

David Sankoff

List of Publications by Year in descending order

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131
papers

7,470
citations

172207

29
h-index

62479

80
g-index

139
all docs

139
docs citations

139
times ranked

9053
citing authors

#	ARTICLE	IF	CITATIONS
1	Polyploidy and angiosperm diversification. <i>American Journal of Botany</i> , 2009, 96, 336-348.	0.8	1,031
2	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	6.0	743
3	Locating rearrangement events in a phylogeny based on highly fragmented assemblies. <i>BMC Genomics</i> , 2016, 17, 1.	1.2	740
4	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	6.0	520
5	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
6	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
7	Structural Dynamics of Eukaryotic Chromosome Evolution. <i>Science</i> , 2003, 301, 793-797.	6.0	357
8	Multiple Genome Rearrangement and Breakpoint Phylogeny. <i>Journal of Computational Biology</i> , 1998, 5, 555-570.	0.8	216
9	Comparable Rates of Gene Loss and Functional Divergence After Genome Duplications Early in Vertebrate Evolution. <i>Genetics</i> , 1997, 147, 1259-1266.	1.2	205
10	Genome rearrangement with gene families. <i>Bioinformatics</i> , 1999, 15, 909-917.	1.8	192
11	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17081-17089.	3.3	134
12	Multichromosomal median and halving problems under different genomic distances. <i>BMC Bioinformatics</i> , 2009, 10, 120.	1.2	123
13	The collapse of gene complement following whole genome duplication. <i>BMC Genomics</i> , 2010, 11, 313.	1.2	114
14	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
15	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441.	3.3	95
16	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. <i>Nature Plants</i> , 2020, 6, 929-941.	4.7	94
17	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	9.4	88
18	The Reconstruction of Doubled Genomes. <i>SIAM Journal on Computing</i> , 2003, 32, 754-792.	0.8	86

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19	Edit distance for genome comparison based on non-local operations. Lecture Notes in Computer Science, 1992, , 121-135.	1.0	78
20	Efficient bounds for oriented chromosome inversion distance. Lecture Notes in Computer Science, 1994, , 307-325.	1.0	74
21	Tests for Gene Clustering. Journal of Computational Biology, 2003, 10, 453-482.	0.8	72
22	Genome sequence and evolution of <i>Betula platyphylla</i> . Horticulture Research, 2021, 8, 37.	2.9	53
23	Scaffold filling, contig fusion and comparative gene order inference. BMC Bioinformatics, 2010, 11, 304.	1.2	50
24	Rearrangements and chromosomal evolution. Current Opinion in Genetics and Development, 2003, 13, 583-587.	1.5	44
25	Chromosomal Breakpoint Reuse in Genome Sequence Rearrangement. Journal of Computational Biology, 2005, 12, 812-821.	0.8	44
26	The median problem for breakpoints in comparative genomics. Lecture Notes in Computer Science, 1997, , 251-263.	1.0	42
27	Chromosome rearrangements in evolution: From gene order to genome sequence and back. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11188-11189.	3.3	41
28	Removing Noise and Ambiguities from Comparative Maps in Rearrangement Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 515-522.	1.9	41
29	Early Eukaryote Evolution Based on Mitochondrial Gene Order Breakpoints. Journal of Computational Biology, 2000, 7, 521-535.	0.8	35
30	Transmission, Education and Integration in Projections of Language Shift in Valencia. Language Policy, 2004, 3, 107-131.	0.4	31
31	The Statistical Analysis of Spatially Clustered Genes under the Maximum Gap Criterion. Journal of Computational Biology, 2005, 12, 1083-1102.	0.8	29
32	Guided genome halving: hardness, heuristics and the history of the Hemiascomycetes. Bioinformatics, 2008, 24, i96-i104.	1.8	29
33	Ancient eudicot hexaploidy meets ancestral eurosid gene order. BMC Genomics, 2013, 14, S3.	1.2	29
34	Chromosomal Distributions of Breakpoints in Cancer, Infertility, and Evolution. Theoretical Population Biology, 2002, 61, 497-501.	0.5	28
35	Common Intervals and Symmetric Difference in a Model-Free Phylogenomics, with an Application to Streptophyte Evolution. Journal of Computational Biology, 2007, 14, 436-445.	0.8	27
36	Genomic features in the breakpoint regions between syntenic blocks. Bioinformatics, 2004, 20, i318-i325.	1.8	26

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37	Algorithms for the Extraction of Synteny Blocks from Comparative Maps. Lecture Notes in Computer Science, 2007, , 277-288.	1.0	26
38	The nuclear genome of <i>Rhazya stricta</i> and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. Scientific Reports, 2016, 6, 33782.	1.6	26
39	Decompositions of Multiple Breakpoint Graphs and Rapid Exact Solutions to the Median Problem. Lecture Notes in Computer Science, 2008, , 25-37.	1.0	26
40	Short inversions and conserved gene cluster. Bioinformatics, 2002, 18, 1305-1305.	1.8	25
41	Fractionation, rearrangement and subgenome dominance. Bioinformatics, 2012, 28, i402-i408.	1.8	25
42	The Signal in the Genomes. PLoS Computational Biology, 2006, 2, e35.	1.5	24
43	The where and wherefore of evolutionary breakpoints. Journal of Biology, 2009, 8, 66.	2.7	24
44	Buxus and Tetracentron genomes help resolve eudicot genome history. Nature Communications, 2022, 13, 643.	5.8	24
45	Reversal distance for partially ordered genomes. Bioinformatics, 2005, 21, i502-i508.	1.8	23
46	Fractionation statistics. BMC Bioinformatics, 2011, 12, S5.	1.2	23
47	Genome Halving with an Outgroup. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	21
48	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. Genome Research, 2021, 31, 799-810.	2.4	21
49	OMG! Orthologs in Multiple Genomes – Competing Graph-Theoretical Formulations. Lecture Notes in Computer Science, 2011, , 364-375.	1.0	21
50	Genome aliquoting with double cut and join. BMC Bioinformatics, 2009, 10, S2.	1.2	20
51	A model for biased fractionation after whole genome duplication. BMC Genomics, 2012, 13, S8.	1.2	20
52	Accurate prediction of orthologs in the presence of divergence after duplication. Bioinformatics, 2018, 34, i366-i375.	1.8	20
53	Generalized Gene Adjacencies, Graph Bandwidth, and Clusters in Yeast Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 213-220.	1.9	18
54	Analysis of Gene Order Evolution Beyond Single-Copy Genes. Methods in Molecular Biology, 2012, 855, 397-429.	0.4	18

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55	Medians seek the corners, and other conjectures. BMC Bioinformatics, 2012, 13, S5.	1.2	17
56	The dynamics of functional classes of plant genes in rediploidized ancient polyploids. BMC Bioinformatics, 2013, 14, S19.	1.2	17
57	Reconstructing the pre-doubling genome. , 1999, , .		16
58	The Distribution of Genomic Distance between Random Genomes. Journal of Computational Biology, 2006, 13, 1005-1012.	0.8	16
59	Stability of Rearrangement Measures in the Comparison of Genome Sequences. Journal of Computational Biology, 2006, 13, 554-566.	0.8	15
60	Whole Genome Duplication in Plants: Implications for Evolutionary Analysis. Methods in Molecular Biology, 2018, 1704, 291-315.	0.4	15
61	Polyploids, genome halving and phylogeny. Bioinformatics, 2007, 23, i433-i439.	1.8	14
62	Descendants of Whole Genome Duplication within Gene Order Phylogeny. Journal of Computational Biology, 2008, 15, 947-964.	0.8	14
63	Power Boosts for Cluster Tests. Lecture Notes in Computer Science, 2005, , 121-130.	1.0	14
64	GENOME HALVING WITH DOUBLE CUT AND JOIN. Journal of Bioinformatics and Computational Biology, 2009, 07, 357-371.	0.3	13
65	Natural Parameter Values for Generalized Gene Adjacency. Journal of Computational Biology, 2010, 17, 1113-1128.	0.8	13
66	Economic importance, taxonomic representation and scientific priority as drivers of genome sequencing projects. BMC Genomics, 2016, 17, 782.	1.2	13
67	Poisson adjacency distributions in genome comparison: multichromosomal, circular, signed and unsigned cases. Bioinformatics, 2008, 24, i146-i152.	1.8	12
68	Towards Improved Reconstruction of Ancestral Gene Order in Angiosperm Phylogeny. Journal of Computational Biology, 2009, 16, 1353-1367.	0.8	12
69	GENE LOSS UNDER NEIGHBORHOOD SELECTION FOLLOWING WHOLE GENOME DUPLICATION AND THE RECONSTRUCTION OF THE ANCESTRAL POPULUS GENOME. Journal of Bioinformatics and Computational Biology, 2009, 07, 499-520.	0.3	12
70	Reconstructing the History of Yeast Genomes. PLoS Genetics, 2009, 5, e1000483.	1.5	11
71	Genome Aliquoting Revisited. Journal of Computational Biology, 2011, 18, 1065-1075.	0.8	11
72	Models for Similarity Distributions of Syntenic Homologs and Applications to Phylogenomics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 727-737.	1.9	11

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73	Pinning down ploidy in paleopolyploid plants. <i>BMC Genomics</i> , 2018, 19, 287.	1.2	10
74	Tests for Gene Clusters Satisfying the Generalized Adjacency Criterion. <i>Lecture Notes in Computer Science</i> , 2008, , 152-160.	1.0	10
75	The ABCs of MGR with DCJ. <i>Evolutionary Bioinformatics</i> , 2008, 4, 69-74.	0.6	10
76	Genome halving with an outgroup. <i>Evolutionary Bioinformatics</i> , 2007, 2, 295-302.	0.6	10
77	Paths and Cycles in Breakpoint Graph of Random Multichromosomal Genomes. <i>Journal of Computational Biology</i> , 2007, 14, 423-435.	0.8	9
78	Detection of gene expression changes at chromosomal rearrangement breakpoints in evolution. <i>BMC Bioinformatics</i> , 2012, 13, S6.	1.2	9
79	Evolutionary Model for the Statistical Divergence of Paralogous and Orthologous Gene Pairs Generated by Whole Genome Duplication and Speciation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1579-1584.	1.9	9
80	The Valencian revival: Why usage lags behind competence. <i>Language in Society</i> , 2004, 33, .	0.3	8
81	A consolidation algorithm for genomes fractionated after higher order polyploidization. <i>BMC Bioinformatics</i> , 2012, 13, S8.	1.2	8
82	Practical aliquoting of flowering plant genomes. <i>BMC Bioinformatics</i> , 2013, 14, S8.	1.2	8
83	Near-medians that avoid the corners; a combinatorial probability approach. <i>BMC Genomics</i> , 2014, 15, S1.	1.2	8
84	Rearrangement Phylogeny of Genomes in Contig Form. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 579-587.	1.9	7
85	Gene order in rosid phylogeny, inferred from pairwise syntenies among extant genomes. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	7
86	Validation of Automated Chromosome Recovery in the Reconstruction of Ancestral Gene Order. <i>Algorithms</i> , 2021, 14, 160.	1.2	7
87	Accuracy and Robustness of Analyses Based on Numbers of Genes in Observed Segments. <i>Computational Biology</i> , 2000, , 299-306.	0.1	7
88	Phase change for the accuracy of the median value in estimating divergence time. <i>BMC Bioinformatics</i> , 2013, 14, S7.	1.2	6
89	Practical halving; the <i>Nelumbo nucifera</i> evidence on early eudicot evolution. <i>Computational Biology and Chemistry</i> , 2014, 50, 75-81.	1.1	6
90	Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-Occurrences. <i>Journal of Computational Biology</i> , 2021, 28, 1156-1179.	0.8	6

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91	Duration of detectible synchrony in a binary branching process. <i>Biometrika</i> , 1971, 58, 77-81.	1.3	5
92	Genome rearrangements with partially ordered chromosomes. <i>Journal of Combinatorial Optimization</i> , 2006, 11, 133-144.	0.8	5
93	Issues in the Reconstruction of Gene Order Evolution. <i>Journal of Computer Science and Technology</i> , 2010, 25, 10-25.	0.9	5
94	Gene expression and fractionation resistance. <i>BMC Genomics</i> , 2014, 15, S19.	1.2	5
95	Excision Dominates Pseudogenization During Fractionation After Whole Genome Duplication and in Gene Loss After Speciation in Plants. <i>Frontiers in Genetics</i> , 2020, 11, 603056.	1.1	5
96	Integrated synteny- and similarity-based inference on the polyploidization-fractionation cycle. <i>Interface Focus</i> , 2021, 11, 20200059.	1.5	5
97	Syntenic block overlap multiplicities with a panel of reference genomes provide a signature of ancient polyploidization events. <i>BMC Genomics</i> , 2015, 16, S8.	1.2	4
98	Structural vs. functional mechanisms of duplicate gene loss following whole genome doubling. <i>BMC Bioinformatics</i> , 2015, 16, S9.	1.2	4
99	A continuous analog of run length distributions reflecting accumulated fractionation events. <i>BMC Bioinformatics</i> , 2016, 17, 412.	1.2	4
100	A branching process for homology distribution-based inference of polyploidy, speciation and loss. <i>Algorithms for Molecular Biology</i> , 2019, 14, 18.	0.3	4
101	Branching Out to Speciation in a Model of Fractionation: The Malvaceae. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1875-1884.	1.9	4
102	RACCROCHE: Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-occurrences. <i>Lecture Notes in Computer Science</i> , 2021, , 97-115.	1.0	4
103	The Trees in the Peaks. <i>Lecture Notes in Computer Science</i> , 2016, , 3-14.	1.0	4
104	Peripheral structures in unlabelled trees and the accumulation of subgenomes in the evolution of polyploids. <i>Journal of Theoretical Biology</i> , 2022, 532, 110924.	0.8	4
105	Sets of medians in the non-geodesic pseudometric space of unsigned genomes with breakpoints. <i>BMC Genomics</i> , 2014, 15, S3.	1.2	3
106	Distinguishing successive ancient polyploidy levels based on genome-internal syntenic alignment. <i>BMC Bioinformatics</i> , 2019, 20, 635.	1.2	3
107	Paths and Cycles in Breakpoint Graphs of Random Multichromosomal Genomes. <i>Lecture Notes in Computer Science</i> , 2006, , 51-62.	1.0	3
108	Speciation and Rate Variation in a Birth-and-Death Account of WGD and Fractionation; the Case of Solanaceae. <i>Lecture Notes in Computer Science</i> , 2018, , 146-160.	1.0	3

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109	THE EFFECT OF MASSIVE GENE LOSS FOLLOWING WHOLE GENOME DUPLICATION ON THE ALGORITHMIC RECONSTRUCTION OF THE ANCESTRAL POPULUS DIPLOID. , 2008, , .		3
110	Gene Order in Rosid Phylogeny, Inferred from Pairwise Syntenies among Extant Genomes. Lecture Notes in Computer Science, 2011, , 99-110.	1.0	3
111	Listing all sorting reversals in quadratic time. Algorithms for Molecular Biology, 2011, 6, 11.	0.3	2
112	Structural vs. functional mechanisms of duplicate gene loss following whole genome doubling. , 2014, , .		2
113	Resolution effects in reconstructing ancestral genomes. BMC Genomics, 2018, 19, 100.	1.2	2
114	Ultrasound tongue contour extraction using BowNet network: A deep learning approach. Proceedings of Meetings on Acoustics, 2019, , .	0.3	2
115	Fractionation, Rearrangement, Consolidation, Reconstruction. Computational Biology, 2013, , 247-260.	0.1	2
116	Rearrangement Phylogeny of Genomes in Contig Form. Lecture Notes in Computer Science, 2009, , 160-172.	1.0	2
117	Natural Parameter Values for Generalized Gene Adjacency. Lecture Notes in Computer Science, 2009, , 13-23.	1.0	2
118	Listing All Sorting Reversals in Quadratic Time. Lecture Notes in Computer Science, 2010, , 102-110.	1.0	2
119	Internal Validation of Ancestral Gene Order Reconstruction in Angiosperm Phylogeny. Lecture Notes in Computer Science, 2008, , 252-264.	1.0	2
120	Stability of Rearrangement Measures in the Comparison of Genome Sequences. Lecture Notes in Computer Science, 2005, , 603-614.	1.0	1
121	Statistical analysis of fractionation resistance by functional category and expression. BMC Genomics, 2017, 18, 366.	1.2	1
122	The Similarity Distribution of Paralogous Gene Pairs Created by Recurrent Alternation of Polyploidization and Fractionation. Lecture Notes in Computer Science, 2017, , 1-13.	1.0	1
123	The monoploid chromosome complement of reconstructed ancestral genomes in a phylogeny. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140008.	0.3	1
124	Generalized Adjacency in Genetic Networks and the Conservation of Functional Gene Clusters. , 2011, , .		0
125	Keynote: Aspects of fractionation. , 2012, , .		0
126	Statistical analysis of fractionation resistance by functional category and expression level. , 2015, , .		0

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127	Compromise or optimize? The breakpoint anti-median. BMC Bioinformatics, 2016, 17, 473.	1.2	0
128	Asymptotic medians of random permutations sampled from reversal random walks. Theoretical Computer Science, 2017, 698, 9-13.	0.5	0
129	Evolutionary Rate Change and the Transformation from Additive to Ultrametric: Modal Similarity of Orthologs in Fish and Flower Phylogenomics. Computational Biology, 2019, , 175-192.	0.1	0
130	Parts of the Problem of Polyploids in Rearrangement Phylogeny. Lecture Notes in Computer Science, 2007, , 162-176.	1.0	0
131	Guest Editorial for the 17th Asia Pacific Bioinformatics Conference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2123-2124.	1.9	0