Stefano Lonardi

List of Publications by Year
in descending order

134 papers	14,397 citations	76196 40 h-index	35952 97 g-index
153 all docs	153 docs citations	153 times ranked	16805 citing authors

#	Article	IF	Citations
1	A Whole-Genome Assembly of Drosophila. Science, 2000, 287, 2196-2204.	6.0	1,449
2	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	13.7	1,416
3	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	13.7	1,365
4	Experiencing SAX: a novel symbolic representation of time series. Data Mining and Knowledge Discovery, 2007, 15, 107-144.	2.4	1,190
5	A symbolic representation of time series, with implications for streaming algorithms. , 2003, , .		919
6	Efficient and Accurate Construction of Genetic Linkage Maps from the Minimum Spanning Tree of a Graph. PLoS Genetics, 2008, 4, e1000212.	1.5	590
7	Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582.	1.2	570
8	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. BMC Genomics, 2015, 16, 236.	1.2	514
9	Towards parameter-free data mining. , 2004, , .		380
10	Probabilistic discovery of time series motifs. , 2003, , .		374
11	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. BMC Bioinformatics, 2007, 8, 211.	1.2	350
12	Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20429-20434.	3.3	327
13	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). Plant Journal, 2019, 98, 767-782.	2.8	264
14	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	3.8	260
15	Finding surprising patterns in a time series database in linear time and space. , 2002, , .		252
16	Genome resources for climate‐resilient cowpea, an essential crop for food security. Plant Journal, 2017, 89, 1042-1054.	2.8	199
17	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. Plant Genome, 2011, 4, 238-249.	1.6	150
18	A multi‐parent advanced generation inter‐cross (<scp>MAGIC</scp>) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). Plant Journal, 2018, 93, 1129-1142.	2.8	132

#	ARTICLE	IF	CITATIONS
19	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L.. Scientific Data, 2017, 4, 170044.	2.4	130
20	Nucleosome landscape and control of transcription in the human malaria parasite. Genome Research, 2010, 20, 228-238.	2.4	126
21	Assignment of Orthologous Genes via Genome Rearrangement. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 302-315.	1.9	120
22	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. BMC Molecular Biology, 2008, 9, 6.	3.0	120
23	Higher classification sensitivity of short metagenomic reads with CLARK-S. Bioinformatics, 2016, 32, 3823-3825.	1.8	116
24	Accurate Construction of Consensus Genetic Maps via Integer Linear Programming. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 381-394.	1.9	105
25	Generating and Reversing Chronic Wounds in Diabetic Mice by Manipulating Wound Redox Parameters. Journal of Diabetes Research, 2014, 2014, 1-18.	1.0	105
26	Visually mining and monitoring massive time series. , 2004, , .		103
27	Visualizing and Discovering Non-Trivial Patterns in Large Time Series Databases. Information Visualization, 2005, 4, 61-82.	1.2	96
28	Time-series Bitmaps: a Practical Visualization Tool for Working with Large Time Series Databases. , 2005, , .		92
29	Mustache: multi-scale detection of chromatin loops from Hi-C and Micro-C maps using scale-space representation. Genome Biology, 2020, 21, 256.	3.8	90
30	Compression-based data mining of sequential data. Data Mining and Knowledge Discovery, 2007, 14, 99-129.	2.4	84
31	Time Series Epenthesis: Clustering Time Series Streams Requires Ignoring Some Data. , 2011, , .		82
32	Genome-wide Mapping of DNA Methylation in the Human Malaria Parasite Plasmodium falciparum. Cell Host and Microbe, 2013, 14, 696-706.	5.1	79
33	Efficient Detection of Unusual Words. Journal of Computational Biology, 2000, 7, 71-94.	0.8	75
34	BRAT-BW: efficient and accurate mapping of bisulfite-treated reads. Bioinformatics, 2012, 28, 1795-1796.	1.8	75
35	Off-line compression by greedy textual substitution. Proceedings of the IEEE, 2000, 88, 1733-1744.	16.4	73
36	Validating genome-wide CRISPR-Cas9 function improves screening in the oleaginous yeast Yarrowia lipolytica. Metabolic Engineering, 2019, 55, 102-110.	3.6	70

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37	A Novel Bit Level Time Series Representation with Implication of Similarity Search and Clustering. Lecture Notes in Computer Science, 2005, , 771-777.	1.0	68
38	BRAT: bisulfite-treated reads analysis tool. Bioinformatics, 2010, 26, 572-573.	1.8	65
39	Identification of candidate genes and molecular markers for heat-induced brown discoloration of seed coats in cowpea [Vigna unguiculata (L.) Walp]. BMC Genomics, 2014, 15, 328.	1.2	65
40	A Bit Level Representation for Time Series Data Mining with Shape Based Similarity. Data Mining and Knowledge Discovery, 2006, 13, 11-40.	2.4	62
41	OligoSpawn: a software tool for the design of overgo probes from large unigene datasets. BMC Bioinformatics, 2006, 7, 7.	1.2	60
42	A comparative evaluation of genome assembly reconciliation tools. Genome Biology, 2017, 18, 93.	3.8	57
43	ON THE ACCURATE CONSTRUCTION OF CONSENSUS GENETIC MAPS. , 2008, , .		57
44	Mechanisms of Small RNA Generation from Cis-NATs in Response to Environmental and Developmental Cues. Molecular Plant, 2013, 6, 704-715.	3.9	53
45	DNA-encoded nucleosome occupancy is associated with transcription levels in the human malaria parasite Plasmodium falciparum. BMC Genomics, 2014, 15, 347.	1.2	52
46	Selfish: discovery of differential chromatin interactions via a self-similarity measure. Bioinformatics, 2019, 35, i145-i153.	1.8	49
47	Monotony of Surprise and Large-Scale Quest for Unusual Words. Journal of Computational Biology, 2003, 10, 283-311.	0.8	48
48	MDL-based time series clustering. Knowledge and Information Systems, 2012, 33, 371-399.	2.1	46
49	Graphlet Kernels for Prediction of Functional Residues in Protein Structures. Journal of Computational Biology, 2010, 17, 55-72.	0.8	44
50	Discovering the Intrinsic Cardinality and Dimensionality of Time Series Using MDL. , 2011, , .		41
51	Gridding and compression of microarray images. , 2004, , 122-30.		38
52	Nucleosome occupancy at transcription start sites in the human malaria parasite: A hard-wired evolution of virulence?. Infection, Genetics and Evolution, 2011, 11, 716-724.	1.0	38
53	String Matching in Hardware Using the FM-Index. , 2011, , .		37
54	Sequencing of 15Â622 geneâ€bearing BAC s clarifies the geneâ€dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	2.8	36

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55	Seed Coat Pattern QTL and Development in Cowpea (Vigna unguiculata [L.] Walp.). Frontiers in Plant Science, 2019, 10, 1346.	1.7	36
56	COMPUTING THE ASSIGNMENT OF ORTHOLOGOUS GENES VIA GENOME REARRANGEMENT. , 2005, , .		36
57	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. PLoS Computational Biology, 2016, 12, e1005107.	1.5	36
58	<sc>FHAST</sc>: FPGA-Based Acceleration of <sc>Bowtie</sc> in Hardware. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 973-981.	1.9	35
59	On the accurate construction of consensus genetic maps. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 285-96.	0.4	35
60	On average sequence complexity. Theoretical Computer Science, 2004, 326, 213-227.	0.5	31
61	Intelligent Icons: Integrating Lite-Weight Data Mining and Visualization into GUI Operating Systems. IEEE International Conference on Data Mining, 2006, , .	0.0	31
62	NO<scp>r</scp>MAL: accurate nucleosome positioning using a modified Gaussian mixture model. Bioinformatics, 2012, 28, i242-i249.	1.8	30
63	When less is more: â€˜slicingâ€™ sequencing data improves read decoding accuracy and <i>de novo</i> assembly quality. Bioinformatics, 2015, 31, 2972-2980.	1.8	25
64	<i>De novo</i> meta-assembly of ultra-deep sequencing data. Bioinformatics, 2015, 31, i9-i16.	1.8	25
65	Genome-wide functional screens enable the prediction of high activity CRISPR-Cas9 and -Cas12a guides in Yarrowia lipolytica. Nature Communications, 2022, 13, 922.	5.8	25
66	Monotony of surprise and large-scale quest for unusual words. , 2002, , .		24
67	A parallel edge-betweenness clustering tool for Protein-Protein Interaction networks. International Journal of Data Mining and Bioinformatics, 2007, 1, 241.	0.1	24
68	Exploration of Short Reads Genome Mapping in Hardware. , 2010, , .		23
69	Efficient selection of unique and popular oligos for large EST databases. Bioinformatics, 2004, 20, 2101-2112.	1.8	22
70	Multithreaded FPGA acceleration of DNA sequence mapping. , 2012, , .		22
71	Finding Biclusters by Random Projections. Lecture Notes in Computer Science, 2004, , 102-116.	1.0	21
72	Soft-core Processor Customization using the Design of Experiments Paradigm. , 2007, , .		20

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73	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. PLoS Computational Biology, 2013, 9, e1003010.	1.5	20
74	Verbumculus and the discovery of unusual words. Journal of Computer Science and Technology, 2004, 19, 22-41.	0.9	19
75	BRAT-nova: fast and accurate mapping of bisulfite-treated reads. Bioinformatics, 2016, 32, 2696-2698.	1.8	18
76	Shape recovery and volume calculation from biplane angiography in the stereotactic radiosurgical treatment of arteriovenous malformations. International Journal of Radiation Oncology Biology Physics, 1996, 35, 565-577.	0.4	17
77	Authentication of LZ-77 compressed data. , 2003, , .		17
78	Dot plots for time series analysis. , 2005, , .		17
79	Using the minimum description length to discover the intrinsic cardinality and dimensionality of time series. Data Mining and Knowledge Discovery, 2015, 29, 358-399.	2.4	17
80	Accurate detection of chimeric contigs via Bionano optical maps. Bioinformatics, 2019, 35, 1760-1762.	1.8	17
81	DeeplyEssential: a deep neural network for predicting essential genes in microbes. BMC Bioinformatics, 2020, 21, 367.	1.2	17
82	Joint source-channel LZ'77 coding. , 0, , .		16
83	Length-Based Encoding of Binary Data in DNA. Langmuir, 2008, 24, 1613-1616.	1.6	16
84	Novo&Stitch: accurate reconciliation of genome assemblies via optical maps. Bioinformatics, 2018, 34, i43-i51.	1.8	16
85	Some theory and practice of greedy off-line textual substitution. , 0, , .		15
86	Error Resilient LZ'77 Data Compression: Algorithms, Analysis, and Experiments. IEEE Transactions on Information Theory, 2007, 53, 1799-1813.	1.5	14
87	OMGS: Optical Map-Based Genome Scaffolding. Journal of Computational Biology, 2020, 27, 519-533.	0.8	14
88	Efficient and Accurate Construction of Genetic Linkage Maps from Noisy and Missing Genotyping Data. Lecture Notes in Computer Science, 2007, , 395-406.	1.0	13
89	PuFFIN - a parameter-free method to build nucleosome maps from paired-end reads. BMC Bioinformatics, 2014, 15, S11.	1.2	12
90	VizTree. , 2004, , 1269-1272.		11

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91	Efficient information compression in sensor networks. International Journal of Sensor Networks, 2006, 1, 229.	0.2	11
92	Finding biclusters by random projections. Theoretical Computer Science, 2006, 368, 217-230.	0.5	11
93	Efficient Discovery of Unusual Patterns in Time Series. New Generation Computing, 2006, 25, 61-93.	2.5	10
94	Chromatin-driven de novo discovery of DNA binding motifs in the human malaria parasite. BMC Genomics, 2011, 12, 601.	1.2	10
95	Storage and transmission of microarray images. Drug Discovery Today, 2005, 10, 1689-1695.	3.2	9
96	Online Information Compression in Sensor Networks. , 2006, , .		9
97	VizTreeA Tool for Visually Mining and Monitoring Massive Time Series Databases. , 2004, , 1269-1272.		8
98	Discovery of Repetitive Patterns in DNA with Accurate Boundaries. , 0, , .		8
99	Efficient Genome-Wide TagSNP Selection Across Populations via the Linkage Disequilibrium Criterion. Journal of Computational Biology, 2010, 17, 21-37.	0.8	8
100	Higher Classification Accuracy of Short Metagenomic Reads by Discriminative Spaced k-mers. Lecture Notes in Computer Science, 2015, , 286-295.	1.0	8
101	A Practical Tool for Visualizing and Data Mining Medical Time Series. , 0, , .		7
102	Error-Resilient LZW Data Compression. , 0, , .		7
103	A Graph-Theoretical Approach to the Selection of the Minimum Tiling Path from a Physical Map. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 352-360.	1.9	7
104	Prediction of histone post-translational modifications using deep learning. Bioinformatics, 2021, 36, 5610-5617.	1.8	7
105	Two-Level Microprocessor-Accelerator Partitioning. , 2007, , .		6
106	A LINEAR-TIME ALGORITHM FOR PREDICTING FUNCTIONAL ANNOTATIONS FROM PPI NETWORKS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1049-1065.	0.3	6
107	Efficient Selection of Unique and Popular Oligos for Large EST Databases. Lecture Notes in Computer Science, 2003, , 384-401.	1.0	6
108	Analysis of secondary structure elements of proteins using indexing techniques. , 0, , .		5

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109	Deciphering histone code of transcriptional regulation in malaria parasites by large-scale data mining. Computational Biology and Chemistry, 2014, 50, 3-10.	1.1	5
110	Analysis of nucleosome positioning landscapes enables gene discovery in the human malaria parasite Plasmodium falciparum. BMC Genomics, 2015, 16, 1005.	1.2	5
111	Accurate Decoding of Pooled Sequenced Data Using Compressed Sensing. Lecture Notes in Computer Science, 2013, , 70-84.	1.0	5
112	EFFICIENT ALGORITHMS FOR GENOME-WIDE TAGSNP SELECTION ACROSS POPULATIONS VIA THE LINKAGE DISEQUILIBRIUM CRITERION. , 2007, , .		5
113	Reference-agnostic representation and visualization of pan-genomes. BMC Bioinformatics, 2021, 22, 502.	1.2	5
114	On the Average Sequence Complexity. Lecture Notes in Computer Science, 2004, , 74-88.	1.0	4
115	A Compartmentalized Approach to the Assembly of Physical Maps. , 2007, , .		4
116	Data Mining in Bioinformatics: Selected Papers from BIOKDD. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 195-196.	1.9	4
117	A speed-up for the commute between subword trees and DAWGs. Information Processing Letters, 2002, 83, 159-161.	0.4	3
118	Augmenting LZ-77 with authentication and integrity assurance capabilities. Concurrency Computation Practice and Experience, 2004, 16, 1063-1076.	1.4	3
119	Clock-Frequency Assignment for Multiple Clock Domain Systems-on-a-Chip. , 2007, , .		3
120	A compartmentalized approach to the assembly of physical maps. BMC Bioinformatics, 2009, 10, 217.	1.2	3
121	Computing the Minimal Tiling Path from a Physical Map by Integer Linear Programming. Lecture Notes in Computer Science, 2008, , 148-161.	1.0	3
122	Fractal image approximation and orthogonal bases. Signal Processing: Image Communication, 1999, 14, 413-423.	1.8	2
123	DECONVOLUTING BACâ€"GENE RELATIONSHIPS USING A PHYSICAL MAP. Journal of Bioinformatics and Computational Biology, 2008, 06, 603-622.	0.3	2
124	Towards Discovering the Intrinsic Cardinality and Dimensionality of Time Series Using MDL. Lecture Notes in Computer Science, 2013, , 184-197.	1.0	2
125	A PROBABILISTIC METHOD FOR SMALL RNA FLOWGRAM MATCHING. , 2007, , .		2
126	Linear global detectors of redundant and rare substrings. , 1999, , .		1

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127	Scrible: Ultra-Accurate Error-Correction of Pooled Sequenced Reads. Lecture Notes in Computer Science, 2015, , 162-174.	1.0	1
128	OMGS: Optical Map-Based Genome Scaffolding. Lecture Notes in Computer Science, 2019, , 190-207.	1.0	1
129	mClass: Cancer Type Classification with Somatic Point Mutation Data. Lecture Notes in Computer Science, 2018, , 131-145.	1.0	1
130	DECONVOLUTING THE BAC-GENE RELATIONSHIPS USING A PHYSICAL MAP. , 2007, , .		1
131	INTRODUCTION. Journal of Bioinformatics and Computational Biology, 2008, 06, v-vi.	0.3	0
132	CLARK, accurate and efficient classification of DNA sequences. , 2014, , .		0
133	BIOKDD 2008. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2008, 10, 51-53.	3.2	0
134	CPMâ€™s 20th Anniversary: A Statistical Retrospective. Lecture Notes in Computer Science, 2009, , 1-11.	1.0	0