

# Burkhard Morgenstern

## List of Publications by Year in descending order

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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	S-conLSH: alignment-free gapped mapping of noisy long reads. BMC Bioinformatics, 2021, 22, 64.	2.6	9
2	â€œMulti-SpaMâ€™: a maximum-likelihood approach to phylogeny reconstruction using multiple spaced-word matches and quartet trees. NAR Genomics and Bioinformatics, 2020, 2, lqz013.	3.2	12
3	Verticillium longisporum Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. Frontiers in Microbiology, 2020, 11, 1876.	3.5	18
4	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
5	Title is missing!. , 2020, 15, e0228070.		0
6	Title is missing!. , 2020, 15, e0228070.		0
7	Title is missing!. , 2020, 15, e0228070.		0
8	Prot-SpaM: fast alignment-free phylogeny reconstruction based on whole-proteome sequences. GigaScience, 2019, 8, .	6.4	19
9	Read-SpaM: assembly-free and alignment-free comparison of bacterial genomes with low sequencing coverage. BMC Bioinformatics, 2019, 20, 638.	2.6	19
10	Phylogeny reconstruction based on the length distribution of k-mismatch common substrings. Algorithms for Molecular Biology, 2017, 12, 27.	1.2	17
11	rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison. PLoS Computational Biology, 2016, 12, e1005107.	3.2	36
12	Estimating evolutionary distances between genomic sequences from spaced-word matches. Algorithms for Molecular Biology, 2015, 10, 5.	1.2	44
13	The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. Nature Communications, 2015, 6, 7822.	12.8	139
14	Meta-Analysis of Pathway Enrichment: Combining Independent and Dependent Omics Data Sets. PLoS ONE, 2014, 9, e89297.	2.5	44
15	Spaced words and kmacs: fast alignment-free sequence comparison based on inexact word matches. Nucleic Acids Research, 2014, 42, W7-W11.	14.5	61
16	DIALIGN at GOBICSâ€™ multiple sequence alignment using various sources of external information. Nucleic Acids Research, 2013, 41, W3-W7.	14.5	45
17	jpHMM: recombination analysis in viruses with circular genomes such as the hepatitis B virus. Nucleic Acids Research, 2012, 40, W193-W198.	14.5	67
18	MolabS - An integrated information system for storing and managing molecular genetics data. BMC Bioinformatics, 2011, 12, 425.	2.6	7

#	ARTICLE	IF	CITATIONS
19	Detection of viral sequence fragments of HIV-1 subfamilies yet unknown. BMC Bioinformatics, 2011, 12, 93.	2.6	37
20	Identification of Novel Plant Peroxisomal Targeting Signals by a Combination of Machine Learning Methods and in Vivo Subcellular Targeting Analyses. Plant Cell, 2011, 23, 1556-1572.	6.6	123
21	Improved Phylogenomic Taxon Sampling Noticeably Affects Nonbilaterian Relationships. Molecular Biology and Evolution, 2010, 27, 1983-1987.	8.9	298
22	The role of recombination in the emergence of a complex and dynamic HIV epidemic. Retrovirology, 2010, 7, 25.	2.0	110
23	<i>Rhizobium</i> sp. Strain NGR234 Possesses a Remarkable Number of Secretion Systems. Applied and Environmental Microbiology, 2009, 75, 4035-4045.	3.1	170
24	OrthoSelect: a protocol for selecting orthologous groups in phylogenomics. BMC Bioinformatics, 2009, 10, 219.	2.6	23
25	Phylogenomics Revives Traditional Views on Deep Animal Relationships. Current Biology, 2009, 19, 706-712.	3.9	611
26	AUGUSTUS at MediGRID: Adaption of a bioinformatics application to grid computing for efficient genome analysis. Future Generation Computer Systems, 2009, 25, 337-345.	7.5	15
27	Local versus Global Alignments. , 2009, , 39-53.		0
28	The genome of the model beetle and pest <i>Tribolium castaneum</i> . Nature, 2008, 452, 949-955.	27.8	1,255
29	Gene prediction in metagenomic fragments: A large scale machine learning approach. BMC Bioinformatics, 2008, 9, 217.	2.6	78
30	Improved coverage of cDNA-AFLP by sequential digestion of immobilized cDNA. BMC Genomics, 2008, 9, 480.	2.8	12
31	Stability of multiple alignments and phylogenetic trees: an analysis of ABC-transporter proteins family. Algorithms for Molecular Biology, 2008, 3, 15.	1.2	6
32	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
33	DIALIGN-TX: greedy and progressive approaches for segment-based multiple sequence alignment. Algorithms for Molecular Biology, 2008, 3, 6.	1.2	197
34	Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium <i>Bacillus amyloliquefaciens</i> FZB42. Nature Biotechnology, 2007, 25, 1007-1014.	17.5	703
35	Multiple sequence alignment with user-defined anchor points. Algorithms for Molecular Biology, 2006, 1, 6.	1.2	52
36	New journal: Algorithms for Molecular Biology. Algorithms for Molecular Biology, 2006, 1, 1.	1.2	44

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37	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
38	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
39	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
40	DIALIGN-T: an improved algorithm for segment-based multiple sequence alignment. <i>BMC Bioinformatics</i> , 2005, 6, 66.	2.6	132
41	Multiple alignment of genomic sequences using CHAOS, DIALIGN and ABC. <i>Nucleic Acids Research</i> , 2005, 33, W532-W534.	14.5	11
42	DIALIGN P: fast pair-wise and multiple sequence alignment using parallel processors. <i>BMC Bioinformatics</i> , 2004, 5, 128.	2.6	35
43	Oligo kernels for datamining on biological sequences: a case study on prokaryotic translation initiation sites. <i>BMC Bioinformatics</i> , 2004, 5, 169.	2.6	47
44	DIALIGN: multiple DNA and protein sequence alignment at BiBiServ. <i>Nucleic Acids Research</i> , 2004, 32, W33-W36.	14.5	200
45	Fast and sensitive multiple alignment of large genomic sequences. <i>BMC Bioinformatics</i> , 2003, 4, 66.	2.6	134
46	A simple and space-efficient fragment-chaining algorithm for alignment of DNA and protein sequences. <i>Applied Mathematics Letters</i> , 2002, 15, 11-16.	2.7	39
47	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	27.8	8,336
48	Evolution of bHLH transcription factors: modular evolution by domain shuffling?. <i>Molecular Biology and Evolution</i> , 1999, 16, 1654-1663.	8.9	97
49	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