

Bruno W S Sobral

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9052313/publications.pdf>

Version: 2024-02-01

123
papers

11,259
citations

41344

49
h-index

30922

102
g-index

131
all docs

131
docs citations

131
times ranked

14459
citing authors

#	ARTICLE	IF	CITATIONS
1	Amazonian deforestation and soil biodiversity. <i>Conservation Biology</i> , 2019, 33, 590-600.	4.7	38
2	From Big Data Analytics and Network Inference to Systems Modeling. , 2016, , 113-144.		0
3	Immunoinformatics Cyberinfrastructure for Modeling and Analytics. , 2016, , 45-61.		0
4	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. <i>Bioinformatics</i> , 2015, 31, 1496-1498.	4.1	11
5	Curation, integration and visualization of bacterial virulence factors in PATRIC. <i>Bioinformatics</i> , 2015, 31, 252-258.	4.1	58
6	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34
7	PATRIC, the bacterial bioinformatics database and analysis resource. <i>Nucleic Acids Research</i> , 2014, 42, D581-D591.	14.5	1,222
8	Comparative nutritional and chemical phenome of <i>Clostridium difficile</i> isolates determined using phenotype microarrays. <i>International Journal of Infectious Diseases</i> , 2014, 27, 20-25.	3.3	24
9	Consensus statement understanding health and malnutrition through a systems approach: the ENOUGH program for early life. <i>Genes and Nutrition</i> , 2014, 9, 378.	2.5	26
10	Comparative Phylogenomics and Evolution of the Brucellae Reveal a Path to Virulence. <i>Journal of Bacteriology</i> , 2014, 196, 920-930.	2.2	122
11	Comparative Genomic Analysis at the PATRIC, A Bioinformatic Resource Center. <i>Methods in Molecular Biology</i> , 2014, 1197, 287-308.	0.9	29
12	Proteomic Comparison of Historic and Recently Emerged Hypervirulent <i>Clostridium difficile</i> Strains. <i>Journal of Proteome Research</i> , 2013, 12, 1151-1161.	3.7	52
13	Functional assignment of <i>Mycobacterium tuberculosis</i> proteome revealed by genome-scale fold-recognition. <i>Tuberculosis</i> , 2013, 93, 40-46.	1.9	18
14	TBCAP; tuberculosis annotation project. <i>Tuberculosis</i> , 2013, 93, 1-5.	1.9	3
15	Database resources for the tuberculosis community. <i>Tuberculosis</i> , 2013, 93, 12-17.	1.9	27
16	Informatics-Driven Infectious Disease Research. <i>Communications in Computer and Information Science</i> , 2013, , 3-11.	0.5	0
17	The Condition-Dependent Transcriptional Landscape of <i>Burkholderia pseudomallei</i> . <i>PLoS Genetics</i> , 2013, 9, e1003795.	3.5	81
18	Bacterial DNA Sifted from the <i>Trichoplax adhaerens</i> (Animalia: Placozoa) Genome Project Reveals a Putative Rickettsial Endosymbiont. <i>Genome Biology and Evolution</i> , 2013, 5, 621-645.	2.5	72

#	ARTICLE	IF	CITATIONS
19	Differential Stress Transcriptome Landscape of Historic and Recently Emerged Hypervirulent Strains of <i>Clostridium difficile</i> Strains Determined Using RNA-seq. <i>PLoS ONE</i> , 2013, 8, e78489.	2.5	22
20	A <i>Rickettsia</i> Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. <i>Journal of Bacteriology</i> , 2012, 194, 376-394.	2.2	152
21	Comparative Genomics of Early-Diverging <i>Brucella</i> Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. <i>MBio</i> , 2012, 3, e00246-11.	4.1	33
22	Comparative Genomics of Early-Diverging <i>Brucella</i> Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. <i>MBio</i> , 2012, 3, e00246-12.	4.1	37
23	<i>Helicobacter pylori</i> Colonization Ameliorates Glucose Homeostasis in Mice through a PPAR β -Dependent Mechanism. <i>PLoS ONE</i> , 2012, 7, e50069.	2.5	37
24	Overview of the ID, EPI and REL tasks of BioNLP Shared Task 2011. <i>BMC Bioinformatics</i> , 2012, 13, S2.	2.6	51
25	Selection of a phylogenetically informative region of the norovirus genome for outbreak linkage. <i>Virus Genes</i> , 2012, 44, 8-18.	1.6	16
26	PATRIC: the Comprehensive Bacterial Bioinformatics Resource with a Focus on Human Pathogenic Species. <i>Infection and Immunity</i> , 2011, 79, 4286-4298.	2.2	252
27	Analysis of High-Throughput Sequencing Data. <i>Methods in Molecular Biology</i> , 2011, 678, 1-11.	0.9	6
28	Supervised learning and prediction of physical interactions between human and HIV proteins. <i>Infection, Genetics and Evolution</i> , 2011, 11, 917-923.	2.3	83
29	Integration and visualization of host-pathogen data related to infectious diseases. <i>Bioinformatics</i> , 2011, 27, 2279-2287.	4.1	17
30	Abscisic Acid Regulates Inflammation via Ligand-binding Domain-independent Activation of Peroxisome Proliferator-activated Receptor β . <i>Journal of Biological Chemistry</i> , 2011, 286, 2504-2516.	3.4	94
31	Immunoregulatory mechanisms of macrophage PPAR β in mice with experimental inflammatory bowel disease. <i>Mucosal Immunology</i> , 2011, 4, 304-313.	6.0	74
32	Named Entity Recognition for Bacterial Type IV Secretion Systems. <i>PLoS ONE</i> , 2011, 6, e14780.	2.5	17
33	<i>Sinorhizobium meliloti</i> 1021 Loss-of-Function Deletion Mutation in <i>chvI</i> and Its Phenotypic Characteristics. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 153-160.	2.6	40
34	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010, 11, 384.	2.8	161
35	Members of the <i>Entamoeba histolytica</i> transmembrane kinase family play non-redundant roles in growth and phagocytosis. <i>International Journal for Parasitology</i> , 2010, 40, 833-843.	3.1	44
36	Data Integration for Dynamic and Sustainable Systems Biology Resources: Challenges and Lessons Learned. <i>Chemistry and Biodiversity</i> , 2010, 7, 1124-1141.	2.1	24

#	ARTICLE	IF	CITATIONS
37	Modulation of hepatic PPAR expression during Ft LVS LPS-induced protection from Francisella tularensis LVS infection. BMC Infectious Diseases, 2010, 10, 10.	2.9	14
38	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
39	The Human-Bacterial Pathogen Protein Interaction Networks of Bacillus anthracis, Francisella tularensis, and Yersinia pestis. PLoS ONE, 2010, 5, e12089.	2.5	131
40	Host-Interactive Genes in Amerindian <i>Helicobacter pylori</i> Diverge from Their Old World Homologs and Mediate Inflammatory Responses. Journal of Bacteriology, 2010, 192, 3078-3092.	2.2	50
41	Phylogeny of Gammaproteobacteria. Journal of Bacteriology, 2010, 192, 2305-2314.	2.2	317
42	Phylogenomics Reveals a Diverse <i>Rickettsiales</i> Type IV Secretion System. Infection and Immunity, 2010, 78, 1809-1823.	2.2	101
43	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. PLoS ONE, 2009, 4, e7162.	2.5	18
44	Detection of Nonstructural Protein 6 in Murine Coronavirus-Infected Cells and Analysis of the Transmembrane Topology by Using Bioinformatics and Molecular Approaches. Journal of Virology, 2009, 83, 6957-6962.	3.4	46
45	PIG—the pathogen interaction gateway. Nucleic Acids Research, 2009, 37, D647-D650.	14.5	57
46	Comparative Genomics Reveal Extensive Transposon-Mediated Genomic Plasticity and Diversity among Potential Effector Proteins within the Genus <i>Coxiella</i> . Infection and Immunity, 2009, 77, 642-656.	2.2	197
47	Variations on the tmRNA gene. RNA Biology, 2009, 6, 355-361.	3.1	26
48	A Typhus Group-Specific Protease Defies Reductive Evolution in Rickettsiae. Journal of Bacteriology, 2009, 191, 7609-7613.	2.2	17
49	Temporal Controls of the Asymmetric Cell Division Cycle in <i>Caulobacter crescentus</i> . PLoS Computational Biology, 2009, 5, e1000463.	3.2	30
50	Analysis of Ten <i>Brucella</i> Genomes Reveals Evidence for Horizontal Gene Transfer Despite a Preferred Intracellular Lifestyle. Journal of Bacteriology, 2009, 191, 3569-3579.	2.2	103
51	Gene expression in primate liver during viral hemorrhagic fever. Virology Journal, 2009, 6, 20.	3.4	30
52	<i>Brucella</i> . , 2009, , 1-64.		5
53	Louse- and flea-borne rickettsioses: biological and genomic analyses. Veterinary Research, 2009, 40, 12.	3.0	52
54	An Anomalous Type IV Secretion System in <i>Rickettsia</i> Is Evolutionarily Conserved. PLoS ONE, 2009, 4, e4833.	2.5	89

#	ARTICLE	IF	CITATIONS
55	Identification of new genes in <i>Sinorhizobium meliloti</i> using the Genome Sequencer FLX system. <i>BMC Microbiology</i> , 2008, 8, 72.	3.3	30
56	Characterization of an <i>Entamoeba histolytica</i> High-Mobility-Group Box Protein Induced during Intestinal Infection. <i>Eukaryotic Cell</i> , 2008, 7, 1565-1572.	3.4	24
57	An emerging cyberinfrastructure for biodefense pathogen and pathogen-host data. <i>Nucleic Acids Research</i> , 2008, 36, D884-D891.	14.5	15
58	A Quantitative Study of the Division Cycle of <i>Caulobacter crescentus</i> Stalked Cells. <i>PLoS Computational Biology</i> , 2008, 4, e9.	3.2	51
59	The Landscape of Human Proteins Interacting with Viruses and Other Pathogens. <i>PLoS Pathogens</i> , 2008, 4, e32.	4.7	297
60	<i>Rickettsia</i> Phylogenomics: Unwinding the Intricacies of Obligate Intracellular Life. <i>PLoS ONE</i> , 2008, 3, e2018.	2.5	175
61	Targets of the <i>Entamoeba histolytica</i> Transcription Factor URE3-BP. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e282.	3.0	34
62	Genome Sequence of <i>Brucella abortus</i> Vaccine Strain S19 Compared to Virulent Strains Yields Candidate Virulence Genes. <i>PLoS ONE</i> , 2008, 3, e2193.	2.5	108
63	Bioinformatics Resources for the Study of Viruses at the Virginia Bioinformatics Institute. , 2008, , 267-287.		0
64	A Robust Species Tree for the Alphaproteobacteria. <i>Journal of Bacteriology</i> , 2007, 189, 4578-4586.	2.2	257
65	Computational Model of the Division Cycle of <i>Caulobacter crescentus</i> . <i>AIP Conference Proceedings</i> , 2007, , .	0.4	0
66	PATRIC: The VBI PathoSystems Resource Integration Center. <i>Nucleic Acids Research</i> , 2007, 35, D401-D406.	14.5	125
67	A versatile computational pipeline for bacterial genome annotation improvement and comparative analysis, with <i>Brucella</i> as a use case. <i>Nucleic Acids Research</i> , 2007, 35, 3953-3962.	14.5	14
68	Roles of poly-3-hydroxybutyrate (PHB) and glycogen in symbiosis of <i>Sinorhizobium meliloti</i> with <i>Medicago sp.</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 388-398.	1.8	57
69	Plasmids and <i>Rickettsial</i> Evolution: Insight from <i>Rickettsia felis</i> . <i>PLoS ONE</i> , 2007, 2, e266.	2.5	212
70	National Institute of Allergy and Infectious Diseases Bioinformatics Resource Centers: New Assets for Pathogen Informatics. <i>Infection and Immunity</i> , 2007, 75, 3212-3219.	2.2	50
71	Loss of a Universal tRNA Feature. <i>Journal of Bacteriology</i> , 2007, 189, 1954-1962.	2.2	31
72	Early Blood Profiles of Virus Infection in a Monkey Model for Lassa Fever. <i>Journal of Virology</i> , 2007, 81, 7960-7973.	3.4	64

#	ARTICLE	IF	CITATIONS
73	Expressed Sequence Tags from <i>Phytophthora sojae</i> Reveal Genes Specific to Development and Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 781-793.	2.6	59
74	Computational prediction of host-pathogen protein-protein interactions. <i>Bioinformatics</i> , 2007, 23, i159-i166.	4.1	164
75	Influence of the Poly-3-Hydroxybutyrate (PHB) Granule-Associated Proteins (PhaP1 and PhaP2) on PHB Accumulation and Symbiotic Nitrogen Fixation in <i>Sinorhizobium meliloti</i> Rm1021. <i>Journal of Bacteriology</i> , 2007, 189, 9050-9056.	2.2	39
76	Gene expression profiling of nonhuman primates exposed to aerosolized Venezuelan equine encephalitis virus. <i>FEMS Immunology and Medical Microbiology</i> , 2007, 51, 462-472.	2.7	20
77	Plant Pathogen Forensics: Capabilities, Needs, and Recommendations. <i>Microbiology and Molecular Biology Reviews</i> , 2006, 70, 450-471.	6.6	143
78	<i>Phytophthora</i> Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	12.6	1,059
79	<i>Brucella melitensis</i> Triggers Time-Dependent Modulation of Apoptosis and Down-Regulation of Mitochondrion-Associated Gene Expression in Mouse Macrophages. <i>Infection and Immunity</i> , 2006, 74, 5035-5046.	2.2	85
80	Developing Bioinformatic Resources for Coronaviruses. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 395-398.	1.6	0
81	The Pathogen Resource Integration Center: Implications for Rickettsial Research. <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 459-465.	3.8	1
82	PIML: the Pathogen Information Markup Language. <i>Bioinformatics</i> , 2005, 21, 116-121.	4.1	88
83	NodMutDB: a database for genes and mutants involved in symbiosis. <i>Bioinformatics</i> , 2005, 21, 2927-2929.	4.1	32
84	Cyberinfrastructure for PathoSystems Biology. <i>Lecture Notes in Computer Science</i> , 2005, , 11-27.	1.3	1
85	A Quantitative Study of the Division Cycle of <i>Caulobacter crescentus</i> Stalked Cells. <i>PLoS Computational Biology</i> , 2005, preprint, e9.	3.2	0
86	Further Investigation of the Roles of Poly-3-Hydroxybutyrate (PHB) and Glycogen in <i>Sinorhizobium meliloti</i> - <i>Medicago</i> SP. <i>Symbiosis</i> , 2005, , 311-312.		0
87	A Life Scientist's Gateway to Distributed Data Management and Computing: The PathPort/ToolBus Framework. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 79-88.	2.0	35
88	ISYS: a decentralized, component-based approach to the integration of heterogeneous bioinformatics resources. <i>Bioinformatics</i> , 2001, 17, 83-94.	4.1	133
89	The Arabidopsis Information Resource (TAIR): a comprehensive database and web-based information retrieval, analysis, and visualization system for a model plant. <i>Nucleic Acids Research</i> , 2001, 29, 102-105.	14.5	497
90	Bioinformatics for Rice Resources. <i>Novartis Foundation Symposium</i> , 2001, 236, 59-84.	1.1	2

#	ARTICLE	IF	CITATIONS
91	Information systems approaches to support discovery in agricultural genomics. <i>Advances in Cellular and Molecular Biology of Plants</i> , 2001, , 139-166.	0.2	1
92	The Phytophthora Genome Initiative Database: informatics and analysis for distributed pathogenomic research. <i>Nucleic Acids Research</i> , 2000, 28, 87-90.	14.5	57
93	Comparative Analysis of Expressed Sequences in <i>Phytophthora sojae</i> . <i>Plant Physiology</i> , 2000, 123, 243-254.	4.8	183
94	Discrimination of <i>Rhizobium tropici</i> and <i>R. leguminosarum</i> strains by PCR-specific amplification of 16S-23S rDNA spacer region fragments and denaturing gradient gel electrophoresis (DGGE). <i>Letters in Applied Microbiology</i> , 1999, 28, 137-141.	2.2	23
95	Initial Assessment of Gene Diversity for the Oomycete Pathogen <i>Phytophthora infestans</i> Based on Expressed Sequences. <i>Fungal Genetics and Biology</i> , 1999, 28, 94-106.	2.1	159
96	Chapter 1.2 Bioinformatics and neuroscience in the post-genomic era. <i>Handbook of Behavioral Neuroscience</i> , 1999, 13, 20-30.	0.0	0
97	Plant disease resistance genes encode members of an ancient and diverse protein family within the nucleotide-binding superfamily. <i>Plant Journal</i> , 1999, 20, 317-332.	5.7	729
98	Genetic maps of <i>Saccharum officinarum</i> L. and <i>Saccharum robustum</i> Brandes & Jew. ex grassl. <i>Genetics and Molecular Biology</i> , 1999, 22, 125-132.	1.3	31
99	Comparative mapping of Andropogoneae: <i>Saccharum</i> L. (sugarcane) and its relation to sorghum and maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 14261-14266.	7.1	119
100	Common language of bioinformatics. <i>Nature</i> , 1997, 389, 418-418.	27.8	1
101	Polymerase Chain Reaction (PCR) Detection and Quantification Using a Short PCR Product and a Synthetic Internal Positive Control. <i>Analytical Biochemistry</i> , 1997, 248, 303-306.	2.4	10
102	Genetics of Polyploids. , 1996, , 3-37.		12
103	Genetic analysis of agronomic traits in a cross between sugarcane (<i>Saccharum officinarum</i> L.) and its presumed progenitor (<i>S. robustum</i> Brandes & Jesw. ex Grassl). <i>Molecular Breeding</i> , 1995, 1, 355-363.	2.1	38
104	<i>Saccharum spontaneum</i> L. SES 208™ genetic linkage map combining RFLP- and PCR-based markers. <i>Molecular Breeding</i> , 1995, 1, 165-179.	2.1	107
105	Genetic Variability among Brazilian Isolates of the Entomopathogenic Fungus <i>Metarhizium anisopliae</i> . <i>Journal of Invertebrate Pathology</i> , 1995, 65, 206-210.	3.2	40
106	Genetic Variability of <i>Paecilomyces fumosoroseus</i> Isolates Revealed by Molecular Markers. <i>Journal of Invertebrate Pathology</i> , 1995, 65, 274-282.	3.2	67
107	Genetics, Plants, and the Polymerase Chain Reaction. , 1994, , 304-319.		12
108	Phylogenetic analysis of organellar DNA sequences in the Andropogoneae: Saccharinae. <i>Theoretical and Applied Genetics</i> , 1994, 88, 933-944.	3.6	111

#	ARTICLE	IF	CITATIONS
109	Phylogenetic analysis of chloroplast restriction enzyme site mutations in the Saccharinae Griseb. subtribe of the Andropogoneae Dumort. tribe. Theoretical and Applied Genetics, 1994, 87, 843-853.	3.6	117
110	Chromosome assortment in Saccharum. Theoretical and Applied Genetics, 1994, 89-89, 959-963.	3.6	29
111	High output genetic mapping of polyploids using PCR-generated markers. Theoretical and Applied Genetics, 1993, 86, 105-112.	3.6	88
112	Physical map of the genome of Rhizobium meliloti 1021. Journal of Bacteriology, 1993, 175, 6945-6952.	2.2	108
113	Methyltransferases as Tools to Alter the Specificity of Restriction Endonucleases. , 1992, 12, 159-172.		2
114	Analysis of large DNA from soybean (Glycine max L. Merr.) by pulsed- field gel electrophoresis.. Plant Journal, 1992, 2, 133-135.	5.7	6
115	A rapid DNA extraction method for sugarcane and its relatives. Plant Molecular Biology Reporter, 1992, 10, 66-72.	1.8	28
116	Analysis of large DMA from soybean (Glycine max L. Merr.) by pulsed-field gel electrophoresis. Plant Journal, 1992, 2, 133-135.	5.7	8
117	Electrophoretic separation of the three Rhizobium meliloti replicons. Journal of Bacteriology, 1991, 173, 5173-5180.	2.2	95
118	The genomes of the family Rhizobiaceae: size, stability, and rarely cutting restriction endonucleases. Journal of Bacteriology, 1991, 173, 704-709.	2.2	31
119	Parentage determination in maize hybrids using the arbitrarily primed polymerase chain reaction (AP-PCR). Theoretical and Applied Genetics, 1991, 82, 473-476.	3.6	165
120	Analysis of rice (Oryza sativa L.) genome using pulsed-field gel electrophoresis and rare-cutting restriction endonucleases. Plant Molecular Biology Reporter, 1990, 8, 253-275.	1.8	19
121	Genome analysis of Bradyrhizobium japonicum serocluster 123 field isolates by using field inversion gel electrophoresis. Applied and Environmental Microbiology, 1990, 56, 1949-1953.	3.1	22
122	Pulse time and agarose concentration affect the electrophoretic mobility of cccDNA during electrophoresis in CHEF and In FIGE. Nucleic Acids Research, 1989, 17, 7359-7369.	14.5	20
123	Phylogeny and Comparative Genomics: the Shifting Landscape in the Genomics Era. , 0, , 84-141.		23