JoÃ£o Eduardo Ferreira

List of Publications by Year
in descending order

79	1,037	516710	477307
papers	citations	16	29
		h-index	g-index

82	82	82	1446
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Validation of physician certified verbal autopsy using conventional autopsy: a large study of adult non-external causes of death in a metropolitan area in Brazil. BMC Public Health, 2022, 22, 748.	2.9	2
2	Robust and Reliable Process-Aware Information Systems. IEEE Transactions on Services Computing, 2021, 14, 820-833.	4.6	1
3	Evaluation of Traditional and Deep Learning Human Detection Techniques Applied to Surveillance: A Performance Comparison at Distinct Object Sizes. , 2021, , .		1
4	Association of HIV infection with clinical and laboratory characteristics of sickle cell disease. BMC Infectious Diseases, 2020, 20, 638.	2.9	4
5	Beyond Artificial Reality. ACM Transactions on Internet Technology, 2020, 20, 1-21.	4.4	5
6	Small, Accurate, and Fast Re-ID on the Edge: The SAFR Approach. Lecture Notes in Computer Science, 2020, , 63-77.	1.3	0
7	Systematic Construction, Execution, and Reproduction of Complex Performance Benchmarks. Lecture Notes in Computer Science, 2019, , 26-37.	1.3	3
8	Intraparticle Connectivity in Sugarcane Bagasse Unveiled by Pore Network Modeling. Bioenergy Research, 2019, 12, 546-557.	3.9	3
9	Robust, Extensible, and Fast: Teamed Classifiers for Vehicle Tracking in Multi-Camera Networks. , 2019, , .		2
10	Clinical and Genetic Predictors of Priapism in Sickle Cell Disease: Results from the Recipient Epidemiology and Donor Evaluation Study III Brazil Cohort Study. Journal of Sexual Medicine, 2019, 16, 1988-1999.	0.6	8
11	Integrating the University of São Paulo Security Mobile App to the Electronic Monitoring System. , 2018, , .		1
12	Beneficial effects of benznidazole in Chagas disease: NIH SaMi-Trop cohort study. PLoS Neglected Tropical Diseases, 2018, 12, e0006814.	3.0	59
13	WED-SQL: An Intermediate Declarative Language for PAIS Execution. Lecture Notes in Computer Science, 2018, , 407-421.	1.3	2
14	Modeling Time-Critical Processes with WED-Flow. Lecture Notes in Computer Science, 2018, , 34-48.	1.3	0
15	Clinical and genetic ancestry profile of a large multiâ€centre sickle cell disease cohort in Brazil. British Journal of Haematology, 2018, 182, 895-908.	2.5	38
16	Visualization properties for data quality visual assessment: An exploratory case study. Information Visualization, 2017, 16, 93-112.	1.9	13
17	Mineral Particles in Sugar Cane Bagasse: Localization and Morphometry Using Microtomography Analysis. Energy & Fuels, 2017, 31, 12288-12296.	5.1	8
18	Dependency Management with WED-flow Techniques and Tools: A Case Study. , 2017, , .		1

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19	Smart services: A case study on smarter public safety by a mobile app for University of São Paulo. , 2017, , .		13
20	Mortality among blood donors seropositive and seronegative for Chagas disease (1996–2000) in São Paulo, Brazil: A death certificate linkage study. PLoS Neglected Tropical Diseases, 2017, 11, e0005542.	3.0	24
21	Longitudinal study of patients with chronic Chagas cardiomyopathy in Brazil (SaMi-Trop project): a cohort profile. BMJ Open, 2016, 6, e011181.	1.9	44
22	A provenance model based on declarative specifications for intensive data analyses in hemotherapy information systems. Future Generation Computer Systems, 2016, 59, 105-113.	7.5	3
23	A computational environment to support research in sugarcane agriculture. Computers and Electronics in Agriculture, 2016, 130, 13-19.	7.7	23
24	Transfusion-Transmitted Dengue and Associated Clinical Symptoms During the 2012 Epidemic in Brazil. Journal of Infectious Diseases, 2016, 213, 694-702.	4.0	114
25	A Formal Taxonomy to Improve Data Defect Description. Lecture Notes in Computer Science, 2016, , 307-320.	1.3	6
26	The Virological and Immunological Characteristics of the HIV-1-Infected Population in Brazil: From Initial Diagnosis to Impact of Antiretroviral Use. PLoS ONE, 2015, 10, e0139677.	2.5	16
27	Data-intensive analysis of HIV mutations. BMC Bioinformatics, 2015, 16, 35.	2.6	1
28	P-SaMI. , 2015, , .		2
29	Accuracy of a probabilistic record-linkage methodology used to track blood donors in the Mortality Information System database. Cadernos De Saude Publica, 2014, 30, 1623-1632.	1.0	17
30	Data Analysis Workflow for Experiments in Sugarcane Precision Agriculture. , 2014, , .		5
31	A Provenance Model Based on Declarative Specifications for Intensive Data Analyses in Hemotherapy Information Systems. , 2014, , .		1
32	Demographic, risk factors and motivations among blood donors with reactive serologic tests for syphilis in São Paulo, Brazil. Transfusion Medicine, 2014, 24, 169-175.	1.1	4
33	Application Configuration Repository for Adaptive Service-Based Systems: Overcoming Challenges in an Evolutionary Online Advertising Environment. , 2014, , .		1
34	Contribution of the Retrovirus Epidemiology Donor Study (REDS) to research on blood transfusion safety in Brazil. Revista Brasileira De Hematologia E Hemoterapia, 2014, 36, 152-158.	0.7	5
35	Prevalence of *Treponema pallidum* DNA among blood donors with two different serologic tests profiles for syphilis in São Paulo, Brazil. Vox Sanguinis, 2014, 106, 376-378.	1.5	6
36	Predictors of low haematocrit among repeat donors in São Paulo, Brazil: Eleven year longitudinal analysis. Transfusion and Apheresis Science, 2013, 49, 553-559.	1.0	8

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37	Analysis of donor deferral at three blood centers in Brazil. Transfusion, 2013, 53, 531-538.	1.6	32
38	Prevalence of serologic markers for hepatitis B and C viruses in Brazilian blood donors and incidence and residual risk of transfusion transmission of hepatitis C virus. Transfusion, 2013, 53, 827-834.	1.6	33
39	Methodological guidelines for reducing the complexity of data warehouse development for transactional blood bank systems. Decision Support Systems, 2013, 55, 728-739.	5.9	12
40	Web Services Composition through Data Events Approach. , 2013, , .		1
41	Prediction of Developer Participation in Issues of Open Source Projects. , 2012, , .		3
42	Transactional Recovery Support for Robust Exception Handling in Business Process Services. , 2012, , .		12
43	Data-intensive analysis of HIV mutations. , 2012, , .		0
44	Number of recent sexual partners among blood donors in Brazil: associations with donor demographics, donation characteristics, and infectious disease markers. Transfusion, 2012, 52, 151-159.	1.6	17
45	Human immunodeficiency virus prevalence, incidence, and residual risk of transmission by transfusions at Retrovirus Epidemiology Donor Study–I blood centers in Brazil. Transfusion, 2012, 52, 870-879.	1.6	51
46	Blood transfusion utilization and recipient survival at Hospital das Clinicas in São Paulo, Brazil. Transfusion, 2012, 52, 729-738.	1.6	18
47	Demographic characteristics and prevalence of serologic markers among blood donors who use confidential unit exclusion (CUE) in São Paulo, Brazil: implications for modification of CUE polices in Brazil. Transfusion, 2011, 51, 191-197.	1.6	17
48	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. Tropical Plant Biology, 2011, 4, 145-156.	1.9	91
49	A rigorous approach to facilitate and guarantee the correctness of the genetic testing management in human genome information systems. BMC Genomics, 2011, 12, S13.	2.8	2
50	Performance Evaluation of Business Processes through a Formal Transformation to SAN. Lecture Notes in Computer Science, 2011, , 42-56.	1.3	5
51	Using LOTOS for rigorous specifications of workflow patterns. , 2010, , .		1
52	Demographic profile of blood donors at three major Brazilian blood centers: results from the International REDS–I study, 2007 to 2008. Transfusion, 2010, 50, 918-925.	1.6	43
53	Towards Flexible Event-Handling in Workflows through Data States. , 2010, , .		10
54	Performance analysis modeling applied to business processes. , 2010, , .		1

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55	A partial persistent data structure to support consistency in real-time collaborative editing. , 2010, , .		10
56	Reducing Exception Handling Complexity in Business Process Modeling and Implementation: The WED-Flow Approach. Lecture Notes in Computer Science, 2010, , 150-167.	1.3	8
57	Algebraic approach to optimal clone selection applied in metagenomic projects. , 2010, , .		1
58	HIVSetSubtype. , 2009, , .		0
59	Implementing rigorous web services with process algebra. , 2009, , .		2
60	The RiverFish Approach to Business Process Modeling: Linking Business Steps to Control-Flow Patterns. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2009, , 179-193.	0.3	5
61	Towards Algorithmic Generation of Business Processes: From Business Step Dependencies to Process Algebra Expressions. Lecture Notes in Computer Science, 2009, , 80-96.	1.3	7
62	NPTool: Towards Scalability and Reliability of Business Process Management. Communications in Computer and Information Science, 2009, , 99-112.	0.5	1
63	Using annotations in the naked objects framework to explore data requirements. , 2008, , .		3
64	Using process algebra to control the execution of business processes. , 2008, , .		2
65	HIV drug resistance analysis tool based on process algebra. , 2008, , .		2
66	Using control-flow patterns for specifying business processes in cooperative environments. , 2007, , .		10
67	Large Scale Order Processing through Navigation Plan Concept. , 2006, , .		7
68	Trends in Antiretroviral Drug Resistance and Clade Distributions Among HIV-1–Infected Blood Donors in Sao Paulo, Brazil. Journal of Acquired Immune Deficiency Syndromes (1999), 2006, 41, 388-341.	2.1	63
69	Synchronization Options for Data Warehouse Designs. Computer, 2006, 39, 53-57.	1.1	23
70	Multi-character population study of the vir subtelomeric multigene superfamily of Plasmodium vivax, a major human malaria parasite. Molecular and Biochemical Parasitology, 2006, 149, 10-16.	1.1	31
71	Extense variant gene family repertoire overlap in Western Amazon Plasmodium falciparum isolates. Molecular and Biochemical Parasitology, 2006, 150, 157-165.	1.1	35
72	DBCollHIV: a database system for collaborative HIV analysis in Brazil. Genetics and Molecular Research, 2006, 5, 203-15.	0.2	3

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73	GenFlow: generic flow for integration, management and analysis of molecular biology data. Genetics and Molecular Biology, 2004, 27, 691-695.	1.3	3
74	An environment for knowledge discovery in biology. Computers in Biology and Medicine, 2004, 34, 427-447.	7.0	15
75	<title>Simulator for gene expression networks</title>. , 2001, 4266, 248.		2
76	Use of a semantically grained database system for distribution and control within design environments. Lecture Notes in Computer Science, 1997, , 1130-1134.	1.3	1
77	A hybrid model for data synchronism in data warehouse projects. , 0, , .		2
78	Data Updating Between the Operational and Analytical Databases Through DW-Log Algorithm. , 0, , .		0
79	Integration of Business Processes with Autonomous Information Systems: A Case Study in Government Services. , 0, , .		7