

Marie-France Sagot

List of Publications by Year in descending order

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141
papers

4,417
citations

117625

34
h-index

133252

59
g-index

152
all docs

152
docs citations

152
times ranked

5876
citing authors

#	ARTICLE	IF	CITATIONS
1	Current methods of gene prediction, their strengths and weaknesses. <i>Nucleic Acids Research</i> , 2002, 30, 4103-4117.	14.5	374
2	M _e D _u S _a : a multi-draft based scaffold. <i>Bioinformatics</i> , 2015, 31, 2443-2451.	4.1	359
3	Algorithms for Extracting Structured Motifs Using a Suffix Tree with an Application to Promoter and Regulatory Site Consensus Identification. <i>Journal of Computational Biology</i> , 2000, 7, 345-362.	1.6	212
4	Current tools for the identification of miRNA genes and their targets. <i>Nucleic Acids Research</i> , 2009, 37, 2419-2433.	14.5	211
5	MetExplore: a web server to link metabolomic experiments and genome-scale metabolic networks. <i>Nucleic Acids Research</i> , 2010, 38, W132-W137.	14.5	148
6	Motif Search in Graphs: Application to Metabolic Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 360-368.	3.0	146
7	An Introduction to Metabolic Networks and Their Structural Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 594-617.	3.0	103
8	Genome reduction and potential metabolic complementation of the dual endosymbionts in the whitefly <i>Bemisia tabaci</i> . <i>BMC Genomics</i> , 2015, 16, 226.	2.8	100
9	Modes and cuts in metabolic networks: Complexity and algorithms. <i>BioSystems</i> , 2009, 95, 51-60.	2.0	88
10	KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. <i>BMC Bioinformatics</i> , 2012, 13, S5.	2.6	85
11	<i>Wolbachia</i> detection: an assessment of standard PCR Protocols. <i>Molecular Ecology Resources</i> , 2011, 11, 567-572.	4.8	83
12	Footprints of Inversions at Present and Past Pseudoautosomal Boundaries in Human Sex Chromosomes. <i>Genome Biology and Evolution</i> , 2009, 1, 56-66.	2.5	82
13	How Long Does <i>Wolbachia</i> Remain on Board?. <i>Molecular Biology and Evolution</i> , 2017, 34, 1183-1193.	8.9	82
14	Advances on sorting by reversals. <i>Discrete Applied Mathematics</i> , 2007, 155, 881-888.	0.9	80
15	Inferring regulatory elements from a whole genome. an analysis of <i>Helicobacter pylori</i> family of promoter signals. <i>Journal of Molecular Biology</i> , 2000, 297, 335-353.	4.2	75
16	Endosymbiosis in trypanosomatids: the genomic cooperation between bacterium and host in the synthesis of essential amino acids is heavily influenced by multiple horizontal gene transfers. <i>BMC Evolutionary Biology</i> , 2013, 13, 190.	3.2	70
17	SNP calling from RNA-seq data without a reference genome: identification, quantification, differential analysis and impact on the protein sequence. <i>Nucleic Acids Research</i> , 2016, 44, gkw655.	14.5	66
18	Analysis of fine-scale mammalian evolutionary breakpoints provides new insight into their relation to genome organisation. <i>BMC Genomics</i> , 2009, 10, 335.	2.8	58

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19	Predicting the Proteins of <i>Angomonas deanei</i> , <i>Strigomonas culicis</i> and Their Respective Endosymbionts Reveals New Aspects of the Trypanosomatidae Family. <i>PLoS ONE</i> , 2013, 8, e60209.	2.5	55
20	Pierce's Disease of Grapevines: A Review of Control Strategies and an Outline of an Epidemiological Model. <i>Frontiers in Microbiology</i> , 2018, 9, 2141.	3.5	55
21	Promoter sequences and algorithmical methods for identifying them. <i>Research in Microbiology</i> , 1999, 150, 779-799.	2.1	52
22	An Efficient Algorithm for the Identification of Structured Motifs in DNA Promoter Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 126-140.	3.0	51
23	RISOTTO: Fast Extraction of Motifs with Mismatches. <i>Lecture Notes in Computer Science</i> , 2006, , 757-768.	1.3	51
24	Bases of Motifs for Generating Repeated Patterns with Wild Cards. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 40-50.	3.0	50
25	An integrative, multi-omics approach towards the prioritization of <i>Klebsiella pneumoniae</i> drug targets. <i>Scientific Reports</i> , 2018, 8, 10755.	3.3	50
26	Systemic analysis of the symbiotic function of <i>Buchnera aphidicola</i> , the primary endosymbiont of the pea aphid <i>Acyrtosiphon pisum</i> . <i>Comptes Rendus - Biologies</i> , 2009, 332, 1034-1049.	0.2	49
27	Biosynthesis of Vitamins and Cofactors in Bacterium-Harboring Trypanosomatids Depends on the Symbiotic Association as Revealed by Genomic Analyses. <i>PLoS ONE</i> , 2013, 8, e79786.	2.5	49
28	Efficient hybrid de novo assembly of human genomes with WENGAN. <i>Nature Biotechnology</i> , 2021, 39, 422-430.	17.5	47
29	A note on the complexity of finding and enumerating elementary modes. <i>BioSystems</i> , 2010, 99, 210-214.	2.0	44
30	Close 3D proximity of evolutionary breakpoints argues for the notion of spatial synteny. <i>BMC Genomics</i> , 2011, 12, 303.	2.8	42
31	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	3.8	40
32	Occurrence Probability of Structured Motifs in Random Sequences. <i>Journal of Computational Biology</i> , 2002, 9, 761-773.	1.6	39
33	A New Distance for High Level RNA Secondary Structure Comparison. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 3-14.	3.0	38
34	Precise detection of rearrangement breakpoints in mammalian chromosomes. <i>BMC Bioinformatics</i> , 2008, 9, 286.	2.6	36
35	Exploring the Solution Space of Sorting by Reversals, with Experiments and an Application to Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 348-356.	3.0	36
36	Metabolic network visualization eliminating node redundancy and preserving metabolic pathways. <i>BMC Systems Biology</i> , 2007, 1, 29.	3.0	35

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37	Identifying SNPs without a Reference Genome by Comparing Raw Reads. Lecture Notes in Computer Science, 2010, , 147-158.	1.3	35
38	Cophylogeny Reconstruction via an Approximate Bayesian Computation. Systematic Biology, 2015, 64, 416-431.	5.6	35
39	Graph-Based Analysis of the Metabolic Exchanges between Two Co-Resident Intracellular Symbionts, <i>Baumannia cicadellinicola</i> and <i>Sulcia muelleri</i> , with Their Insect Host, <i>Homalodisca coagulata</i> . PLoS Computational Biology, 2010, 6, e1000904.	3.2	34
40	Insights on the virulence of swine respiratory tract mycoplasmas through genome-scale metabolic modeling. BMC Genomics, 2016, 17, 353.	2.8	34
41	Identifying Satellites and Periodic Repetitions in Biological Sequences. Journal of Computational Biology, 1998, 5, 539-553.	1.6	33
42	EUCALYPT: efficient tree reconciliation enumerator. Algorithms for Molecular Biology, 2015, 10, 3.	1.2	33
43	Repetition-free longest common subsequence. Discrete Applied Mathematics, 2010, 158, 1315-1324.	0.9	32
44	The maximum agreement forest problem: Approximation algorithms and computational experiments. Theoretical Computer Science, 2007, 374, 91-110.	0.9	31
45	A HIGHLY SCALABLE ALGORITHM FOR THE EXTRACTION OF CIS-REGULATORY REGIONS. , 2005, , .		31
46	Mycoplasma non-coding RNA: identification of small RNAs and targets. BMC Genomics, 2016, 17, 743.	2.8	27
47	Structural and dynamical analysis of biological networks. Briefings in Functional Genomics, 2012, 11, 420-433.	2.7	26
48	Two Host Clades, Two Bacterial Arsenals: Evolution through Gene Losses in Facultative Endosymbionts. Genome Biology and Evolution, 2015, 7, 839-855.	2.5	26
49	A Combinatorial Algorithm for Microbial Consortia Synthetic Design. Scientific Reports, 2016, 6, 29182.	3.3	24
50	A FIRST APPROACH TO FINDING COMMON MOTIFS WITH GAPS. International Journal of Foundations of Computer Science, 2005, 16, 1145-1154.	1.1	23
51	Cassis: detection of genomic rearrangement breakpoints. Bioinformatics, 2010, 26, 1897-1898.	4.1	22
52	DegreeCox " a network-based regularization method for survival analysis. BMC Bioinformatics, 2016, 17, 449.	2.6	22
53	Hydrogen peroxide production and myo"inositol metabolism as important traits for virulence of <i>Mycoplasma hyopneumoniae</i> . Molecular Microbiology, 2018, 108, 683-696.	2.5	22
54	A parallel algorithm for the extraction of structured motifs. , 2004, , .		20

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55	Identification of expressed transposable element insertions in the sequenced genome of <i>Drosophila melanogaster</i> . <i>Gene</i> , 2009, 439, 55-62.	2.2	19
56	Playing hide and seek with repeats in local and global de novo transcriptome assembly of short RNA-seq reads. <i>Algorithms for Molecular Biology</i> , 2017, 12, 2.	1.2	18
57	Algorithms and complexity of enumerating minimal precursor sets in genome-wide metabolic networks. <i>Bioinformatics</i> , 2012, 28, 2474-2483.	4.1	17
58	On the Genetic Architecture of Cytoplasmic Incompatibility: Inference from Phenotypic Data. <i>American Naturalist</i> , 2013, 182, E15-E24.	2.1	17
59	Evolution under Reversals: Parsimony and Conservation of Common Intervals. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 301-309.	3.0	16
60	CycADS: an annotation database system to ease the development and update of BioCyc databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar008-bar008.	3.0	16
61	Mirinho: An efficient and general plant and animal pre-miRNA predictor for genomic and deep sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, 179.	2.6	16
62	Orphan gene finding – an exon assembly approach. <i>Theoretical Computer Science</i> , 2003, 290, 1407-1431.	0.9	15
63	Combination of measures distinguishes pre-miRNAs from other stem-loops in the genome of the newly sequenced <i>Anopheles darlingi</i> . <i>BMC Genomics</i> , 2010, 11, 529.	2.8	15
64	BRASERO: A Resource for Benchmarking RNA Secondary Structure Comparison Algorithms. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-5.	5.7	15
65	MOOMIN – Mathematical exploration of –Omics data on a Metabolic Network. <i>Bioinformatics</i> , 2020, 36, 514-523.	4.1	15
66	Assessing the Exceptionality of Coloured Motifs in Networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 616234.	1.4	15
67	Efficiently Listing Bounded Length st-Paths. <i>Lecture Notes in Computer Science</i> , 2015, , 318-329.	1.3	14
68	Multiple sequence comparison – a peptide matching approach. <i>Theoretical Computer Science</i> , 1997, 180, 115-137.	0.9	13
69	Lossless filter for multiple repeats with bounded edit distance. <i>Algorithms for Molecular Biology</i> , 2009, 4, 3.	1.2	13
70	Telling metabolic stories to explore metabolomics data: a case study on the yeast response to cadmium exposure. <i>Bioinformatics</i> , 2014, 30, 61-70.	4.1	13
71	Enumeration of minimal stoichiometric precursor sets in metabolic networks. <i>Algorithms for Molecular Biology</i> , 2016, 11, 25.	1.2	13
72	OptPipe - a pipeline for optimizing metabolic engineering targets. <i>BMC Systems Biology</i> , 2017, 11, 143.	3.0	13

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73	The Solution Space of Sorting by Reversals. , 2007, , 293-304.		13
74	Enumerating Precursor Sets of Target Metabolites in a Metabolic Network. Lecture Notes in Computer Science, 2008, , 233-244.	1.3	13
75	Efficient Bubble Enumeration in Directed Graphs. Lecture Notes in Computer Science, 2012, , 118-129.	1.3	13
76	Longest repeats with a block of k don't care. Theoretical Computer Science, 2006, 362, 248-254.	0.9	12
77	Lossless filter for multiple repetitions with Hamming distance. Journal of Discrete Algorithms, 2008, 6, 497-509.	0.7	12
78	BachBerry: BACTERIAL Hosts for production of Bioactive phenolics from bERRY fruits. Phytochemistry Reviews, 2018, 17, 291-326.	6.5	12
79	Assessing the Exceptionality of Coloured Motifs in Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-9.	1.4	11
80	Exploration of the core metabolism of symbiotic bacteria. BMC Genomics, 2012, 13, 438.	2.8	11
81	Mitochondrial respiration and genomic analysis provide insight into the influence of the symbiotic bacterium on host trypanosomatid oxygen consumption. Parasitology, 2015, 142, 352-362.	1.5	11
82	A multiple layer model to compare RNA secondary structures. Software - Practice and Experience, 2008, 38, 775-792.	3.6	10
83	Geometric medians in reconciliation spaces of phylogenetic trees. Information Processing Letters, 2018, 136, 96-101.	0.6	10
84	Metabolic Games. Frontiers in Applied Mathematics and Statistics, 2019, 5, .	1.3	10
85	Multiple Alignment of Biological Networks: A Flexible Approach. Lecture Notes in Computer Science, 2009, , 263-273.	1.3	10
86	Bacterial synteny: an exact approach with gene quorum. BMC Bioinformatics, 2011, 12, 193.	2.6	9
87	Short and long-term genome stability analysis of prokaryotic genomes. BMC Genomics, 2013, 14, 309.	2.8	9
88	Perfect Sorting by Reversals. Lecture Notes in Computer Science, 2005, , 42-51.	1.3	9
89	Telling stories: Enumerating maximal directed acyclic graphs with a constrained set of sources and targets. Theoretical Computer Science, 2012, 457, 1-9.	0.9	8
90	Computing and Listing st-Paths in Public Transportation Networks. Theory of Computing Systems, 2018, 62, 600-621.	1.1	8

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91	Fast-SG: an alignment-free algorithm for hybrid assembly. GigaScience, 2018, 7, .	6.4	8
92	MOMO - multi-objective metabolic mixed integer optimization: application to yeast strain engineering. BMC Bioinformatics, 2020, 21, 69.	2.6	8
93	The relevance of enzyme specificity for coenzymes and the presence of 6-phosphogluconate dehydrogenase for polyhydroxyalkanoates production in the metabolism of Pseudomonas sp. LFM046. International Journal of Biological Macromolecules, 2020, 163, 240-250.	7.5	8
94	Repetition-free longest common subsequence. Electronic Notes in Discrete Mathematics, 2008, 30, 243-248.	0.4	7
95	Exploring and Visualizing Spaces of Tree Reconciliations. Systematic Biology, 2019, 68, 607-618.	5.6	7
96	Capybara: equivalence ClAss enumeration of coPhylogenY event-BAsed ReconciliAtions. Bioinformatics, 2020, 36, 4197-4199.	4.1	7
97	Reaction Motifs in Metabolic Networks. Lecture Notes in Computer Science, 2005, , 178-191.	1.3	7
98	Amortized $\mathcal{O}(V)$ -Delay Algorithm for Listing Chordless Cycles in Undirected Graphs. Lecture Notes in Computer Science, 2014, , 418-429.	1.3	7
99	Further Thoughts on the Syntenic Distance between Genomes. Algorithmica, 2002, 34, 157-180.	1.3	6
100	Efficient representation and $\langle i \rangle P \langle i \rangle$ -value computation for high-order Markov motifs. Bioinformatics, 2008, 24, i160-i166.	4.1	6
101	Navigating the unexplored seascape of pre-miRNA candidates in single-genome approaches. Bioinformatics, 2012, 28, 3034-3041.	4.1	6
102	Mod/Resc Parsimony Inference: Theory and application. Information and Computation, 2012, 213, 23-32.	0.7	6
103	Mycoplasma hyopneumoniae J elicits an antioxidant response and decreases the expression of ciliary genes in infected swine epithelial cells. Scientific Reports, 2020, 10, 13707.	3.3	6
104	Multiple sequence comparison: A peptide matching approach. Lecture Notes in Computer Science, 1995, , 366-385.	1.3	6
105	A Polynomial Delay Algorithm for the Enumeration of Bubbles with Length Constraints in Directed Graphs and Its Application to the Detection of Alternative Splicing in RNA-seq Data. Lecture Notes in Computer Science, 2013, , 99-111.	1.3	6
106	An asymmetric approach to preserve common intervals while sorting by reversals. Algorithms for Molecular Biology, 2009, 4, 16.	1.2	5
107	A comprehensive evaluation of binning methods to recover human gut microbial species from a non-redundant reference gene catalog. NAR Genomics and Bioinformatics, 2021, 3, lqab009.	3.2	5
108	Flexible identification of structural objects in nucleic acid sequences: Palindromes, mirror repeats, pseudoknots and triple helices. Lecture Notes in Computer Science, 1997, , 224-246.	1.3	5

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109	A small trip in the untranquil world of genomes. Theoretical Computer Science, 2008, 395, 171-192.	0.9	4
110	INDEXING GAPPED-FACTORS USING A TREE. International Journal of Foundations of Computer Science, 2008, 19, 71-87.	1.1	4
111	Longest Repeats with a Block of Don't Cares. Lecture Notes in Computer Science, 2004, , 271-278.	1.3	3
112	EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1-1.	3.0	3
113	Robustness of the Parsimonious Reconciliation Method in Cophylogeny. Lecture Notes in Computer Science, 2016, , 119-130.	1.3	3
114	On Bubble Generators in Directed Graphs. Lecture Notes in Computer Science, 2017, , 18-31.	1.3	3
115	Exploring the Robustness of the Parsimonious Reconciliation Method in Host-Symbiont Cophylogeny. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 738-748.	3.0	3
116	Computing and Listing st-Paths in Public Transportation Networks. Lecture Notes in Computer Science, 2016, , 102-116.	1.3	3
117	Mod/Resc Parsimony Inference. Lecture Notes in Computer Science, 2010, , 202-213.	1.3	3
118	All maximal-pairs in step-leap representation of melodic sequence. Information Sciences, 2007, 177, 1954-1962.	6.9	2
119	Rime : Repeat identification. Discrete Applied Mathematics, 2014, 163, 275-286.	0.9	2
120	A polynomial delay algorithm for the enumeration of bubbles with length constraints in directed graphs. Algorithms for Molecular Biology, 2015, 10, 20.	1.2	2
121	Extracting Few Representative Reconciliations with Host Switches. Lecture Notes in Computer Science, 2019, , 9-18.	1.3	2
122	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.3	2
123	Motifs in Sequences. , 2004, , 47-97.		2
124	Finding flexible patterns in a text: an application to three-dimensional molecular matching. Bioinformatics, 1995, 11, 59-70.	4.1	1
125	New EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 3-3.	3.0	1
126	Sampling solution traces for the problem of sorting permutations by signed reversals. Algorithms for Molecular Biology, 2012, 7, 18.	1.2	1

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127	Algorithms for the quantitative Lock/Key model of cytoplasmic incompatibility. Algorithms for Molecular Biology, 2020, 15, 14.	1.2	1
128	Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms. Lecture Notes in Computer Science, 2010, , 226-237.	1.3	1
129	EIC Editorial: Introducing New Associate Editors. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 369-369.	3.0	0
130	EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 177-177.	3.0	0
131	EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 193-194.	3.0	0
132	EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 289-291.	3.0	0
133	EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1553-1557.	3.0	0
134	On Maximal Chain Subgraphs and Covers of Bipartite Graphs. Lecture Notes in Computer Science, 2016, , 137-150.	1.3	0
135	On Bubble Generators in Directed Graphs. Algorithmica, 2020, 82, 898-914.	1.3	0
136	Longest Motifs with a Functionally Equivalent Central Block. Lecture Notes in Computer Science, 2004, , 298-309.	1.3	0
137	Incremental Complexity of a Bi-objective Hypergraph Transversal Problem. Lecture Notes in Computer Science, 2015, , 202-213.	1.3	0
138	A Family of Tree-Based Generators for Bubbles in Directed Graphs. Lecture Notes in Computer Science, 2020, , 17-29.	1.3	0
139	A family of tree-based generators for bubbles in directed graphs. Journal of Graph Algorithms and Applications, 2021, 25, 563-580.	0.4	0
140	Totoro: Identifying Active Reactions During the Transient State for Metabolic Perturbations. Frontiers in Genetics, 2022, 13, 815476.	2.3	0
141	Efficiently sparse listing of classes of optimal cophylogeny reconciliations. Algorithms for Molecular Biology, 2022, 17, 2.	1.2	0