

Burkhard Morgenstern

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

14,976
citations

147801

31
h-index

233421

45
g-index

52
all docs

52
docs citations

52
times ranked

19537
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815. | 27.8 | 8,336 |
| 2 | The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955. | 27.8 | 1,255 |
| 3 | Gene prediction in eukaryotes with a generalized hidden Markov model that uses hints from external sources. <i>BMC Bioinformatics</i> , 2006, 7, 62. | 2.6 | 968 |
| 4 | Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium <i>Bacillus amyloliquefaciens</i> FZB42. <i>Nature Biotechnology</i> , 2007, 25, 1007-1014. | 17.5 | 703 |
| 5 | Phylogenomics Revives Traditional Views on Deep Animal Relationships. <i>Current Biology</i> , 2009, 19, 706-712. | 3.9 | 611 |
| 6 | Improved Phylogenomic Taxon Sampling Noticeably Affects Nonbilaterian Relationships. <i>Molecular Biology and Evolution</i> , 2010, 27, 1983-1987. | 8.9 | 298 |
| 7 | Multiple DNA and protein sequence alignment based on segment-to-segment comparison.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 12098-12103. | 7.1 | 269 |
| 8 | AUGUSTUS at EGASP: using EST, protein and genomic alignments for improved gene prediction in the human genome. <i>Genome Biology</i> , 2006, 7, S11. | 9.6 | 263 |
| 9 | DIALIGN: multiple DNA and protein sequence alignment at BiBiServ. <i>Nucleic Acids Research</i> , 2004, 32, W33-W36. | 14.5 | 200 |
| 10 | DIALIGN-TX: greedy and progressive approaches for segment-based multiple sequence alignment. <i>Algorithms for Molecular Biology</i> , 2008, 3, 6. | 1.2 | 197 |
| 11 | <i>Rhizobium</i> sp. Strain NGR234 Possesses a Remarkable Number of Secretion Systems. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4035-4045. | 3.1 | 170 |
| 12 | The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. <i>Nature Communications</i> , 2015, 6, 7822. | 12.8 | 139 |
| 13 | Fast and sensitive multiple alignment of large genomic sequences. <i>BMC Bioinformatics</i> , 2003, 4, 66. | 2.6 | 134 |
| 14 | DIALIGN-T: an improved algorithm for segment-based multiple sequence alignment. <i>BMC Bioinformatics</i> , 2005, 6, 66. | 2.6 | 132 |
| 15 | Identification of Novel Plant Peroxisomal Targeting Signals by a Combination of Machine Learning Methods and in Vivo Subcellular Targeting Analyses. <i>Plant Cell</i> , 2011, 23, 1556-1572. | 6.6 | 123 |
| 16 | The role of recombination in the emergence of a complex and dynamic HIV epidemic. <i>Retrovirology</i> , 2010, 7, 25. | 2.0 | 110 |
| 17 | Evolution of bHLH transcription factors: modular evolution by domain shuffling?. <i>Molecular Biology and Evolution</i> , 1999, 16, 1654-1663. | 8.9 | 97 |
| 18 | A jumping profile Hidden Markov Model and applications to recombination sites in HIV and HCV genomes. <i>BMC Bioinformatics</i> , 2006, 7, 265. | 2.6 | 85 |

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|----|---|------|-----------|
| 19 | Gene prediction in metagenomic fragments: A large scale machine learning approach. BMC Bioinformatics, 2008, 9, 217. | 2.6 | 78 |
| 20 | jpHMM: recombination analysis in viruses with circular genomes such as the hepatitis B virus. Nucleic Acids Research, 2012, 40, W193-W198. | 14.5 | 67 |
| 21 | Spaced words and kmacs: fast alignment-free sequence comparison based on inexact word matches. Nucleic Acids Research, 2014, 42, W7-W11. | 14.5 | 61 |
| 22 | Metabolite-based clustering and visualization of mass spectrometry data using one-dimensional self-organizing maps. Algorithms for Molecular Biology, 2008, 3, 9. | 1.2 | 57 |
| 23 | Multiple sequence alignment with user-defined anchor points. Algorithms for Molecular Biology, 2006, 1, 6. | 1.2 | 52 |
| 24 | Oligo kernels for datamining on biological sequences: a case study on prokaryotic translation initiation sites. BMC Bioinformatics, 2004, 5, 169. | 2.6 | 47 |
| 25 | DIALIGN at GOBICSâ€™ multiple sequence alignment using various sources of external information. Nucleic Acids Research, 2013, 41, W3-W7. | 14.5 | 45 |
| 26 | New journal: Algorithms for Molecular Biology. Algorithms for Molecular Biology, 2006, 1, 1. | 1.2 | 44 |
| 27 | Meta-Analysis of Pathway Enrichment: Combining Independent and Dependent Omics Data Sets. PLoS ONE, 2014, 9, e89297. | 2.5 | 44 |
| 28 | Estimating evolutionary distances between genomic sequences from spaced-word matches. Algorithms for Molecular Biology, 2015, 10, 5. | 1.2 | 44 |
| 29 | A simple and space-efficient fragment-chaining algorithm for alignment of DNA and protein sequences. Applied Mathematics Letters, 2002, 15, 11-16. | 2.7 | 39 |
| 30 | Detection of viral sequence fragments of HIV-1 subfamilies yet unknown. BMC Bioinformatics, 2011, 12, 93. | 2.6 | 37 |
| 31 | rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. PLoS Computational Biology, 2016, 12, e1005107. | 3.2 | 36 |
| 32 | DIALIGN P: fast pair-wise and multiple sequence alignment using parallel processors. BMC Bioinformatics, 2004, 5, 128. | 2.6 | 35 |
| 33 | The number of k-mer matches between two DNA sequences as a function of k and applications to estimate phylogenetic distances. PLoS ONE, 2020, 15, e0228070. | 2.5 | 30 |
| 34 | OrthoSelect: a protocol for selecting orthologous groups in phylogenomics. BMC Bioinformatics, 2009, 10, 219. | 2.6 | 23 |
| 35 | Prot-SpaM: fast alignment-free phylogeny reconstruction based on whole-proteome sequences. GigaScience, 2019, 8, . | 6.4 | 19 |
| 36 | Read-SpaM: assembly-free and alignment-free comparison of bacterial genomes with low sequencing coverage. BMC Bioinformatics, 2019, 20, 638. | 2.6 | 19 |

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|----|---|------|-----------|
| 37 | Verticillium longisporum Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. <i>Frontiers in Microbiology</i> , 2020, 11, 1876. | 3.5 | 18 |
| 38 | Phylogeny reconstruction based on the length distribution of k-mismatch common substrings. <i>Algorithms for Molecular Biology</i> , 2017, 12, 27. | 1.2 | 17 |
| 39 | AUGUSTUS at MediGRID: Adaption of a bioinformatics application to grid computing for efficient genome analysis. <i>Future Generation Computer Systems</i> , 2009, 25, 337-345. | 7.5 | 15 |
| 40 | Improved coverage of cDNA-AFLP by sequential digestion of immobilized cDNA. <i>BMC Genomics</i> , 2008, 9, 480. | 2.8 | 12 |
| 41 | â€œMulti-SpaMâ€™: a maximum-likelihood approach to phylogeny reconstruction using multiple spaced-word matches and quartet trees. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz013. | 3.2 | 12 |
| 42 | Multiple alignment of genomic sequences using CHAOS, DIALIGN and ABC. <i>Nucleic Acids Research</i> , 2005, 33, W532-W534. | 14.5 | 11 |
| 43 | S-conLSH: alignment-free gapped mapping of noisy long reads. <i>BMC Bioinformatics</i> , 2021, 22, 64. | 2.6 | 9 |
| 44 | MolabIS - An integrated information system for storing and managing molecular genetics data. <i>BMC Bioinformatics</i> , 2011, 12, 425. | 2.6 | 7 |
| 45 | Stability of multiple alignments and phylogenetic trees: an analysis of ABC-transporter proteins family. <i>Algorithms for Molecular Biology</i> , 2008, 3, 15. | 1.2 | 6 |
| 46 | Local versus Global Alignments. , 2009, , 39-53. | | 0 |
| 47 | Title is missing!. , 2020, 15, e0228070. | | 0 |
| 48 | Title is missing!. , 2020, 15, e0228070. | | 0 |
| 49 | Title is missing!. , 2020, 15, e0228070. | | 0 |