Jens Stoye

List of Publications by Year
in descending order

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	REPuter: the manifold applications of repeat analysis on a genomic scale. Nucleic Acids Research, 2001, 29, 4633-4642.	14.5	1,660
2	Updating benchtop sequencing performance comparison. Nature Biotechnology, 2013, 31, 294-296.	17.5	423
3	Phylogenetic classification of short environmental DNA fragments. Nucleic Acids Research, 2008, 36, 2230-2239.	14.5	246
4	Based Upon Repeat Pattern (BURP): an algorithm to characterize the long-term evolution of Staphylococcus aureus populations based on spa polymorphisms. BMC Microbiology, 2007, 7, 98.	3.3	203
5	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. Journal of Biotechnology, 2008, 136, 91-101.	3.8	202
6	Linear time algorithms for finding and representing all the tandem repeats in a string. Journal of Computer and System Sciences, 2004, 69, 525-546.	1.2	147
7	r2cat: synteny plots and comparative assembly. Bioinformatics, 2010, 26, 570-571.	4.1	134
8	ReadXplorer—visualization and analysis of mapped sequences. Bioinformatics, 2014, 30, 2247-2254.	4.1	127
9	MeltDB: a software platform for the analysis and integration of metabolomics experiment data. Bioinformatics, 2008, 24, 2726-2732.	4.1	100
10	Benchmarking tools for the alignment of functional noncoding DNA. BMC Bioinformatics, 2004, 5, 6.	2.6	99
11	Taxonomic classification of metagenomic shotgun sequences with CARMA3. Nucleic Acids Research, 2011, 39, e91-e91.	14.5	99
12	Efficient q-Gram Filters for Finding All ϵ-Matches over a Given Length. Journal of Computational Biology, 2006, 13, 296-308.	1.6	90
13	The complete genome sequence of Corynebacterium pseudotuberculosis 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
14	Efficient implementation of lazy suffix trees. Software - Practice and Experience, 2003, 33, 1035-1049.	3.6	87
15	Orthology Detection Combining Clustering and Synteny for Very Large Datasets. PLoS ONE, 2014, 9, e105015.	2.5	86
16	Partitioning biological data with transitivity clustering. Nature Methods, 2010, 7, 419-420.	19.0	84
17	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	3.8	84
18	WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads. BMC Bioinformatics, 2009, 10, 430.	2.6	78

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19	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. Bioinformatics, 2011, 27, 1351-1358.	4.1	78
20	Multiple sequence alignment with the divide-and-conquer method. Gene, 1998, 211, GC45-GC56.	2.2	77
21	The complete genome sequence of the acarbose producer Actinoplanes sp. SE50/110. BMC Genomics, 2012, 13, 112.	2.8	69
22	Bloom Filter Trie: an alignment-free and reference-free data structure for pan-genome storage. Algorithms for Molecular Biology, 2016, 11, 3.	1.2	69
23	Finding novel genes in bacterial communities isolated from the environment. Bioinformatics, 2006, 22, e281-e289.	4.1	68
24	Simple and flexible detection of contiguous repeats using a suffix tree. Theoretical Computer Science, 2002, 270, 843-856.	0.9	67
25	Finding All Common Intervals of k Permutations. Lecture Notes in Computer Science, 2001, , 207-218.	1.3	65
26	Double Cut and Join with Insertions and Deletions. Journal of Computational Biology, 2011, 18, 1167-1184.	1.6	63
27	Large scale hierarchical clustering of protein sequences. BMC Bioinformatics, 2005, 6, 15.	2.6	62
28	Whole-genome sequence of the bovine blood fluke Schistosoma bovis supports interspecific hybridization with S. haematobium. PLoS Pathogens, 2019, 15, e1007513.	4.7	49
29	On Sorting by Translocations. Journal of Computational Biology, 2006, 13, 567-578.	1.6	48
30	Quadratic Time Algorithms for Finding Common Intervals in Two and More Sequences. Lecture Notes in Computer Science, 2004, , 347-358.	1.3	47
31	GISMO--gene identification using a support vector machine for ORF classification. Nucleic Acids Research, 2006, 35, 540-549.	14.5	47
32	DCA: An efficient implementation of the divide-and-conquer approach to simultaneous multiple sequence alignment. Bioinformatics, 1997, 13, 625-626.	4.1	46
33	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. Carcinogenesis, 2016, 37, 356-365.	2.8	46
34	Reversal Distance without Hurdles and Fortresses. Lecture Notes in Computer Science, 2004, , 388-399.	1.3	44
35	HASLR: Fast Hybrid Assembly of Long Reads. IScience, 2020, 23, 101389.	4.1	44
36	The Solution Space of Sorting by DCJ. Journal of Computational Biology, 2010, 17, 1145-1165.	1.6	42

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37	On the Similarity of Sets of Permutations and Its Applications to Genome Comparison. Lecture Notes in Computer Science, 2003, , 68-79.	1.3	41
38	UniMoGâ€"a unifying framework for genomic distance calculation and sorting based on DCJ. Bioinformatics, 2012, 28, 2509-2511.	4.1	38
39	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. Journal of Biotechnology, 2009, 140, 3-12.	3.8	37
40	On the Similarity of Sets of Permutations and Its Applications to Genome Comparison. Journal of Computational Biology, 2006, 13, 1340-1354.	1.6	36
41	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
42	A Novel Approach to Remote Homology Detection: Jumping Alignments. Journal of Computational Biology, 2002, 9, 747-760.	1.6	33
43	Combining peak- and chromatogram-based retention time alignment algorithms for multiple chromatography-mass spectrometry datasets. BMC Bioinformatics, 2012, 13, 214.	2.6	33
44	BACCardI--a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. Bioinformatics, 2005, 21, 853-859.	4.1	32
45	Computation of Median Gene Clusters. Journal of Computational Biology, 2009, 16, 1085-1099.	1.6	32
46	ChromA: signal-based retention time alignment for chromatographyâ€"mass spectrometry data. Bioinformatics, 2009, 25, 2080-2081.	4.1	32
47	Mycoplasma salivarium as a Dominant Coloniser of Fanconi Anaemia Associated Oral Carcinoma. PLoS ONE, 2014, 9, e92297.	2.5	32
48	Sequencing of high G+C microbial genomes using the ultrafast pyrosequencing technology. Journal of Biotechnology, 2011, 155, 68-77.	3.8	29
49	GABenchToB: A Genome Assembly Benchmark Tuned on Bacteria and Benchtop Sequencers. PLoS ONE, 2014, 9, e107014.	2.5	29
50	Flexible metagenome analysis using the MGX framework. Microbiome, 2018, 6, 76.	11.1	29
51	A general method for fast multiple sequence alignment. Gene, 1996, 172, GC33-GC41.	2.2	26
52	A Unified Approach for Reconstructing Ancient Gene Clusters. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 387-400.	3.0	26
53	Algorithms for Finding Gene Clusters. Lecture Notes in Computer Science, 2001, , 252-263.	1.3	26
54	Character sets of strings. Journal of Discrete Algorithms, 2007, 5, 330-340.	0.7	25

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55	Pan-Genome Storage and Analysis Techniques. Methods in Molecular Biology, 2018, 1704, 29-53.	0.9	24
56	Finding approximate gene clusters with Gecko 3. Nucleic Acids Research, 2016, 44, gkw843.	14.5	23
57	Comparing Tandem Repeats with Duplications and Excisions of Variable Degree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 395-407.	3.0	22
58	An incomplex algorithm for fast suffix array construction. Software - Practice and Experience, 2007, 37, 309-329.	3.6	21
59	Genomic Distance with DCJ and Indels. Lecture Notes in Computer Science, 2010, , 90-101.	1.3	20
60	Comparative RNA-sequencing of the acarbose producer Actinoplanes sp. SE50/110 cultivated in different growth media. Journal of Biotechnology, 2013, 167, 166-177.	3.8	20
61	On the family-free DCJ distance and similarity. Algorithms for Molecular Biology, 2015, 10, 13.	1.2	19
62	Algorithmic complexity of protein identification: combinatorics of weighted strings. Discrete Applied Mathematics, 2004, 137, 27-46.	0.9	18
63	On Sorting by Translocations. Lecture Notes in Computer Science, 2005, , 615-629.	1.3	18
64	Divide-and-conquer multiple alignment with segment-based constraints. Bioinformatics, 2003, 19, ii189-ii195.	4.1	17
65	Gene family assignment-free comparative genomics. BMC Bioinformatics, 2012, 13, S3.	2.6	17
66	MetaSAMSâ€"A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. Journal of Biotechnology, 2013, 167, 156-165.	3.8	17
67	Computing the Rearrangement Distance of Natural Genomes. Journal of Computational Biology, 2021, 28, 410-431.	1.6	17
68	Counting suffix arrays and strings. Theoretical Computer Science, 2008, 395, 220-234.	0.9	16
69	On the inversion-indel distance. BMC Bioinformatics, 2013, 14, S3.	2.6	16
70	Phylogenetic comparative assembly. Algorithms for Molecular Biology, 2010, 5, 3.	1.2	15
71	Improving the genome annotation of the acarbose producer Actinoplanes sp. SE50/110 by sequencing enriched 5â€²-ends of primary transcripts. Journal of Biotechnology, 2014, 190, 85-95.	3.8	15
72	On the weight of indels in genomic distances. BMC Bioinformatics, 2011, 12, S13.	2.6	14

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73	Restricted DCJ Model: Rearrangement Problems with Chromosome Reincorporation. Journal of Computational Biology, 2011, 18, 1231-1241.	1.6	14
74	metaBEETL: high-throughput analysis of heterogeneous microbial populations from shotgun DNA sequences. BMC Bioinformatics, 2013, 14, S2.	2.6	14
75	Comparative Pathway Analyzerâ€"a web server for comparative analysis, clustering and visualization of metabolic networks in multiple organisms. Nucleic Acids Research, 2008, 36, W433-W437.	14.5	13
76	The Potential of Family-Free Genome Comparison. Computational Biology, 2013, , 287-307.	0.2	12
77	Common Intervals of Multiple Permutations. Algorithmica, 2011, 60, 175-206.	1.3	11
78	Statistics for approximate gene clusters. BMC Bioinformatics, 2013, 14, S14.	2.6	11
79	Swiftly Computing Center Strings. Lecture Notes in Computer Science, 2010, , 325-336.	1.3	11
80	Finding Nested Common Intervals Efficiently. Journal of Computational Biology, 2010, 17, 1183-1194.	1.6	10
81	Genomic distance under gene substitutions. BMC Bioinformatics, 2011, 12, S8.	2.6	10
82	Consistency of Sequence-Based Gene Clusters. Journal of Computational Biology, 2011, 18, 1023-1039.	1.6	9
83	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. Journal of Biotechnology, 2014, 190, 64-75.	3.8	9
84	Approximating the DCJ distance of balanced genomes in linear time. Algorithms for Molecular Biology, 2017, 12, 3.	1.2	9
85	Finding all maximal perfect haplotype blocks in linear time. Algorithms for Molecular Biology, 2020, 15, 2.	1.2	9
86	Computing the Inversion-Indel Distance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2314-2326.	3.0	8
87	HP Distance Via Double Cut and Join Distance. , 2008, , 56-68.		8
88	Computation of Median Gene Clusters. Lecture Notes in Computer Science, 2008, , 331-345.	1.3	8
89	Alignment of Tandem Repeats with Excision, Duplication, Substitution and Indels (EDSI). Lecture Notes in Computer Science, 2005, , 276-290.	1.3	7
90	Sorting Linear Genomes with Rearrangements and Indels. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 500-506.	3.0	7

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91	Dynamic Alignment-Free and Reference-Free Read Compression. Lecture Notes in Computer Science, 2017, , 50-65.	1.3	7
92	Identifying Maximal Perfect Haplotype Blocks. Lecture Notes in Computer Science, 2018, , 26-37.	1.3	7
93	Dynamic Alignment-Free and Reference-Free Read Compression. Journal of Computational Biology, 2018, 25, 825-836.	1.6	7
94	Reconstructing tumor evolutionary histories and clone trees in polynomial-time with SubMARine. PLoS Computational Biology, 2021, 17, e1008400.	3.2	7
95	On Computing the Breakpoint Reuse Rate in Rearrangement Scenarios. Lecture Notes in Computer Science, 2008, , 226-240.	1.3	7
96	Panta rhei (QAlign2): an open graphical environment for sequence analysis. Bioinformatics, 2006, 22, 889-890.	4.1	6
97	Balanced vertices in trees and a simpler algorithm to compute the genomic distance. Applied Mathematics Letters, 2011, 24, 82-86.	2.7	6
98	Multiple genome comparison based on overlap regions of pairwise local alignments. BMC Bioinformatics, 2012, 13, S7.	2.6	6
99	Family-Free Genome Comparison. Methods in Molecular Biology, 2018, 1704, 331-342.	0.9	6
100	Detecting high-scoring local alignments in pangenome graphs. Bioinformatics, 2021, 37, 2266-2274.	4.1	6
101	Gecko and GhostFam. Methods in Molecular Biology, 2007, 396, 165-182.	0.9	6
102	Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework. Lecture Notes in Computer Science, 2014, 15, 135-143.	1.3	6
103	Rearrangement Models and Single-Cut Operations. Journal of Computational Biology, 2010, 17, 1213-1225.	1.6	5
104	Horizontal Gene Transfer Phylogenetics: A Random Walk Approach. Molecular Biology and Evolution, 2020, 37, 1470-1479.	8.9	5
105	Computing the Rearrangement Distance of Natural Genomes. Lecture Notes in Computer Science, 2020, , 3-18.	1.3	5
106	Sequence-based pangenomic core detection. IScience, 2022, 25, 104413.	4.1	5
107	Swiftly Computing Center Strings. BMC Bioinformatics, 2011, 12, 106.	2.6	4
108	Identifying gene clusters by discovering common intervals in indeterminate strings. BMC Genomics, 2014, 15, S2.	2.8	4

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109	Analysis of local genome rearrangement improves resolution of ancestral genomic maps in plants. BMC Genomics, 2020, 21, 273.	2.8	4
110	Contig Selection in Physical Mapping. Journal of Computational Biology, 2000, 7, 395-408.	1.6	2
111	New Genome Similarity Measures Based on Conserved Gene Adjacencies. Lecture Notes in Computer Science, 2016, , 204-224.	1.3	2
112	A Linear Time Approximation Algorithm for the DCJ Distance for Genomes with Bounded Number of Duplicates. Lecture Notes in Computer Science, 2016, , 293-306.	1.3	2
113	Computing the family-free DCJ similarity. BMC Bioinformatics, 2018, 19, 152.	2.6	2
114	The Problem of Chromosome Reincorporation in DCJ Sorting and Halving. Lecture Notes in Computer Science, 2010, , 13-24.	1.3	2
115	Consistency of Sequence-Based Gene Clusters. Lecture Notes in Computer Science, 2010, , 252-263.	1.3	2
116	Finding Nested Common Intervals Efficiently. Lecture Notes in Computer Science, 2009, , 59-69.	1.3	2
117	The Genesis of the DCJ Formula. Computational Biology, 2013, , 63-81.	0.2	1
118	New Genome Similarity Measures based on Conserved Gene Adjacencies. Journal of Computational Biology, 2017, 24, 616-634.	1.6	1
119	Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 2094-2100.	3.0	1
120	Suboptimal Local Alignments Across Multiple Scoring Schemes. Lecture Notes in Computer Science, 2004, , 99-110.	1.3	1
121	Rearrangement Models and Single-Cut Operations. Lecture Notes in Computer Science, 2009, , 84-97.	1.3	1
122	Restricted DCJ-Indel Model Revisited. Lecture Notes in Computer Science, 2013, , 36-46.	1.3	1
123	A report on the 2009 SIG on short read sequencing and algorithms (Short-SIG). Bioinformatics, 2009, 25, 2863-2864.	4.1	0
124	Algorithms for Computing the Family-Free Genomic Similarity Under DCJ. Lecture Notes in Computer Science, 2017, , 76-100.	1.3	0
125	Editorial: Computational Methods for Microbiome Analysis. Frontiers in Genetics, 2020, 11, 623897.	2.3	0
126	Searching and inferring colorful topological motifs in vertex-colored graphs. Journal of Combinatorial Optimization, 2020, 40, 379-411.	1.3	0

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127	Protein Annotation by Secondary Structure Based Alignments (PASSTA). Lecture Notes in Computer Science, 2005, , 79-90.	1.3	0
128	Phylogenetic Comparative Assembly. Lecture Notes in Computer Science, 2009, , 145-156.	1.3	0
129	Taxonomic Classification of Metagenomic Shotgun Sequences with CARMA3. , 2013, , 1-8.		0