	1.6	13

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55	DNA Barcoding and Genomics in the Megadiverse Amazon Altitude Fields. IBOL Barcode Bulletin, 2019, 9, .	0.2	1
56	Computational and Experimental Approaches to Predict Host-Parasite Protein-Protein Interactions. Methods in Molecular Biology, 2018, 1819, 153-173.	0.4	13
57	A multiscale study of fungal endophyte communities of the foliar endosphere of native rubber trees in Eastern Amazon. Scientific Reports, 2018, 8, 16151.	1.6	42
58	Metagenomics-based signature clustering and interactive visualization analysis. , 2018, , .		2
59	PIPEBAR and OverlapPER: tools for a fast and accurate DNA barcoding analysis and paired-end assembly. BMC Bioinformatics, 2018, 19, 297.	1.2	10
60	New insights on the phylogenetic relationships among the traditional <i>Philodendron</i> subgenera and the other groups of the <i>Homalomena</i> clade (Araceae). Molecular Phylogenetics and Evolution, 2018, 127, 168-178.	1.2	9
61	Differential accumulation of proteins in oil palms affected by fatal yellowing disease. PLoS ONE, 2018, 13, e0195538.	1.1	13
62	Landscape Genomic Conservation Assessment of a Narrow-Endemic and a Widespread Morning Glory From Amazonian Savannas. Frontiers in Plant Science, 2018, 9, 532.	1.7	48
63	Pleiotropic alterations in gene expression in Latin American <i>Fasciola hepatica</i> isolates with different susceptibility to drugs. Parasites and Vectors, 2018, 11, 56.	1.0	17
64	Quillworts from the Amazon: A multidisciplinary populational study on <i>Isoetes serracarajensis</i> and <i>Isoetes cangae</i> . PLoS ONE, 2018, 13, e0201417.	1.1	20
65	Adaptation and tolerance mechanisms developed by mycorrhizal <i>Bipinnula fimbriata</i> plantlets (Orchidaceae) in a heavy metal-polluted ecosystem. Mycorrhiza, 2018, 28, 651-663.	1.3	33
66	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.	1.7	7
67	Whole genome analysis of codon usage in <i>Echinococcus</i> . Molecular and Biochemical Parasitology, 2018, 225, 54-66.	0.5	21
68	USING Next-Generation Sequencing (NGS) TO UNCOVER DIVERSITY OF WOOD-DECAYING FUNGI IN NEOTROPICAL ATLANTIC FORESTS. Phytotaxa, 2017, 295, 1.	0.1	22
69	Bioleaching of electronic waste using bacteria isolated from the marine sponge <i>Hymeniacidon heliophila</i> (Porifera). Journal of Hazardous Materials, 2017, 329, 120-130.	6.5	45
70	Effectiveness of ITS and sub-regions as DNA barcode markers for the identification of Basidiomycota (Fungi). BMC Microbiology, 2017, 17, 42.	1.3	126
71	The <i>Echinococcus canadensis</i> (G7) genome: a key knowledge of parasitic platyhelminth human diseases. BMC Genomics, 2017, 18, 204.	1.2	42
72	Evolutionary relationships among protein lysine deacetylases of parasites causing neglected diseases. Infection, Genetics and Evolution, 2017, 53, 175-188.	1.0	20

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73	Schistosoma mansoni: Off-target analyses using nonspecific double-stranded RNAs as control for RNAi experiments in schistosomula. <i>Experimental Parasitology</i> , 2017, 177, 98-103.	0.5	8
74	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. <i>Nature Communications</i> , 2017, 8, 15451.	5.8	216
75	Helminth secretomes reflect different lifestyles and parasitized hosts. <i>International Journal for Parasitology</i> , 2017, 47, 529-544.	1.3	50
76	Metagenomic analysis and performance of a mesophilic anaerobic reactor treating food waste at various load rates. <i>Environmental Technology (United Kingdom)</i> , 2017, 38, 2153-2163.	1.2	12
77	Natural history of the narrow endemics <i>Ipomoea cavalcantei</i> and <i>I. marabaensis</i> from Amazon Canga savannahs. <i>Scientific Reports</i> , 2017, 7, 7493.	1.6	28
78	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
79	Single-cell sequencing unveils the lifestyle and CRISPR-based population history of <i>Hydrothalea</i> sp. in acid mine drainage. <i>Molecular Ecology</i> , 2017, 26, 5541-5551.	2.0	8
80	Whole genome sequencing of Guzzeri cattle reveals genetic variants in candidate genes for production, disease resistance, and heat tolerance. <i>Mammalian Genome</i> , 2017, 28, 66-80.	1.0	15
81	Recent Developments for Remediating Acidic Mine Waters Using Sulfidogenic Bacteria. <i>BioMed Research International</i> , 2017, 2017, 1-17.	0.9	34
82	Illumina sequencing-based analysis of a microbial community enriched under anaerobic methane oxidation condition coupled to denitrification revealed coexistence of aerobic and anaerobic methanotrophs. <i>Environmental Science and Pollution Research</i> , 2017, 24, 16751-16764.	2.7	20
83	Expression of myogenes in longissimus dorsi muscle during prenatal development in commercial and local Piau pigs. <i>Genetics and Molecular Biology</i> , 2016, 39, 589-599.	0.6	8
84	Reconciling Mining with the Conservation of Cave Biodiversity: A Quantitative Baseline to Help Establish Conservation Priorities. <i>PLoS ONE</i> , 2016, 11, e0168348.	1.1	37
85	Draft Genome Sequence of <i>Acidibacillus ferrooxidans</i> strain TV01, a Novel Acidophilic Firmicute Isolated from a Chalcopyrite Mine Drainage Site in Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
86	Draft Genome Sequence of a Novel Acidophilic Iron-Oxidizing Firmicutes Species, <i>Acidibacillus ferrooxidans</i> strain (SLC66). <i>Genome Announcements</i> , 2016, 4, .	0.8	5
87	Draft Genome Sequence of <i>Hydrothalea flava</i> Strain CCUG 51397. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
88	Isolation and characterisation of mineral-oxidising <i>Acidibacillus</i> spp. from mine sites and geothermal environments in different global locations. <i>Research in Microbiology</i> , 2016, 167, 613-623.	1.0	32
89	BMPOS: a Flexible and User-Friendly Tool Sets for Microbiome Studies. <i>Microbial Ecology</i> , 2016, 72, 443-447.	1.4	45
90	A next-generation proteome array for <i>Schistosoma mansoni</i> . <i>International Journal for Parasitology</i> , 2016, 46, 411-415.	1.3	22

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91	Independent origins of loss-of-function mutations conferring oxamniquine resistance in a Brazilian schistosome population. <i>International Journal for Parasitology</i> , 2016, 46, 417-424.	1.3	31
92	Draft Genome Sequences of <i>Staphylococcus aureus</i> Strains Isolated from Subclinical Bovine Mastitis in Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
93	Metagenomic signatures of a tropical mining-impacted stream reveal complex microbial and metabolic networks. <i>Chemosphere</i> , 2016, 161, 266-273.	4.2	39
94	Hybrid agent-based model for quantitative in-silico cell-free protein synthesis. <i>BioSystems</i> , 2016, 150, 22-34.	0.9	7
95	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. <i>BMC Genomics</i> , 2016, 17, 623.	1.2	35
96	Estimation of genetic diversity in viral populations from next generation sequencing data with extremely deep coverage. <i>Algorithms for Molecular Biology</i> , 2016, 11, 2.	0.3	6
97	Complete mitochondrial genome sequence of <i>Melipona scutellaris</i> , a Brazilian stingless bee. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3387-3388.	0.7	5
98	Metagenomic analysis of a desulphurisation system used to treat biogas from vinasse methanisation. <i>Bioresource Technology</i> , 2016, 205, 58-66.	4.8	11
99	The <i>Leishmania</i> metaphylome: a comprehensive survey of <i>Leishmania</i> protein phylogenetic relationships. <i>BMC Genomics</i> , 2015, 16, 887.	1.2	21
100	Taxonomic and functional diversity of microbial community from a mining environment. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	8
101	Comparative proteomics of cerebrospinal fluid reveals a predictive model for differential diagnosis of pneumococcal, meningococcal, and enteroviral meningitis, and novel putative therapeutic targets. <i>BMC Genomics</i> , 2015, 16, S11.	1.2	13
102	Medicinal Plants Recommended by the World Health Organization: DNA Barcode Identification Associated with Chemical Analyses Guarantees Their Quality. <i>PLoS ONE</i> , 2015, 10, e0127866.	1.1	130
103	Synergy of Omeprazole and Praziquantel In Vitro Treatment against <i>Schistosoma mansoni</i> Adult Worms. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004086.	1.3	17
104	Vaginal Microbiome Characterization of Nellore Cattle Using Metagenomic Analysis. <i>PLoS ONE</i> , 2015, 10, e0143294.	1.1	92
105	HDAC8: a multifaceted target for therapeutic interventions. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 481-492.	4.0	210
106	How has the genomics era impacted schistosomiasis drug discovery?. <i>Future Medicinal Chemistry</i> , 2015, 7, 685-687.	1.1	6
107	Electropolymerization of hydroxyphenylacetic acid isomers and the development of a bioelectrode for the diagnosis of bacterial meningitis. <i>Journal of Applied Electrochemistry</i> , 2015, 45, 1277-1287.	1.5	9
108	Drugging the schistosome zinc-dependent HDACs: current progress and future perspectives. <i>Future Medicinal Chemistry</i> , 2015, 7, 783-800.	1.1	22

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109	Metagenome of a Microbial Community Inhabiting a Metal-Rich Tropical Stream Sediment. PLoS ONE, 2015, 10, e0119465.	1.1	95
110	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.	1.3	21
111	Epigenetic control of gene function in schistosomes: a source of therapeutic targets?. Frontiers in Genetics, 2014, 5, 317.	1.1	34
112	Regulation of Schistosoma mansoni Development and Reproduction by the Mitogen-Activated Protein Kinase Signaling Pathway. PLoS Neglected Tropical Diseases, 2014, 8, e2949.	1.3	73
113	Serological Screening of the Schistosoma mansoni Adult Worm Proteome. PLoS Neglected Tropical Diseases, 2014, 8, e2745.	1.3	48
114	An Immunomics Approach to Schistosome Antigen Discovery: Antibody Signatures of Naturally Resistant and Chronically Infected Individuals from Endemic Areas. PLoS Pathogens, 2014, 10, e1004033.	2.1	78
115	Heterologous expression in Caenorhabditis elegans as an alternative approach to functional studies in Schistosoma mansoni. Frontiers in Genetics, 2014, 5, 120.	1.1	0
116	Preliminary Characterization of Mitochondrial Genome of <i>Melipona scutellaris</i> , a Brazilian Stingless Bee. BioMed Research International, 2014, 2014, 1-6.	0.9	7
117	Evolutionary analysis of the cystatin family in three Schistosoma species. Frontiers in Genetics, 2014, 5, 206.	1.1	13
118	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.	0.7	16
119	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.	2.0	12
120	Assessing the efficiency of multiple sequence alignment programs. Algorithms for Molecular Biology, 2014, 9, 4.	0.3	87
121	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.	0.4	32
122	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.	1.0	26
123	Mitochondrial Cardioencephalomyopathy Due to a Novel SCO2 Mutation in a Brazilian Patient. JAMA Neurology, 2013, 70, 258.	4.5	8
124	Praziquantel Treatment Decreases Schistosoma mansoni Genetic Diversity in Experimental Infections. PLoS Neglected Tropical Diseases, 2013, 7, e2596.	1.3	47
125	Schistosoma mansoni Sirtuins: Characterization and Potential as Chemotherapeutic Targets. PLoS Neglected Tropical Diseases, 2013, 7, e2428.	1.3	77
126	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.	2.1	136

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127	Elucidating the temporal and spatial dynamics of <i>Trypanosoma brucei</i> genetic diversity in three Brazilian villages. <i>Tropical Medicine and International Health</i> , 2013, 18, 1164-1173.	1.0	11
128	Complete genome sequence of <i>Streptococcus agalactiae</i> strain SA20-06, a fish pathogen associated to meningoenzephalitis outbreaks. <i>Standards in Genomic Sciences</i> , 2013, 8, 188-197.	1.5	33
129	Higher Expression of CCL2, CCL4, CCL5, CCL21, and CXCL8 Chemokines in the Skin Associated with Parasite Density in Canine Visceral Leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1566.	1.3	39
130	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1455.	1.3	400
131	Use of Indicator Kriging to Investigate Schistosomiasis in Minas Gerais State, Brazil. <i>Journal of Tropical Medicine</i> , 2012, 2012, 1-10.	0.6	7
132	Serological-proteome analysis of the parasite <i>Schistosoma mansoni</i> . <i>International Journal of Infectious Diseases</i> , 2012, 16, e402.	1.5	0
133	Utilizing environmental, socioeconomic data and GIS techniques to estimate the risk for ascariasis and trichuriasis in Minas Gerais, Brazil. <i>Acta Tropica</i> , 2012, 121, 112-117.	0.9	13
134	The <i>Schistosoma mansoni</i> phylome: using evolutionary genomics to gain insight into a parasite's biology. <i>BMC Genomics</i> , 2012, 13, 617.	1.2	28
135	Molecular characterization of the hexose transporter gene in benzimidazole resistant and susceptible populations of <i>Trypanosoma cruzi</i> . <i>Parasites and Vectors</i> , 2012, 5, 161.	1.0	11
136	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
137	SchistoDB: an updated genome resource for the three key schistosomes of humans. <i>Nucleic Acids Research</i> , 2012, 41, D728-D731.	6.5	45
138	Automatic Assignment of Prokaryotic Genes to Functional Categories Using Literature Profiling. <i>PLoS ONE</i> , 2012, 7, e47436.	1.1	6
139	New Frontiers in <i>Schistosoma</i> Genomics and Transcriptomics. <i>Journal of Parasitology Research</i> , 2012, 2012, 1-11.	0.5	61
140	Recent advances in <i>Schistosoma</i> genomics. <i>Parasite Immunology</i> , 2012, 34, 151-162.	0.7	14
141	Targeting schistosome histone modifying enzymes for drug development. <i>Current Pharmaceutical Design</i> , 2012, 18, 3567-78.	0.9	48
142	Developmental Regulation of Genes Encoding Universal Stress Proteins in <i>Schistosoma mansoni</i> . <i>Gene Regulation and Systems Biology</i> , 2011, 5, GRSB.S7491.	2.3	27
143	Evolutionary histories of expanded peptidase families in <i>Schistosoma mansoni</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 864-877.	0.8	12
144	Functional Diversity of the <i>Schistosoma mansoni</i> Tyrosine Kinases. <i>Journal of Signal Transduction</i> , 2011, 2011, 1-11.	2.0	19

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145	Cytokine and transcription factor profiles in the skin of dogs naturally infected by <i>Leishmania (Leishmania) chagasi</i> presenting distinct cutaneous parasite density and clinical status. <i>Veterinary Parasitology</i> , 2011, 177, 39-49.	0.7	46
146	Phred-Phrap package to analyses tools: a pipeline to facilitate population genetics re-sequencing studies. <i>Investigative Genetics</i> , 2011, 2, 3.	3.3	42
147	Eukaryotic Protein Kinases (ePKs) of the Helminth Parasite <i>Schistosoma mansoni</i> . <i>BMC Genomics</i> , 2011, 12, 215.	1.2	90
148	Identification of <i>Schistosoma mansoni</i> microRNAs. <i>BMC Genomics</i> , 2011, 12, 47.	1.2	62
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