

Jens Stoye

List of Publications by Year in descending order

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129
papers

6,470
citations

94433

37
h-index

69250

77
g-index

136
all docs

136
docs citations

136
times ranked

7193
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence-based pangenomic core detection. <i>IScience</i> , 2022, 25, 104413.	4.1	5
2	Computing the Inversion-Indel Distance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2314-2326.	3.0	8
3	Detecting high-scoring local alignments in pangenome graphs. <i>Bioinformatics</i> , 2021, 37, 2266-2274.	4.1	6
4	Computing the Rearrangement Distance of Natural Genomes. <i>Journal of Computational Biology</i> , 2021, 28, 410-431.	1.6	17
5	Reconstructing tumor evolutionary histories and clone trees in polynomial-time with SubMARine. <i>PLoS Computational Biology</i> , 2021, 17, e1008400.	3.2	7
6	Horizontal Gene Transfer Phylogenetics: A Random Walk Approach. <i>Molecular Biology and Evolution</i> , 2020, 37, 1470-1479.	8.9	5
7	HASLR: Fast Hybrid Assembly of Long Reads. <i>IScience</i> , 2020, 23, 101389.	4.1	44
8	Editorial: Computational Methods for Microbiome Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 623897.	2.3	0
9	Searching and inferring colorful topological motifs in vertex-colored graphs. <i>Journal of Combinatorial Optimization</i> , 2020, 40, 379-411.	1.3	0
10	Finding all maximal perfect haplotype blocks in linear time. <i>Algorithms for Molecular Biology</i> , 2020, 15, 2.	1.2	9
11	Analysis of local genome rearrangement improves resolution of ancestral genomic maps in plants. <i>BMC Genomics</i> , 2020, 21, 273.	2.8	4
12	Computing the Rearrangement Distance of Natural Genomes. <i>Lecture Notes in Computer Science</i> , 2020, , 3-18.	1.3	5
13	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	4.7	49
14	Pan-Genome Storage and Analysis Techniques. <i>Methods in Molecular Biology</i> , 2018, 1704, 29-53.	0.9	24
15	Family-Free Genome Comparison. <i>Methods in Molecular Biology</i> , 2018, 1704, 331-342.	0.9	6
16	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018, 6, 76.	11.1	29
17	Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 2094-2100.	3.0	1
18	Identifying Maximal Perfect Haplotype Blocks. <i>Lecture Notes in Computer Science</i> , 2018, , 26-37.	1.3	7

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19	Dynamic Alignment-Free and Reference-Free Read Compression. <i>Journal of Computational Biology</i> , 2018, 25, 825-836.	1.6	7
20	Computing the family-free DCJ similarity. <i>BMC Bioinformatics</i> , 2018, 19, 152.	2.6	2
21	Dynamic Alignment-Free and Reference-Free Read Compression. <i>Lecture Notes in Computer Science</i> , 2017, , 50-65.	1.3	7
22	New Genome Similarity Measures based on Conserved Gene Adjacencies. <i>Journal of Computational Biology</i> , 2017, 24, 616-634.	1.6	1
23	Algorithms for Computing the Family-Free Genomic Similarity Under DCJ. <i>Lecture Notes in Computer Science</i> , 2017, , 76-100.	1.3	0
24	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	3.8	84
25	Approximating the DCJ distance of balanced genomes in linear time. <i>Algorithms for Molecular Biology</i> , 2017, 12, 3.	1.2	9
26	Finding approximate gene clusters with Gecko 3. <i>Nucleic Acids Research</i> , 2016, 44, gkw843.	14.5	23
27	New Genome Similarity Measures Based on Conserved Gene Adjacencies. <i>Lecture Notes in Computer Science</i> , 2016, , 204-224.	1.3	2
28	A Linear Time Approximation Algorithm for the DCJ Distance for Genomes with Bounded Number of Duplicates. <i>Lecture Notes in Computer Science</i> , 2016, , 293-306.	1.3	2
29	Bloom Filter Trie: an alignment-free and reference-free data structure for pan-genome storage. <i>Algorithms for Molecular Biology</i> , 2016, 11, 3.	1.2	69
30	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. <i>Carcinogenesis</i> , 2016, 37, 356-365.	2.8	46
31	On the family-free DCJ distance and similarity. <i>Algorithms for Molecular Biology</i> , 2015, 10, 13.	1.2	19
32	Sorting Linear Genomes with Rearrangements and Indels. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 500-506.	3.0	7
33	Orthology Detection Combining Clustering and Synteny for Very Large Datasets. <i>PLoS ONE</i> , 2014, 9, e105015.	2.5	86
34	GABenchToB: A Genome Assembly Benchmark Tuned on Bacteria and Benchtop Sequencers. <i>PLoS ONE</i> , 2014, 9, e107014.	2.5	29
35	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. <i>Journal of Biotechnology</i> , 2014, 190, 64-75.	3.8	9
36	ReadXplorerâ€™ visualization and analysis of mapped sequences. <i>Bioinformatics</i> , 2014, 30, 2247-2254.	4.1	127

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37	Improving the genome annotation of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 by sequencing enriched 5' ends of primary transcripts. <i>Journal of Biotechnology</i> , 2014, 190, 85-95.	3.8	15
38	Identifying gene clusters by discovering common intervals in indeterminate strings. <i>BMC Genomics</i> , 2014, 15, S2.	2.8	4
39	Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework. <i>Lecture Notes in Computer Science</i> , 2014, 15, 135-143.	1.3	6
40	<i>Mycoplasma salivarium</i> as a Dominant Coloniser of Fanconi Anaemia Associated Oral Carcinoma. <i>PLoS ONE</i> , 2014, 9, e92297.	2.5	32
41	metaBEETL: high-throughput analysis of heterogeneous microbial populations from shotgun DNA sequences. <i>BMC Bioinformatics</i> , 2013, 14, S2.	2.6	14
42	MetaSAMS: A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. <i>Journal of Biotechnology</i> , 2013, 167, 156-165.	3.8	17
43	On the inversion-indel distance. <i>BMC Bioinformatics</i> , 2013, 14, S3.	2.6	16
44	Statistics for approximate gene clusters. <i>BMC Bioinformatics</i> , 2013, 14, S14.	2.6	11
45	Comparative RNA-sequencing of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 cultivated in different growth media. <i>Journal of Biotechnology</i> , 2013, 167, 166-177.	3.8	20
46	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , 2013, 31, 294-296.	17.5	423
47	The Genesis of the DCJ Formula. <i>Computational Biology</i> , 2013, , 63-81.	0.2	1
48	The Potential of Family-Free Genome Comparison. <i>Computational Biology</i> , 2013, , 287-307.	0.2	12
49	Taxonomic Classification of Metagenomic Shotgun Sequences with CARMA3. , 2013, , 1-8.		0
50	Restricted DCJ-Indel Model Revisited. <i>Lecture Notes in Computer Science</i> , 2013, , 36-46.	1.3	1
51	UniMoG: a unifying framework for genomic distance calculation and sorting based on DCJ. <i>Bioinformatics</i> , 2012, 28, 2509-2511.	4.1	38
52	Combining peak- and chromatogram-based retention time alignment algorithms for multiple chromatography-mass spectrometry datasets. <i>BMC Bioinformatics</i> , 2012, 13, 214.	2.6	33
53	The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2012, 13, 112.	2.8	69
54	Multiple genome comparison based on overlap regions of pairwise local alignments. <i>BMC Bioinformatics</i> , 2012, 13, S7.	2.6	6

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55	Gene family assignment-free comparative genomics. BMC Bioinformatics, 2012, 13, S3.	2.6	17
56	Consistency of Sequence-Based Gene Clusters. Journal of Computational Biology, 2011, 18, 1023-1039.	1.6	9
57	Taxonomic classification of metagenomic shotgun sequences with CARMA3. Nucleic Acids Research, 2011, 39, e91-e91.	14.5	99
58	Common Intervals of Multiple Permutations. Algorithmica, 2011, 60, 175-206.	1.3	11
59	Swiftly Computing Center Strings. BMC Bioinformatics, 2011, 12, 106.	2.6	4
60	On the weight of indels in genomic distances. BMC Bioinformatics, 2011, 12, S13.	2.6	14
61	Genomic distance under gene substitutions. BMC Bioinformatics, 2011, 12, S8.	2.6	10
62	Balanced vertices in trees and a simpler algorithm to compute the genomic distance. Applied Mathematics Letters, 2011, 24, 82-86.	2.7	6
63	Sequencing of high G+C microbial genomes using the ultrafast pyrosequencing technology. Journal of Biotechnology, 2011, 155, 68-77.	3.8	29
64	Restricted DCJ Model: Rearrangement Problems with Chromosome Reincorporation. Journal of Computational Biology, 2011, 18, 1231-1241.	1.6	14
65	Double Cut and Join with Insertions and Deletions. Journal of Computational Biology, 2011, 18, 1167-1184.	1.6	63
66	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. Bioinformatics, 2011, 27, 1351-1358.	4.1	78
67	The complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence. BMC Genomics, 2010, 11, 728.	2.8	89
68	Phylogenetic comparative assembly. Algorithms for Molecular Biology, 2010, 5, 3.	1.2	15
69	Partitioning biological data with transitivity clustering. Nature Methods, 2010, 7, 419-420.	19.0	84
70	Genomic Distance with DCJ and Indels. Lecture Notes in Computer Science, 2010, , 90-101.	1.3	20
71	Finding Nested Common Intervals Efficiently. Journal of Computational Biology, 2010, 17, 1183-1194.	1.6	10
72	Rearrangement Models and Single-Cut Operations. Journal of Computational Biology, 2010, 17, 1213-1225.	1.6	5

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73	The Solution Space of Sorting by DCJ. <i>Journal of Computational Biology</i> , 2010, 17, 1145-1165.	1.6	42
74	r2cat: synteny plots and comparative assembly. <i>Bioinformatics</i> , 2010, 26, 570-571.	4.1	134
75	Swiftly Computing Center Strings. <i>Lecture Notes in Computer Science</i> , 2010, , 325-336.	1.3	11
76	The Problem of Chromosome Reincorporation in DCJ Sorting and Halving. <i>Lecture Notes in Computer Science</i> , 2010, , 13-24.	1.3	2
77	Consistency of Sequence-Based Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2010, , 252-263.	1.3	2
78	Computation of Median Gene Clusters. <i>Journal of Computational Biology</i> , 2009, 16, 1085-1099.	1.6	32
79	ChromA: signal-based retention time alignment for chromatographyâ€“mass spectrometry data. <i>Bioinformatics</i> , 2009, 25, 2080-2081.	4.1	32
80	A report on the 2009 SIG on short read sequencing and algorithms (Short-SIG). <i>Bioinformatics</i> , 2009, 25, 2863-2864.	4.1	0
81	WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads. <i>BMC Bioinformatics</i> , 2009, 10, 430.	2.6	78
82	A new linear time algorithm to compute the genomic distance via the double cut and join distance. <i>Theoretical Computer Science</i> , 2009, 410, 5300-5316.	0.9	35
83	The Sequence Analysis and Management System â€“ SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12.	3.8	37
84	A Unified Approach for Reconstructing Ancient Gene Clusters. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 387-400.	3.0	26
85	Rearrangement Models and Single-Cut Operations. <i>Lecture Notes in Computer Science</i> , 2009, , 84-97.	1.3	1
86	Finding Nested Common Intervals Efficiently. <i>Lecture Notes in Computer Science</i> , 2009, , 59-69.	1.3	2
87	Phylogenetic Comparative Assembly. <i>Lecture Notes in Computer Science</i> , 2009, , 145-156.	1.3	0
88	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	3.8	202
89	Counting suffix arrays and strings. <i>Theoretical Computer Science</i> , 2008, 395, 220-234.	0.9	16
90	MeltDB: a software platform for the analysis and integration of metabolomics experiment data. <i>Bioinformatics</i> , 2008, 24, 2726-2732.	4.1	100

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91	Comparative Pathway Analyzer—a web server for comparative analysis, clustering and visualization of metabolic networks in multiple organisms. <i>Nucleic Acids Research</i> , 2008, 36, W433-W437.	14.5	13
92	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	14.5	246
93	HP Distance Via Double Cut and Join Distance. , 2008, , 56-68.		8
94	Computation of Median Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2008, , 331-345.	1.3	8
95	On Computing the Breakpoint Reuse Rate in Rearrangement Scenarios. <i>Lecture Notes in Computer Science</i> , 2008, , 226-240.	1.3	7
96	Character sets of strings. <i>Journal of Discrete Algorithms</i> , 2007, 5, 330-340.	0.7	25
97	An incomplex algorithm for fast suffix array construction. <i>Software - Practice and Experience</i> , 2007, 37, 309-329.	3.6	21
98	Based Upon Repeat Pattern (BURP): an algorithm to characterize the long-term evolution of <i>Staphylococcus aureus</i> populations based on <i>spa</i> polymorphisms. <i>BMC Microbiology</i> , 2007, 7, 98.	3.3	203
99	Gecko and GhostFam. <i>Methods in Molecular Biology</i> , 2007, 396, 165-182.	0.9	6
100	Comparing Tandem Repeats with Duplications and Excisions of Variable Degree. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 395-407.	3.0	22
101	Efficient q-Gram Filters for Finding All $\hat{\mu}$ -Matches over a Given Length. <i>Journal of Computational Biology</i> , 2006, 13, 296-308.	1.6	90
102	GISMO—gene identification using a support vector machine for ORF classification. <i>Nucleic Acids Research</i> , 2006, 35, 540-549.	14.5	47
103	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , 2006, 22, e281-e289.	4.1	68
104	Panta rhei (QAlign2): an open graphical environment for sequence analysis. <i>Bioinformatics</i> , 2006, 22, 889-890.	4.1	6
105	On Sorting by Translocations. <i>Journal of Computational Biology</i> , 2006, 13, 567-578.	1.6	48
106	On the Similarity of Sets of Permutations and Its Applications to Genome Comparison. <i>Journal of Computational Biology</i> , 2006, 13, 1340-1354.	1.6	36
107	Large scale hierarchical clustering of protein sequences. <i>BMC Bioinformatics</i> , 2005, 6, 15.	2.6	62
108	Alignment of Tandem Repeats with Excision, Duplication, Substitution and Indels (EDSI). <i>Lecture Notes in Computer Science</i> , 2005, , 276-290.	1.3	7

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109	BACCardI—a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , 2005, 21, 853-859.	4.1	32
110	On Sorting by Translocations. <i>Lecture Notes in Computer Science</i> , 2005, , 615-629.	1.3	18
111	Protein Annotation by Secondary Structure Based Alignments (PASSTA). <i>Lecture Notes in Computer Science</i> , 2005, , 79-90.	1.3	0
112	Reversal Distance without Hurdles and Fortresses. <i>Lecture Notes in Computer Science</i> , 2004, , 388-399.	1.3	44
113	Benchmarking tools for the alignment of functional noncoding DNA. <i>BMC Bioinformatics</i> , 2004, 5, 6.	2.6	99
114	Algorithmic complexity of protein identification: combinatorics of weighted strings. <i>Discrete Applied Mathematics</i> , 2004, 137, 27-46.	0.9	18
115	Linear time algorithms for finding and representing all the tandem repeats in a string. <i>Journal of Computer and System Sciences</i> , 2004, 69, 525-546.	1.2	147
116	Quadratic Time Algorithms for Finding Common Intervals in Two and More Sequences. <i>Lecture Notes in Computer Science</i> , 2004, , 347-358.	1.3	47
117	Suboptimal Local Alignments Across Multiple Scoring Schemes. <i>Lecture Notes in Computer Science</i> , 2004, , 99-110.	1.3	1
118	Efficient implementation of lazy suffix trees. <i>Software - Practice and Experience</i> , 2003, 33, 1035-1049.	3.6	87
119	Divide-and-conquer multiple alignment with segment-based constraints. <i>Bioinformatics</i> , 2003, 19, ii189-ii195.	4.1	17
120	On the Similarity of Sets of Permutations and Its Applications to Genome Comparison. <i>Lecture Notes in Computer Science</i> , 2003, , 68-79.	1.3	41
121	A Novel Approach to Remote Homology Detection: Jumping Alignments. <i>Journal of Computational Biology</i> , 2002, 9, 747-760.	1.6	33
122	Simple and flexible detection of contiguous repeats using a suffix tree. <i>Theoretical Computer Science</i> , 2002, 270, 843-856.	0.9	67
123	REPuter: the manifold applications of repeat analysis on a genomic scale. <i>Nucleic Acids Research</i> , 2001, 29, 4633-4642.	14.5	1,660
124	Algorithms for Finding Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2001, , 252-263.	1.3	26
125	Finding All Common Intervals of k Permutations. <i>Lecture Notes in Computer Science</i> , 2001, , 207-218.	1.3	65
126	Contig Selection in Physical Mapping. <i>Journal of Computational Biology</i> , 2000, 7, 395-408.	1.6	2

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127	Multiple sequence alignment with the divide-and-conquer method. <i>Gene</i> , 1998, 211, GC45-GC56.	2.2	77
128	DCA: An efficient implementation of the divide-and-conquer approach to simultaneous multiple sequence alignment. <i>Bioinformatics</i> , 1997, 13, 625-626.	4.1	46
129	A general method for fast multiple sequence alignment. <i>Gene</i> , 1996, 172, GC33-GC41.	2.2	26