

Stefano Lonardi

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

138
papers

10,243
citations

39
h-index

100
g-index

153
ext. papers

12,618
ext. citations

5.8
avg, IF

5.92
L-index

#	Paper	IF	Citations
138	A whole-genome assembly of <i>Drosophila</i> . <i>Science</i> , 2000 , 287, 2196-204	33.3	1204
137	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124
136	Experiencing SAX: a novel symbolic representation of time series. <i>Data Mining and Knowledge Discovery</i> , 2007 , 15, 107-144	5.6	870
135	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017 , 544, 427-433	33.4	822
134	A symbolic representation of time series, with implications for streaming algorithms 2003 ,		552
133	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009 , 10, 582	4.5	477
132	Efficient and accurate construction of genetic linkage maps from the minimum spanning tree of a graph. <i>PLoS Genetics</i> , 2008 , 4, e1000212	6	399
131	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , 2015 , 16, 236	4.5	347
130	Probabilistic discovery of time series motifs 2003 ,		278
129	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. <i>BMC Bioinformatics</i> , 2007 , 8, 211	3.6	276
128	Towards parameter-free data mining 2004 ,		275
127	Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 20429-34	11.5	257
126	Finding surprising patterns in a time series database in linear time and space 2002 ,		179
125	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017 , 18, 182	18.3	152
124	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019 , 98, 767-782	6.9	128
123	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017 , 89, 1042-1054	6.9	118
122	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011 , 4, 238-249	4.4	111

121	Nucleosome landscape and control of transcription in the human malaria parasite. <i>Genome Research</i> , 2010 , 20, 228-38	9.7	109
120	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. <i>BMC Molecular Biology</i> , 2008 , 9, 6	4.5	105
119	Assignment of orthologous genes via genome rearrangement. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005 , 2, 302-15	3	101
118	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L. <i>Scientific Data</i> , 2017 , 4, 170044	8.2	93
117	Accurate construction of consensus genetic maps via integer linear programming. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 381-94	3	88
116	Generating and reversing chronic wounds in diabetic mice by manipulating wound redox parameters. <i>Journal of Diabetes Research</i> , 2014 , 2014, 562625	3.9	81
115	Visually mining and monitoring massive time series 2004 ,		75
114	Higher classification sensitivity of short metagenomic reads with CLARK-S. <i>Bioinformatics</i> , 2016 , 32, 3823-3825	7.1	71
113	Time-series Bitmaps: a Practical Visualization Tool for Working with Large Time Series Databases 2005 ,		71
112	Visualizing and Discovering Non-Trivial Patterns in Large Time Series Databases. <i>Information Visualization</i> , 2005 , 4, 61-82	2.4	71
111	BRAT-BW: efficient and accurate mapping of bisulfite-treated reads. <i>Bioinformatics</i> , 2012 , 28, 1795-6	7.2	69
110	A multi-parent advanced generation inter-cross (MAGIC) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). <i>Plant Journal</i> , 2018 , 93, 1129-1142	6.9	65
109	Compression-based data mining of sequential data. <i>Data Mining and Knowledge Discovery</i> , 2007 , 14, 99-120	3.0	63
108	Genome-wide mapping of DNA methylation in the human malaria parasite <i>Plasmodium falciparum</i> . <i>Cell Host and Microbe</i> , 2013 , 14, 696-706	23.4	60
107	BRAT: bisulfite-treated reads analysis tool. <i>Bioinformatics</i> , 2010 , 26, 572-3	7.2	60
106	. <i>Proceedings of the IEEE</i> , 2000 , 88, 1733-1744	14.3	59
105	Time Series Epenthesis: Clustering Time Series Streams Requires Ignoring Some Data 2011 ,		58
104	Efficient detection of unusual words. <i>Journal of Computational Biology</i> , 2000 , 7, 71-94	1.7	50

103	A Bit Level Representation for Time Series Data Mining with Shape Based Similarity. <i>Data Mining and Knowledge Discovery</i> , 2006 , 13, 11-40	5.6	47
102	Validating genome-wide CRISPR-Cas9 function improves screening in the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2019 , 55, 102-110	9.7	46
101	A Novel Bit Level Time Series Representation with Implication of Similarity Search and Clustering. <i>Lecture Notes in Computer Science</i> , 2005 , 771-777	0.9	46
100	Mechanisms of small RNA generation from cis-NATs in response to environmental and developmental cues. <i>Molecular Plant</i> , 2013 , 6, 704-15	14.4	40
99	ON THE ACCURATE CONSTRUCTION OF CONSENSUS GENETIC MAPS 2008 ,		39
98	DNA-encoded nucleosome occupancy is associated with transcription levels in the human malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2014 , 15, 347	4.5	38
97	OligoSpawn: a software tool for the design of overgo probes from large unigene datasets. <i>BMC Bioinformatics</i> , 2006 , 7, 7	3.6	38
96	MDL-based time series clustering. <i>Knowledge and Information Systems</i> , 2012 , 33, 371-399	2.4	37
95	Graphlet kernels for prediction of functional residues in protein structures. <i>Journal of Computational Biology</i> , 2010 , 17, 55-72	1.7	36
94	Monotony of surprise and large-scale quest for unusual words. <i>Journal of Computational Biology</i> , 2003 , 10, 283-311	1.7	35
93	On the accurate construction of consensus genetic maps. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008 , 7, 285-96		35
92	Identification of candidate genes and molecular markers for heat-induced brown discoloration of seed coats in cowpea [<i>Vigna unguiculata</i> (L.) Walp]. <i>BMC Genomics</i> , 2014 , 15, 328	4.5	34
91	Nucleosome occupancy at transcription start sites in the human malaria parasite: a hard-wired evolution of virulence?. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 716-24	4.5	33
90	Sequencing of 15 \times 22 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015 , 84, 216-27	6.9	31
89	Discovering the Intrinsic Cardinality and Dimensionality of Time Series Using MDL 2011 ,		28
88	COMPUTING THE ASSIGNMENT OF ORTHOLOGOUS GENES VIA GENOME REARRANGEMENT 2005 ,		28
87	A comparative evaluation of genome assembly reconciliation tools. <i>Genome Biology</i> , 2017 , 18, 93	18.3	27
86	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. <i>PLoS Computational Biology</i> , 2016 , 12, e1005107	5	26

85	String Matching in Hardware Using the FM-Index 2011 ,		25
84	Mustache: multi-scale detection of chromatin loops from Hi-C and Micro-C maps using scale-space representation. <i>Genome Biology</i> , 2020 , 21, 256	18.3	25
83	FHAST: FPGA-Based Acceleration of Bowtie in Hardware. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 973-81	3	24
82	NORMAL: accurate nucleosome positioning using a modified Gaussian mixture model. <i>Bioinformatics</i> , 2012 , 28, i242-9	7.2	24
81	When less is more: 'slicing' sequencing data improves read decoding accuracy and de novo assembly quality. <i>Bioinformatics</i> , 2015 , 31, 2972-80	7.2	23
80	Monotony of surprise and large-scale quest for unusual words 2002 ,		22
79	De novo meta-assembly of ultra-deep sequencing data. <i>Bioinformatics</i> , 2015 , 31, i9-16	7.2	21
78	On average sequence complexity. <i>Theoretical Computer Science</i> , 2004 , 326, 213-227	1.1	20
77	Gridding and compression of microarray images 2004 , 122-30		20
76	Intelligent Icons: Integrating Lite-Weight Data Mining and Visualization into GUI Operating Systems. <i>IEEE International Conference on Data Mining</i> , 2006 ,		19
75	Selfish: discovery of differential chromatin interactions via a self-similarity measure. <i>Bioinformatics</i> , 2019 , 35, i145-i153	7.2	18
74	Exploration of Short Reads Genome Mapping in Hardware 2010 ,		18
73	Soft-core Processor Customization using the Design of Experiments Paradigm 2007 ,		17
72	A parallel edge-betweenness clustering tool for Protein-Protein Interaction networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2007 , 1, 241-7	0.5	17
71	Efficient selection of unique and popular oligos for large EST databases. <i>Bioinformatics</i> , 2004 , 20, 2101-122		17
70	Verbumculus and the discovery of unusual words. <i>Journal of Computer Science and Technology</i> , 2004 , 19, 22-41	1.7	16
69	Multithreaded FPGA acceleration of DNA sequence mapping 2012 ,		15
68	Combinatorial pooling enables selective sequencing of the barley gene space. <i>PLoS Computational Biology</i> , 2013 , 9, e1003010	5	15

67	Finding Biclusters by Random Projections. <i>Lecture Notes in Computer Science</i> , 2004 , 102-116	0.9	15
66	Novo&Stitch: accurate reconciliation of genome assemblies via optical maps. <i>Bioinformatics</i> , 2018 , 34, i43-i51	7.2	12
65	Using the minimum description length to discover the intrinsic cardinality and dimensionality of time series. <i>Data Mining and Knowledge Discovery</i> , 2015 , 29, 358-399	5.6	11
64	Seed Coat Pattern QTL and Development in Cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Frontiers in Plant Science</i> , 2019 , 10, 1346	6.2	11
63	Dot plots for time series analysis 2005 ,		11
62	Shape recovery and volume calculation from biplane angiography in the stereotactic radiosurgical treatment of arteriovenous malformations. <i>International Journal of Radiation Oncology Biology Physics</i> , 1996 , 35, 565-77	4	11
61	BRAT-nova: fast and accurate mapping of bisulfite-treated reads. <i>Bioinformatics</i> , 2016 , 32, 2696-8	7.2	11
60			10
59	Length-based encoding of binary data in DNA. <i>Langmuir</i> , 2008 , 24, 1613-6	4	9
58	Efficient and Accurate Construction of Genetic Linkage Maps from Noisy and Missing Genotyping Data. <i>Lecture Notes in Computer Science</i> , 2007 , 395-406	0.9	9
57	OMGS: Optical Map-Based Genome Scaffolding. <i>Journal of Computational Biology</i> , 2020 , 27, 519-533	1.7	9
56	Higher Classification Accuracy of Short Metagenomic Reads by Discriminative Spaced k-mers. <i>Lecture Notes in Computer Science</i> , 2015 , 286-295	0.9	8
55	PuFFIN--a parameter-free method to build nucleosome maps from paired-end reads. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 9, S11	3.6	8
54	Chromatin-driven de novo discovery of DNA binding motifs in the human malaria parasite. <i>BMC Genomics</i> , 2011 , 12, 601	4.5	8
53	Error Resilient LZ'77 Data Compression: Algorithms, Analysis, and Experiments. <i>IEEE Transactions on Information Theory</i> , 2007 , 53, 1799-1813	2.8	8
52	Efficient information compression in sensor networks. <i>International Journal of Sensor Networks</i> , 2006 , 1, 229	0.8	8
51	Finding biclusters by random projections. <i>Theoretical Computer Science</i> , 2006 , 368, 217-230	1.1	8
50	Efficient Discovery of Unusual Patterns in Time Series. <i>New Generation Computing</i> , 2006 , 25, 61-93	0.9	8

49	Efficient genome-wide TagSNP selection across populations via the linkage disequilibrium criterion. <i>Journal of Computational Biology</i> , 2010 , 17, 21-37	1.7	7
48	Joint source-channel LZ'77 coding		7
47	DeeplyEssential: a deep neural network for predicting essential genes in microbes. <i>BMC Bioinformatics</i> , 2020 , 21, 367	3.6	7
46	Accurate detection of chimeric contigs via Bionano optical maps. <i>Bioinformatics</i> , 2019 , 35, 1760-1762	7.2	7
45	A graph-theoretical approach to the selection of the minimum tiling path from a physical map. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 352-60	3	6
44	Storage and transmission of microarray images. <i>Drug Discovery Today</i> , 2005 , 10, 1689-95	8.8	6
43	Deciphering histone code of transcriptional regulation in malaria parasites by large-scale data mining. <i>Computational Biology and Chemistry</i> , 2014 , 50, 3-10	3.6	5
42	Analysis of nucleosome positioning landscapes enables gene discovery in the human malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2015 , 16, 1005	4.5	5
41	A linear-time algorithm for predicting functional annotations from PPI networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 1049-65	1	5
40	Online Information Compression in Sensor Networks 2006 ,		5
39	Authentication of LZ-77 compressed data 2003 ,		5
38	VizTree: A Tool for Visually Mining and Monitoring Massive Time Series Databases 2004 , 1269-1272		5
37	EFFICIENT ALGORITHMS FOR GENOME-WIDE TAGSNP SELECTION ACROSS POPULATIONS VIA THE LINKAGE DISEQUILIBRIUM CRITERION 2007 ,		5
36	Two-Level Microprocessor-Accelerator Partitioning 2007 ,		4
35	Discovery of Repetitive Patterns in DNA with Accurate Boundaries		4
34	Accurate Decoding of Pooled Sequenced Data Using Compressed Sensing. <i>Lecture Notes in Computer Science</i> , 2013 , 70-84	0.9	4
33	A multi-parent advanced generation inter-cross population for genetic analysis of multiple traits in cowpea (<i>Vigna unguiculata</i> L. Walp.)		4
32	Efficient Selection of Unique and Popular Oligos for Large EST Databases. <i>Lecture Notes in Computer Science</i> , 2003 , 384-401	0.9	4

31	Data mining in bioinformatics: selected papers from BIODKDD. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010 , 7, 195-6	3	3
30	A speed-up for the commute between subword trees and DAWGs. <i>Information Processing Letters</i> , 2002 , 83, 159-161	0.8	3
29	Analysis of secondary structure elements of proteins using indexing techniques		3
28	Comprehensive Benchmarking and Ensemble Approaches for Metagenomic Classifiers		3
27	Mustache: Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation		3
26	Higher classification sensitivity of short metagenomic reads with CLARK-S		3
25	A compartmentalized approach to the assembly of physical maps. <i>BMC Bioinformatics</i> , 2009 , 10, 217	3.6	2
24	Deconvoluting BAC-gene relationships using a physical map. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 603-22	1	2
23	Clock-Frequency Assignment for Multiple Clock Domain Systems-on-a-Chip 2007 ,		2
22	A Compartmentalized Approach to the Assembly of Physical Maps 2007 ,		2
21	A Practical Tool for Visualizing and Data Mining Medical Time Series		2
20	Error-resilient LZW data compression		2
19	VizTree: A Tool for Visually Mining and Monitoring Massive Time Series Databases 2004 , 1269-1272		2
18	Augmenting LZ-77 with authentication and integrity assurance capabilities. <i>Concurrency Computation Practice and Experience</i> , 2004 , 16, 1063-1076	1.4	2
17	On the Average Sequence Complexity. <i>Lecture Notes in Computer Science</i> , 2004 , 74-88	0.9	2
16	Computing the Minimal Tiling Path from a Physical Map by Integer Linear Programming. <i>Lecture Notes in Computer Science</i> , 2008 , 148-161	0.9	2
15	Reference-agnostic representation and visualization of pan-genomes. <i>BMC Bioinformatics</i> , 2021 , 22, 5023.6		2
14	Genome resources for climate-resilient cowpea, an essential crop for food security		2

13	Seed Coat Pattern QTL and Development in Cowpea (<i>Vigna unguiculata</i> [L.] Walp.)		2
12	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.)		2
11	Genome-wide functional screens enable the prediction of high activity CRISPR-Cas9 and -Cas12a guides in <i>Yarrowia lipolytica</i> . <i>Nature Communications</i> , 2022 , 13, 922	17.4	2
10	Scribe: Ultra-Accurate Error-Correction of Pooled Sequenced Reads. <i>Lecture Notes in Computer Science</i> , 2015 , 162-174	0.9	1
9	A Compression-Boosting Transform for Two-Dimensional Data. <i>Lecture Notes in Computer Science</i> , 2006 , 126-137	0.9	1
8	mClass: Cancer Type Classification with Somatic Point Mutation Data. <i>Lecture Notes in Computer Science</i> , 2018 , 131-145	0.9	1
7	Towards Discovering the Intrinsic Cardinality and Dimensionality of Time Series Using MDL. <i>Lecture Notes in Computer Science</i> , 2013 , 184-197	0.9	1
6	Prediction Of Histone Post-Translational Modifications Using Deep Learning. <i>Bioinformatics</i> , 2020 ,	7.2	1
5	Bisulfite-Conversion-Based Methods for DNA Methylation Sequencing Data Analysis 2016 , 227-243		1
4	Fractal image approximation and orthogonal bases. <i>Signal Processing: Image Communication</i> , 1999 , 14, 413-423	2.8	0
3	OMGS: Optical Map-Based Genome Scaffolding. <i>Lecture Notes in Computer Science</i> , 2019 , 190-207	0.9	
2	BIOKDD 2008. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2008 , 10, 51-53	4.6	
1	CPM 20th Anniversary: A Statistical Retrospective. <i>Lecture Notes in Computer Science</i> , 2009 , 1-11	0.9	