

Stefano Lonardi

List of Publications by Year in Descending Order

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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	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
137	Reference-agnostic representation and visualization of pan-genomes. <i>BMC Bioinformatics</i> , 2021 , 22, 5023.6	3.6	2
136	DeeplyEssential: a deep neural network for predicting essential genes in microbes. <i>BMC Bioinformatics</i> , 2020 , 21, 367	3.6	7
135	Prediction Of Histone Post-Translational Modifications Using Deep Learning. <i>Bioinformatics</i> , 2020 ,	7.2	1
134	OMGS: Optical Map-Based Genome Scaffolding. <i>Journal of Computational Biology</i> , 2020 , 27, 519-533	1.7	9
133	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
132	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
131	OMGS: Optical Map-Based Genome Scaffolding. <i>Lecture Notes in Computer Science</i> , 2019 , 190-207	0.9	
130	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019 , 98, 767-782	6.9	128
129	Selfish: discovery of differential chromatin interactions via a self-similarity measure. <i>Bioinformatics</i> , 2019 , 35, i145-i153	7.2	18
128	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
127	Accurate detection of chimeric contigs via Bionano optical maps. <i>Bioinformatics</i> , 2019 , 35, 1760-1762	7.2	7
126	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
125	mClass: Cancer Type Classification with Somatic Point Mutation Data. <i>Lecture Notes in Computer Science</i> , 2018 , 131-145	0.9	1
124	Novo&Stitch: accurate reconciliation of genome assemblies via optical maps. <i>Bioinformatics</i> , 2018 , 34, i43-i51	7.2	12
123	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017 , 544, 427-433.4	33.4	822
122	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

121	A comparative evaluation of genome assembly reconciliation tools. <i>Genome Biology</i> , 2017 , 18, 93	18.3	27
120	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017 , 18, 182	18.3	152
119	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017 , 89, 1042-1054	6.9	118
118	Higher classification sensitivity of short metagenomic reads with CLARK-S. <i>Bioinformatics</i> , 2016 , 32, 3823-3825	7.1	71
117	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. <i>PLoS Computational Biology</i> , 2016 , 12, e1005107	5	26
116	BRAT-nova: fast and accurate mapping of bisulfite-treated reads. <i>Bioinformatics</i> , 2016 , 32, 2696-8	7.2	11
115	Bisulfite-Conversion-Based Methods for DNA Methylation Sequencing Data Analysis 2016 , 227-243		1
114	CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. <i>BMC Genomics</i> , 2015 , 16, 236	4.5	347
113	Sequencing of 15622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015 , 84, 216-27	6.9	31
112	FHAST: FPGA-Based Acceleration of Bowtie in Hardware. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 973-81	3	24
111	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
110	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
109	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
108	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
107	De novo meta-assembly of ultra-deep sequencing data. <i>Bioinformatics</i> , 2015 , 31, i9-16	7.2	21
106	Scribe: Ultra-Accurate Error-Correction of Pooled Sequenced Reads. <i>Lecture Notes in Computer Science</i> , 2015 , 162-174	0.9	1
105	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
104	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

103	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
102	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
101	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
100	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
99	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
98	Combinatorial pooling enables selective sequencing of the barley gene space. <i>PLoS Computational Biology</i> , 2013 , 9, e1003010	5	15
97	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
96	Accurate Decoding of Pooled Sequenced Data Using Compressed Sensing. <i>Lecture Notes in Computer Science</i> , 2013 , 70-84	0.9	4
95	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
94	MDL-based time series clustering. <i>Knowledge and Information Systems</i> , 2012 , 33, 371-399	2.4	37
93	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124
92	Multithreaded FPGA acceleration of DNA sequence mapping 2012 ,		15
91	BRAT-BW: efficient and accurate mapping of bisulfite-treated reads. <i>Bioinformatics</i> , 2012 , 28, 1795-6	7.2	69
90	NORMAL: accurate nucleosome positioning using a modified Gaussian mixture model. <i>Bioinformatics</i> , 2012 , 28, i242-9	7.2	24
89	String Matching in Hardware Using the FM-Index 2011 ,		25
88	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
87	Chromatin-driven de novo discovery of DNA binding motifs in the human malaria parasite. <i>BMC Genomics</i> , 2011 , 12, 601	4.5	8
86	Time Series Epenthesis: Clustering Time Series Streams Requires Ignoring Some Data 2011 ,		58

85	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
84	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
83	Discovering the Intrinsic Cardinality and Dimensionality of Time Series Using MDL 2011 ,		28
82	Nucleosome landscape and control of transcription in the human malaria parasite. <i>Genome Research</i> , 2010 , 20, 228-38	9.7	109
81	BRAT: bisulfite-treated reads analysis tool. <i>Bioinformatics</i> , 2010 , 26, 572-3	7.2	60
80	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
79	Data mining in bioinformatics: selected papers from BIODDD. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010 , 7, 195-6	3	3
78	Exploration of Short Reads Genome Mapping in Hardware 2010 ,		18
77	Graphlet kernels for prediction of functional residues in protein structures. <i>Journal of Computational Biology</i> , 2010 , 17, 55-72	1.7	36
76	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
75	A compartmentalized approach to the assembly of physical maps. <i>BMC Bioinformatics</i> , 2009 , 10, 217	3.6	2
74	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009 , 10, 582	4.5	477
73	CPM's 20th Anniversary: A Statistical Retrospective. <i>Lecture Notes in Computer Science</i> , 2009 , 1-11	0.9	
72	Length-based encoding of binary data in DNA. <i>Langmuir</i> , 2008 , 24, 1613-6	4	9
71	Deconvoluting BAC-gene relationships using a physical map. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 603-22	1	2
70	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
69	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
68	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. <i>BMC Molecular Biology</i> , 2008 , 9, 6	4.5	105

67	ON THE ACCURATE CONSTRUCTION OF CONSENSUS GENETIC MAPS 2008 ,		39
66	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
65	BIOKDD 2008. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2008 , 10, 51-53	4.6	
64	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
63	Clock-Frequency Assignment for Multiple Clock Domain Systems-on-a-Chip 2007 ,		2
62	Two-Level Microprocessor-Accelerator Partitioning 2007 ,		4
61	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. <i>BMC Bioinformatics</i> , 2007 , 8, 211	3.6	276
60	Error Resilient LZ'77 Data Compression: Algorithms, Analysis, and Experiments. <i>IEEE Transactions on Information Theory</i> , 2007 , 53, 1799-1813	2.8	8
59	Compression-based data mining of sequential data. <i>Data Mining and Knowledge Discovery</i> , 2007 , 14, 99-120		63
58	Experiencing SAX: a novel symbolic representation of time series. <i>Data Mining and Knowledge Discovery</i> , 2007 , 15, 107-144	5.6	870
57	A Compartmentalized Approach to the Assembly of Physical Maps 2007 ,		2
56	Soft-core Processor Customization using the Design of Experiments Paradigm 2007 ,		17
55	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
54	EFFICIENT ALGORITHMS FOR GENOME-WIDE TAGSNP SELECTION ACROSS POPULATIONS VIA THE LINKAGE DISEQUILIBRIUM CRITERION 2007 ,		5
53	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
52	OligoSpawn: a software tool for the design of overgo probes from large unigene datasets. <i>BMC Bioinformatics</i> , 2006 , 7, 7	3.6	38
51	Online Information Compression in Sensor Networks 2006 ,		5
50	Intelligent Icons: Integrating Lite-Weight Data Mining and Visualization into GUI Operating Systems. <i>IEEE International Conference on Data Mining</i> , 2006 ,		19

49	Efficient information compression in sensor networks. <i>International Journal of Sensor Networks</i> , 2006 , 1, 229	0.8	8
48	Finding biclusters by random projections. <i>Theoretical Computer Science</i> , 2006 , 368, 217-230	1.1	8
47	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
46	Efficient Discovery of Unusual Patterns in Time Series. <i>New Generation Computing</i> , 2006 , 25, 61-93	0.9	8
45	A Compression-Boosting Transform for Two-Dimensional Data. <i>Lecture Notes in Computer Science</i> , 2006 , 126-137	0.9	1
44	Time-series Bitmaps: a Practical Visualization Tool for Working with Large Time Series Databases 2005 ,		71
43	Dot plots for time series analysis 2005 ,		11
42	Assignment of orthologous genes via genome rearrangement. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005 , 2, 302-15	3	101
41	Storage and transmission of microarray images. <i>Drug Discovery Today</i> , 2005 , 10, 1689-95	8.8	6
40	Visualizing and Discovering Non-Trivial Patterns in Large Time Series Databases. <i>Information Visualization</i> , 2005 , 4, 61-82	2.4	71
39	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
38	COMPUTING THE ASSIGNMENT OF ORTHOLOGOUS GENES VIA GENOME REARRANGEMENT 2005 ,		28
37	VizTree: A Tool for Visually Mining and Monitoring Massive Time Series Databases 2004 , 1269-1272		2
36	VizTree: A Tool for Visually Mining and Monitoring Massive Time Series Databases 2004 , 1269-1272		5
35	Efficient selection of unique and popular oligos for large EST databases. <i>Bioinformatics</i> , 2004 , 20, 2101-122		17
34	Visually mining and monitoring massive time series 2004 ,		75
33	Verbumculus and the discovery of unusual words. <i>Journal of Computer Science and Technology</i> , 2004 , 19, 22-41	1.7	16
32	On average sequence complexity. <i>Theoretical Computer Science</i> , 2004 , 326, 213-227	1.1	20

31	Augmenting LZ-77 with authentication and integrity assurance capabilities. <i>Concurrency Computation Practice and Experience</i> , 2004 , 16, 1063-1076	1.4	2
30	Gridding and compression of microarray images 2004 , 122-30		20
29	Towards parameter-free data mining 2004 ,		275
28	On the Average Sequence Complexity. <i>Lecture Notes in Computer Science</i> , 2004 , 74-88	0.9	2
27	Finding Biclusters by Random Projections. <i>Lecture Notes in Computer Science</i> , 2004 , 102-116	0.9	15
26	Monotony of surprise and large-scale quest for unusual words. <i>Journal of Computational Biology</i> , 2003 , 10, 283-311	1.7	35
25	Probabilistic discovery of time series motifs 2003 ,		278
24	Authentication of LZ-77 compressed data 2003 ,		5
23	A symbolic representation of time series, with implications for streaming algorithms 2003 ,		552
22	Efficient Selection of Unique and Popular Oligos for Large EST Databases. <i>Lecture Notes in Computer Science</i> , 2003 , 384-401	0.9	4
21	A speed-up for the commute between subword trees and DAWGs. <i>Information Processing Letters</i> , 2002 , 83, 159-161	0.8	3
20	Monotony of surprise and large-scale quest for unusual words 2002 ,		22
19	Finding surprising patterns in a time series database in linear time and space 2002 ,		179
18	Efficient detection of unusual words. <i>Journal of Computational Biology</i> , 2000 , 7, 71-94	1.7	50
17	A whole-genome assembly of Drosophila. <i>Science</i> , 2000 , 287, 2196-204	33.3	1204
16	. <i>Proceedings of the IEEE</i> , 2000 , 88, 1733-1744	14.3	59
15	Fractal image approximation and orthogonal bases. <i>Signal Processing: Image Communication</i> , 1999 , 14, 413-423	2.8	0
14	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

13		10
12	Discovery of Repetitive Patterns in DNA with Accurate Boundaries	4
11	A Practical Tool for Visualizing and Data Mining Medical Time Series	2
10	Error-resilient LZW data compression	2
9	Joint source-channel LZ'77 coding	7
8	Analysis of secondary structure elements of proteins using indexing techniques	3
7	Genome resources for climate-resilient cowpea, an essential crop for food security	2
6	A multi-parent advanced generation inter-cross population for genetic analysis of multiple traits in cowpea (<i>Vigna unguiculata</i> L. Walp.)	4
5	Comprehensive Benchmarking and Ensemble Approaches for Metagenomic Classifiers	3
4	Mustache: Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation	3
3	Seed Coat Pattern QTL and Development in Cowpea (<i>Vigna unguiculata</i> [L.] Walp.)	2
2	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.)	2
1	Higher classification sensitivity of short metagenomic reads with CLARK-S	3