

Anne Bergeron

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

794
citations

516710

16
h-index

642732

23
g-index

25
all docs

25
docs citations

25
times ranked

584
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genesis of the DCJ Formula. Computational Biology, 2013, , 63-81.	0.2	1
2	The evolution of the tape measure protein: units, duplications and losses. BMC Bioinformatics, 2011, 12, S10.	2.6	34
3	Theory and Practice of Ultra-Perfection. Journal of Computational Biology, 2011, 18, 1219-1230.	1.6	2
4	Combinatorial Structure of Genome Rearrangements Scenarios. Journal of Computational Biology, 2010, 17, 1129-1144.	1.6	17
5	Rearrangement Models and Single-Cut Operations. Journal of Computational Biology, 2010, 17, 1213-1225.	1.6	5
6	Mosaic Graphs and Comparative Genomics in Phage Communities. Journal of Computational Biology, 2010, 17, 1315-1326.	1.6	22
7	Ultra-Perfect Sorting Scenarios. Lecture Notes in Computer Science, 2010, , 50-61.	1.3	0
8	A new linear time algorithm to compute the genomic distance via the double cut and join distance. Theoretical Computer Science, 2009, 410, 5300-5316.	0.9	35
9	Parking Functions, Labeled Trees and DCJ Sorting Scenarios. Lecture Notes in Computer Science, 2009, , 24-35.	1.3	2
10	HP Distance Via Double Cut and Join Distance. , 2008, , 56-68.		8
11	Perfect Sorting by Reversals Is Not Always Difficult. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 4-16.	3.0	42
12	Divide and Conquer: Enriching Environmental Sequencing Data. PLoS ONE, 2007, 2, e830.	2.5	6
13	Advances on sorting by reversals. Discrete Applied Mathematics, 2007, 155, 881-888.	0.9	80
14	On Sorting by Translocations. Journal of Computational Biology, 2006, 13, 567-578.	1.6	48
15	On the Similarity of Sets of Permutations and Its Applications to Genome Comparison. Journal of Computational Biology, 2006, 13, 1340-1354.	1.6	36
16	Conservation of Combinatorial Structures in Evolution Scenarios. Lecture Notes in Computer Science, 2005, , 1-14.	1.3	20
17	Identification of genomic features using microsynteny of domains: Domain teams. Genome Research, 2005, 15, 867-874.	5.5	37
18	From cascade decompositions to bit-vector algorithms. Theoretical Computer Science, 2004, 313, 3-16.	0.9	1

#	ARTICLE	IF	CITATIONS
19	An algorithmic view of gene teams. Theoretical Computer Science, 2004, 320, 395-418.	0.9	31
20	Gene teams: a new formalization of gene clusters for comparative genomics. Computational Biology and Chemistry, 2003, 27, 59-67.	2.3	52
21	On the Similarity of Sets of Permutations and Its Applications to Genome Comparison. Lecture Notes in Computer Science, 2003, , 68-79.	1.3	41
22	VECTOR ALGORITHMS FOR APPROXIMATE STRING MATCHING. International Journal of Foundations of Computer Science, 2002, 13, 53-65.	1.1	15
23	The Algorithmic of Gene Teams. Lecture Notes in Computer Science, 2002, , 464-476.	1.3	49