Oswaldo Trelles Salazar

List of Publications by Year
in descending order

62 papers	1,299 citations	361413 20 h-index	361022 35 g-index
64 all docs	64 docs citations	64 times ranked	1830 citing authors

#	Article	IF	Citations
1	Big data, but are we ready?. Nature Reviews Genetics, 2011, 12, 224-224.	16.3	126
2	Integrated analysis of gene expression by Association Rules Discovery. BMC Bioinformatics, 2006, 7, 54.	2.6	100
3	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	6.5	91
4	De Novo Assembly and Functional Annotation of the Olive (Olea europaea) Transcriptome. DNA Research, 2013, 20, 93-108.	3.4	84
5	Sma3s: A Three-Step Modular Annotator for Large Sequence Datasets. DNA Research, 2014, 21, 341-353.	3.4	80
6	The 800-nm diode laser in the treatment of leg veins: Assessment at 6 months. Journal of the American Academy of Dermatology, 2006, 54, 282-289.	1.2	71
7	Early and delayed long-term transcriptional changes and short-term transient responses during cold acclimation in olive leaves. DNA Research, 2015, 22, 1-11.	3.4	67
8	Assessment of the Efficacy of Nonablative Long-Pulsed 1064-nm Nd:YAG Laser Treatment of Wrinkles Compared at 2, 4, and 6 Months. Facial Plastic Surgery, 2005, 21, 145-153.	0.9	43
9	Mammalian l-amino acid decarboxylases producing 1,4-diamines: analogies among differences. Trends in Biochemical Sciences, 1994, 19, 318-319.	7.5	38
10	Development of EST-derived SSR Markers with Long-core Repeat in Olive and Their Use for Paternity Testing. Journal of the American Society for Horticultural Science, 2013, 138, 290-296.	1.0	38
11	Engene: the processing and exploratory analysis of gene expression data. Bioinformatics, 2003, 19, 657-658.	4.1	34
12	Intelligent client for integrating bioinformatics services. Bioinformatics, 2006, 22, 106-111.	4.1	34
13	Genetic and genome-wide transcriptomic analyses identify co-regulation of oxidative response and hormone transcript abundance with vitamin C content in tomato fruit. BMC Genomics, 2012, 13, 187.	2.8	33
14	Microbiome overview in swine lungs. PLoS ONE, 2017, 12, e0181503.	2.5	33
15	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31
16	Magallanes: a web services discovery and automatic workflow composition tool. BMC Bioinformatics, 2009, 10, 334.	2.6	27
17	PreP: gene expression data pre-processing. Bioinformatics, 2003, 19, 2328-2329.	4.1	26
18	Transcriptomic Analysis Using Olive Varieties and Breeding Progenies Identifies Candidate Genes Involved in Plant Architecture. Frontiers in Plant Science, 2016, 7, 240.	3.6	25

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19	Building an open source cloud environment with auto-scaling resources for executing bioinformatics and biomedical workflows. Future Generation Computer Systems, 2017, 67, 329-340.	7.5	24
20	Ultra-fast genome comparison for large-scale genomic experiments. Scientific Reports, 2019, 9, 10274.	3.3	24
21	jORCA: easily integrating bioinformatics Web Services. Bioinformatics, 2010, 26, 553-559.	4.1	23
22	Mining association rules from biological databases. Journal of the Association for Information Science and Technology, 2005, 56, 493-504.	2.6	20
23	Supervised Lowess normalization of comparative genome hybridization data â€" application to lactococcal strain comparisons. BMC Bioinformatics, 2008, 9, 93.	2.6	20
24	Genetic changes involved in the juvenile-to-adult transition in the shoot apex of Olea europaea L. occur years before the first flowering. Tree Genetics and Genomes, 2014, 10, 585.	1.6	20
25	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	1.6	19
26	Saturation and Quantization Reduction in Microarray Experiments using Two Scans at Different Sensitivities. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-16.	0.6	18
27	Breaking the computational barriers of pairwise genome comparison. BMC Bioinformatics, 2015, 16, 250.	2.6	16
28	Histological correlation in laser skin resurfacing. Lasers in Medical Science, 1995, 10, 279-282.	2.1	13
29	A Computational Strategy for Protein Function Assignment which Addresses the Multidomain Problem. Comparative and Functional Genomics, 2002, 3, 423-440.	2.0	12
30	PreP+07: improvements of a user friendly tool to preprocess and analyse microarray data. BMC Bioinformatics, 2009, 10, 16.	2.6	12
31	A metadata classification schema for semantic content analysis of videos. Journal of Microscopy, 2002, 205, 33-42.	1.8	9
32	An 810ï¿½nm diode laser in the treatment of small (?1.0ï¿½mm) leg veins: a preliminary assessment. Lasers in Medical Science, 2004, 19, 21-6.	2.1	9
33	MAPI: a software framework for distributed biomedical applications. Journal of Biomedical Semantics, 2013, 4, 4.	1.6	9
34	A new user-friendly software platform for systematic classification of skin lesions to aid in their diagnosis and prognosis. Lasers in Medical Science, 2006, 21, 54-60.	2.1	8
35	Workflow Composition and Enactment Using jORCA. Lecture Notes in Computer Science, 2010, , 328-339.	1.3	7
36	Long-pulsed Nd:YAG 1064nm in the treatment of leg veins: Check up of results at 6 months in 100 patients. Medical Laser Application: International Journal for Laser Treatment and Research, 2005, 20, 255-266.	0.3	6

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37	Computational workflow for the fine-grained analysis of metagenomic samples. BMC Genomics, 2016, 17, 802.	2.8	6
38	Bio-Broker: a tool for integration of biological data sources and data analysis tools. Software - Practice and Experience, 2006, 36, 1585-1604.	3.6	5
39	Training bioinformaticians in High Performance Computing. Heliyon, 2018, 4, e01057.	3.2	5
40	Automatic Analysis of the Content of Cell Biological Videos and Database Organization of Their Metadata Descriptors. IEEE Transactions on Multimedia, 2004, 6, 119-128.	7.2	4
41	Analysis and Description of the Semantic Content of Cell Biological Videos. Multimedia Tools and Applications, 2005, 25, 37-58.	3.9	4
42	MOWServ: a web client for integration of bioinformatic resources. Nucleic Acids Research, 2010, 38, W671-W676.	14.5	4
43	Pairwise Genome Comparison Workflow in the Cloud Using Galaxy. Procedia Computer Science, 2015, 51, 2864-2868.	2.0	3
44	Command-line interfaces can be efficiently brought to graphics: COLIMATE (the COmmand LIne MATE). Software - Practice and Experience, 2002, 32, 873-887.	3.6	2
45	Bioinformatics and Parallel Metaheuristics. , 2005, , 517-549.		2
46	Using Graphics Processors for a High Performance Normalization of Gene Expressions. , 2011, , .		2
47	Two level parallelism and I/O reduction in genome comparisons. Cluster Computing, 2017, 20, 1925-1936.	5.0	2
48	PLIDflow: an open-source workflow for the online analysis of protein–ligand docking using galaxy. Bioinformatics, 2020, 36, 4203-4205.	4.1	2
49	MAPI: towards the integrated exploitation of bioinformatics Web Services. BMC Bioinformatics, 2011, 12, 419.	2.6	1
50	Bio-Cirrus: A Framework for Running Legacy Bioinformatics Applications with Cloud Computing Resources. Lecture Notes in Computer Science, 2013, , 200-207.	1.3	1
51	Accelerating Exhaustive Pairwise Metagenomic Comparisons. Lecture Notes in Computer Science, 2017, , 611-620.	1.3	1
52	mORCA: sailing bioinformatics world with mobile devices. Bioinformatics, 2018, 34, 869-870.	4.1	1
53	Precise and Parallel Pairwise Metagenomic Comparisons. Journal of Computational Biology, 2018, 25, 841-849.	1.6	1
54	Combining Strengths for Multi-genome Visual Analytics Comparison. Bioinformatics and Biology Insights, 2019, 13, 117793221882512.	2.0	1

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55	Two-Level Parallelism to Accelerate Multiple Genome Comparisons. Lecture Notes in Computer Science, 2017, , 445-456.	1.3	1
56	jORCA and Magallanes Sailing Together towards Integration of Web Services. Lecture Notes in Computer Science, 2012, , 94-101.	1.3	1
57	Clinical and histologic effects of facial skin rejuvenation with pulsed- and continuous-wave flash-scanned CO_2 lasers. Aesthetic Surgery Journal, 2001, 21, 399-411.	1.6	0
58	mORCA: ubiquitous access to life science web services. BMC Genomics, 2018, 19, 56.	2.8	0
59	Unraveling Genome Evolution Throughout Visual Analysis: The XCout Portal. Bioinformatics and Biology Insights, 2021, 15, 117793222110214.	2.0	0
60	Statistical Significance for NGS Reads Similarities. Lecture Notes in Computer Science, 2012, , 1-7.	1.3	0
61	Mobile Access to On-line Analytic Bioinformatics Tools. Lecture Notes in Computer Science, 2015, , 555-565.	1.3	0
62	Workflows and Service Discovery: A Mobile Device Approach. Lecture Notes in Computer Science, 2018, , 177-185.	1.3	0