

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
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152
all docs

152
docs citations

152
times ranked

5876
citing authors

#	ARTICLE	IF	CITATIONS
1	Totoro: Identifying Active Reactions During the Transient State for Metabolic Perturbations. <i>Frontiers in Genetics</i> , 2022, 13, 815476.	2.3	0
2	Efficiently sparse listing of classes of optimal cophylogeny reconciliations. <i>Algorithms for Molecular Biology</i> , 2022, 17, 2.	1.2	0
3	Efficient hybrid de novo assembly of human genomes with WENGAN. <i>Nature Biotechnology</i> , 2021, 39, 422-430.	17.5	47
4	A comprehensive evaluation of binning methods to recover human gut microbial species from a non-redundant reference gene catalog. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab009.	3.2	5
5	A family of tree-based generators for bubbles in directed graphs. <i>Journal of Graph Algorithms and Applications</i> , 2021, 25, 563-580.	0.4	0
6	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	3.8	40
7	MOOMIN – Mathematical exploration of –Omics data on a Metabolic Network. <i>Bioinformatics</i> , 2020, 36, 514-523.	4.1	15
8	On Bubble Generators in Directed Graphs. <i>Algorithmica</i> , 2020, 82, 898-914.	1.3	0
9	Algorithms for the quantitative Lock/Key model of cytoplasmic incompatibility. <i>Algorithms for Molecular Biology</i> , 2020, 15, 14.	1.2	1
10	<i>Mycoplasma hyopneumoniae</i> J elicits an antioxidant response and decreases the expression of ciliary genes in infected swine epithelial cells. <i>Scientific Reports</i> , 2020, 10, 13707.	3.3	6
11	Capybara: equivalence Class enumeration of coPhylogenY event-BAsed ReconciliAtions. <i>Bioinformatics</i> , 2020, 36, 4197-4199.	4.1	7
12	MOMO - multi-objective metabolic mixed integer optimization: application to yeast strain engineering. <i>BMC Bioinformatics</i> , 2020, 21, 69.	2.6	8
13	The relevance of enzyme specificity for coenzymes and the presence of 6-phosphogluconate dehydrogenase for polyhydroxyalkanoates production in the metabolism of <i>Pseudomonas</i> sp. LFM046. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 240-250.	7.5	8
14	A Family of Tree-Based Generators for Bubbles in Directed Graphs. <i>Lecture Notes in Computer Science</i> , 2020, , 17-29.	1.3	0
15	Exploring the Robustness of the Parsimonious Reconciliation Method in Host-Symbiont Cophylogeny. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 738-748.	3.0	3
16	Extracting Few Representative Reconciliations with Host Switches. <i>Lecture Notes in Computer Science</i> , 2019, , 9-18.	1.3	2
17	Metabolic Games. <i>Frontiers in Applied Mathematics and Statistics</i> , 2019, 5, .	1.3	10
18	Exploring and Visualizing Spaces of Tree Reconciliations. <i>Systematic Biology</i> , 2019, 68, 607-618.	5.6	7

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19	Hydrogen peroxide production and myoâ€inositol metabolism as important traits for virulence of <i>Mycoplasma hyopneumoniae</i> . <i>Molecular Microbiology</i> , 2018, 108, 683-696.	2.5	22
20	Computing and Listing st-Paths in Public Transportation Networks. <i>Theory of Computing Systems</i> , 2018, 62, 600-621.	1.1	8
21	BachBerry: BACTERIAL Hosts for production of Bioactive phenolics from bERRY fruits. <i>Phytochemistry Reviews</i> , 2018, 17, 291-326.	6.5	12
22	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
23	Geometric medians in reconciliation spaces of phylogenetic trees. <i>Information Processing Letters</i> , 2018, 136, 96-101.	0.6	10
24	Fast-SG: an alignment-free algorithm for hybrid assembly. <i>GigaScience</i> , 2018, 7, .	6.4	8
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	How Long Does Wolbachia Remain on Board?. <i>Molecular Biology and Evolution</i> , 2017, 34, 1183-1193.	8.9	82
27	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
28	On Bubble Generators in Directed Graphs. <i>Lecture Notes in Computer Science</i> , 2017, , 18-31.	1.3	3
29	OptPipe - a pipeline for optimizing metabolic engineering targets. <i>BMC Systems Biology</i> , 2017, 11, 143.	3.0	13
30	Insights on the virulence of swine respiratory tract mycoplasmas through genome-scale metabolic modeling. <i>BMC Genomics</i> , 2016, 17, 353.	2.8	34
31	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
32	On Maximal Chain Subgraphs and Covers of Bipartite Graphs. <i>Lecture Notes in Computer Science</i> , 2016, , 137-150.	1.3	0
33	A Combinatorial Algorithm for Microbial Consortia Synthetic Design. <i>Scientific Reports</i> , 2016, 6, 29182.	3.3	24
34	DegreeCox â€“ a network-based regularization method for survival analysis. <i>BMC Bioinformatics</i> , 2016, 17, 449.	2.6	22
35	<i>Mycoplasma</i> non-coding RNA: identification of small RNAs and targets. <i>BMC Genomics</i> , 2016, 17, 743.	2.8	27
36	Enumeration of minimal stoichiometric precursor sets in metabolic networks. <i>Algorithms for Molecular Biology</i> , 2016, 11, 25.	1.2	13

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37	Robustness of the Parsimonious Reconciliation Method in Cophylogeny. Lecture Notes in Computer Science, 2016, , 119-130.	1.3	3
38	Computing and Listing st-Paths in Public Transportation Networks. Lecture Notes in Computer Science, 2016, , 102-116.	1.3	3
39	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
40	Cophylogeny Reconstruction via an Approximate Bayesian Computation. Systematic Biology, 2015, 64, 416-431.	5.6	35
41	EUCALYPT: efficient tree reconciliation enumerator. Algorithms for Molecular Biology, 2015, 10, 3.	1.2	33
42	Two Host Clades, Two Bacterial Arsenals: Evolution through Gene Losses in Facultative Endosymbionts. Genome Biology and Evolution, 2015, 7, 839-855.	2.5	26
43	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
44	M _e D _u S _a : a multi-draft based scaffold. Bioinformatics, 2015, 31, 2443-2451.	4.1	359
45	Genome reduction and potential metabolic complementation of the dual endosymbionts in the whitefly Bemisia tabaci. BMC Genomics, 2015, 16, 226.	2.8	100
46	Mirinho: An efficient and general plant and animal pre-miRNA predictor for genomic and deep sequencing data. BMC Bioinformatics, 2015, 16, 179.	2.6	16
47	Efficiently Listing Bounded Length st-Paths. Lecture Notes in Computer Science, 2015, , 318-329.	1.3	14
48	Incremental Complexity of a Bi-objective Hypergraph Transversal Problem. Lecture Notes in Computer Science, 2015, , 202-213.	1.3	0
49	Telling metabolic stories to explore metabolomics data: a case study on the yeast response to cadmium exposure. Bioinformatics, 2014, 30, 61-70.	4.1	13
50	Rime : Repeat identification. Discrete Applied Mathematics, 2014, 163, 275-286.	0.9	2
51	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.3	2
52	Amortized $\mathcal{O}(V)$ -Delay Algorithm for Listing Chordless Cycles in Undirected Graphs. Lecture Notes in Computer Science, 2014, , 418-429.	1.3	7
53	Short and long-term genome stability analysis of prokaryotic genomes. BMC Genomics, 2013, 14, 309.	2.8	9
54	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. BMC Evolutionary Biology, 2013, 13, 190.	3.2	70

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55	On the Genetic Architecture of Cytoplasmic Incompatibility: Inference from Phenotypic Data. <i>American Naturalist</i> , 2013, 182, E15-E24.	2.1	17
56	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
57	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
58	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. <i>Lecture Notes in Computer Science</i> , 2013, , 99-111.	1.3	6
59	Navigating the unexplored seascape of pre-miRNA candidates in single-genome approaches. <i>Bioinformatics</i> , 2012, 28, 3034-3041.	4.1	6
60	Algorithms and complexity of enumerating minimal precursor sets in genome-wide metabolic networks. <i>Bioinformatics</i> , 2012, 28, 2474-2483.	4.1	17
61	EIC Editorial. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1553-1557.	3.0	0
62	Exploration of the core metabolism of symbiotic bacteria. <i>BMC Genomics</i> , 2012, 13, 438.	2.8	11
63	Telling stories: Enumerating maximal directed acyclic graphs with a constrained set of sources and targets. <i>Theoretical Computer Science</i> , 2012, 457, 1-9.	0.9	8
64	Structural and dynamical analysis of biological networks. <i>Briefings in Functional Genomics</i> , 2012, 11, 420-433.	2.7	26
65	Sampling solution traces for the problem of sorting permutations by signed reversals. <i>Algorithms for Molecular Biology</i> , 2012, 7, 18.	1.2	1
66	BRASERO: A Resource for Benchmarking RNA Secondary Structure Comparison Algorithms. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-5.	5.7	15
67	Mod/Resc Parsimony Inference: Theory and application. <i>Information and Computation</i> , 2012, 213, 23-32.	0.7	6
68	KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. <i>BMC Bioinformatics</i> , 2012, 13, S5.	2.6	85
69	Efficient Bubble Enumeration in Directed Graphs. <i>Lecture Notes in Computer Science</i> , 2012, , 118-129.	1.3	13
70	<i>Wolbachia</i> detection: an assessment of standard PCR Protocols. <i>Molecular Ecology Resources</i> , 2011, 11, 567-572.	4.8	83
71	EIC Editorial. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1-1.	3.0	3
72	EIC Editorial. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 289-291.	3.0	0

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73	Bacterial synteny: an exact approach with gene quorum. BMC Bioinformatics, 2011, 12, 193.	2.6	9
74	Close 3D proximity of evolutionary breakpoints argues for the notion of spatial synteny. BMC Genomics, 2011, 12, 303.	2.8	42
75	CycADS: an annotation database system to ease the development and update of BioCyc databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar008-bar008.	3.0	16
76	EIC Editorial. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 193-194.	3.0	0
77	Identifying SNPs without a Reference Genome by Comparing Raw Reads. Lecture Notes in Computer Science, 2010, , 147-158.	1.3	35
78	Combination of measures distinguishes pre-miRNAs from other stem-loops in the genome of the newly sequenced Anopheles darlingi. BMC Genomics, 2010, 11, 529.	2.8	15
79	A note on the complexity of finding and enumerating elementary modes. BioSystems, 2010, 99, 210-214.	2.0	44
80	Repetition-free longest common subsequence. Discrete Applied Mathematics, 2010, 158, 1315-1324.	0.9	32
81	MetExplore: a web server to link metabolomic experiments and genome-scale metabolic networks. Nucleic Acids Research, 2010, 38, W132-W137.	14.5	148
82	Cassis: detection of genomic rearrangement breakpoints. Bioinformatics, 2010, 26, 1897-1898.	4.1	22
83	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
84	Mod/Resc Parsimony Inference. Lecture Notes in Computer Science, 2010, , 202-213.	1.3	3
85	Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms. Lecture Notes in Computer Science, 2010, , 226-237.	1.3	1
86	Assessing the Exceptionality of Coloured Motifs in Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-9.	1.4	11
87	Footprints of Inversions at Present and Past Pseudoautosomal Boundaries in Human Sex Chromosomes. Genome Biology and Evolution, 2009, 1, 56-66.	2.5	82
88	Analysis of fine-scale mammalian evolutionary breakpoints provides new insight into their relation to genome organisation. BMC Genomics, 2009, 10, 335.	2.8	58
89	Modes and cuts in metabolic networks: Complexity and algorithms. BioSystems, 2009, 95, 51-60.	2.0	88
90	Systemic analysis of the symbiotic function of <i>Buchnera aphidicola</i> , the primary endosymbiont of the pea aphid <i>Acyrtosiphon pisum</i> . Comptes Rendus - Biologies, 2009, 332, 1034-1049.	0.2	49

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91	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
92	Current tools for the identification of miRNA genes and their targets. <i>Nucleic Acids Research</i> , 2009, 37, 2419-2433.	14.5	211
93	An asymmetric approach to preserve common intervals while sorting by reversals. <i>Algorithms for Molecular Biology</i> , 2009, 4, 16.	1.2	5
94	Lossless filter for multiple repeats with bounded edit distance. <i>Algorithms for Molecular Biology</i> , 2009, 4, 3.	1.2	13
95	EIC Editorial: Introducing New Associate Editors. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 369-369.	3.0	0
96	EIC Editorial. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 177-177.	3.0	0
97	New EIC Editorial. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 3-3.	3.0	1
98	Multiple Alignment of Biological Networks: A Flexible Approach. <i>Lecture Notes in Computer Science</i> , 2009, , 263-273.	1.3	10
99	Assessing the Exceptionality of Coloured Motifs in Networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 616234.	1.4	15
100	A multiple layer model to compare RNA secondary structures. <i>Software - Practice and Experience</i> , 2008, 38, 775-792.	3.6	10
101	Lossless filter for multiple repetitions with Hamming distance. <i>Journal of Discrete Algorithms</i> , 2008, 6, 497-509.	0.7	12
102	Repetition-free longest common subsequence. <i>Electronic Notes in Discrete Mathematics</i> , 2008, 30, 243-248.	0.4	7
103	A small trip in the untranquil world of genomes. <i>Theoretical Computer Science</i> , 2008, 395, 171-192.	0.9	4
104	Precise detection of rearrangement breakpoints in mammalian chromosomes. <i>BMC Bioinformatics</i> , 2008, 9, 286.	2.6	36
105	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
106	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
107	INDEXING GAPPED-FACTORS USING A TREE. <i>International Journal of Foundations of Computer Science</i> , 2008, 19, 71-87.	1.1	4
108	Efficient representation and $\langle i \rangle P \langle i \rangle$ -value computation for high-order Markov motifs. <i>Bioinformatics</i> , 2008, 24, i160-i166.	4.1	6

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109	Enumerating Precursor Sets of Target Metabolites in a Metabolic Network. Lecture Notes in Computer Science, 2008, , 233-244.	1.3	13
110	Evolution under Reversals: Parsimony and Conservation of Common Intervals. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 301-309.	3.0	16
111	The maximum agreement forest problem: Approximation algorithms and computational experiments. Theoretical Computer Science, 2007, 374, 91-110.	0.9	31
112	Advances on sorting by reversals. Discrete Applied Mathematics, 2007, 155, 881-888.	0.9	80
113	All maximal-pairs in stepâ€‘leap representation of melodic sequence. Information Sciences, 2007, 177, 1954-1962.	6.9	2
114	Metabolic network visualization eliminating node redundance and preserving metabolic pathways. BMC Systems Biology, 2007, 1, 29.	3.0	35
115	The Solution Space of Sorting by Reversals. , 2007, , 293-304.		13
116	An Efficient Algorithm for the Identification of Structured Motifs in DNA Promoter Sequences. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 126-140.	3.0	51
117	Motif Search in Graphs: Application to Metabolic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 360-368.	3.0	146
118	Longest repeats with a block of k donâ€™t cares. Theoretical Computer Science, 2006, 362, 248-254.	0.9	12
119	RISOTTO: Fast Extraction of Motifs with Mismatches. Lecture Notes in Computer Science, 2006, , 757-768.	1.3	51
120	Bases of Motifs for Generating Repeated Patterns with Wild Cards. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 40-50.	3.0	50
121	A FIRST APPROACH TO FINDING COMMON MOTIFS WITH GAPS. International Journal of Foundations of Computer Science, 2005, 16, 1145-1154.	1.1	23
122	A New Distance for High Level RNA Secondary Structure Comparison. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 3-14.	3.0	38
123	Perfect Sorting by Reversals. Lecture Notes in Computer Science, 2005, , 42-51.	1.3	9
124	Reaction Motifs in Metabolic Networks. Lecture Notes in Computer Science, 2005, , 178-191.	1.3	7
125	A HIGHLY SCALABLE ALGORITHM FOR THE EXTRACTION OF CIS-REGULATORY REGIONS. , 2005, , .		31
126	A parallel algorithm for the extraction of structured motifs. , 2004, , .		20

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127	Longest Repeats with a Block of Donâ€™t Cares. Lecture Notes in Computer Science, 2004, , 271-278.	1.3	3
128	Longest Motifs with a Functionally Equivalent Central Block. Lecture Notes in Computer Science, 2004, , 298-309.	1.3	0
129	Motifs in Sequences. , 2004, , 47-97.		2
130	Orphan gene findingâ€™ an exon assembly approach. Theoretical Computer Science, 2003, 290, 1407-1431.	0.9	15
131	Occurrence Probability of Structured Motifs in Random Sequences. Journal of Computational Biology, 2002, 9, 761-773.	1.6	39
132	Current methods of gene prediction, their strengths and weaknesses. Nucleic Acids Research, 2002, 30, 4103-4117.	14.5	374
133	Further Thoughts on the Syntenic Distance between Genomes. Algorithmica, 2002, 34, 157-180.	1.3	6
134	Algorithms for Extracting Structured Motifs Using a Suffix Tree with an Application to Promoter and Regulatory Site Consensus Identification. Journal of Computational Biology, 2000, 7, 345-362.	1.6	212
135	Inferring regulatory elements from a whole genome. an analysis of Helicobacter pylori’s family of promoter signals. Journal of Molecular Biology, 2000, 297, 335-353.	4.2	75
136	Promoter sequences and algorithmical methods for identifying them. Research in Microbiology, 1999, 150, 779-799.	2.1	52
137	Identifying Satellites and Periodic Repetitions in Biological Sequences. Journal of Computational Biology, 1998, 5, 539-553.	1.6	33
138	Multiple sequence comparison â€™ a peptide matching approach. Theoretical Computer Science, 1997, 180, 115-137.	0.9	13
139	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
140	Finding flexible patterns in a text: an application to three-dimensional molecular matching. Bioinformatics, 1995, 11, 59-70.	4.1	1
141	Multiple sequence comparison: A peptide matching approach. Lecture Notes in Computer Science, 1995, , 366-385.	1.3	6