

Mario Stanke

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

23,071
citations

50276

46
h-index

88630

70
g-index

90
all docs

90
docs citations

90
times ranked

29555
citing authors

#	ARTICLE	IF	CITATIONS
1	AUGUSTUS: ab initio prediction of alternative transcripts. <i>Nucleic Acids Research</i> , 2006, 34, W435-W439.	14.5	1,851
2	Using native and syntenically mapped cDNA alignments to improve <i>de novo</i> gene finding. <i>Bioinformatics</i> , 2008, 24, 637-644.	4.1	1,618
3	Gene prediction with a hidden Markov model and a new intron submodel. <i>Bioinformatics</i> , 2003, 19, ii215-ii225.	4.1	1,294
4	AUGUSTUS: a web server for gene prediction in eukaryotes that allows user-defined constraints. <i>Nucleic Acids Research</i> , 2005, 33, W465-W467.	14.5	1,286
5	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	27.8	1,255
6	AUGUSTUS: a web server for gene finding in eukaryotes. <i>Nucleic Acids Research</i> , 2004, 32, W309-W312.	14.5	1,068
7	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
8	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
9	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
10	BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS. <i>Bioinformatics</i> , 2016, 32, 767-769.	4.1	918
11	The <i>Amphimedon queenslandica</i> genome and the evolution of animal complexity. <i>Nature</i> , 2010, 466, 720-726.	27.8	917
12	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
13	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	12.6	808
14	BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa108.	3.2	803
15	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
16	A novel hybrid gene prediction method employing protein multiple sequence alignments. <i>Bioinformatics</i> , 2011, 27, 757-763.	4.1	468
17	Whole-Genome Annotation with BRAKER. <i>Methods in Molecular Biology</i> , 2019, 1962, 65-95.	0.9	461
18	Draft genome sequence of the oilseed species <i>Ricinus communis</i> . <i>Nature Biotechnology</i> , 2010, 28, 951-956.	17.5	449

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19	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	12.6	439
20	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	12.6	424
21	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11889-11894.	7.1	389
22	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	2.8	375
23	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	3.8	286
24	Discovery and revision of <i>Arabidopsis</i> genes by proteogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 21034-21038.	7.1	268
25	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
26	WebAUGUSTUS--a web service for training AUGUSTUS and predicting genes in eukaryotes. <i>Nucleic Acids Research</i> , 2013, 41, W123-W128.	14.5	253
27	Predicting Genes in Single Genomes with AUGUSTUS. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e57.	25.8	225
28	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	21.4	169
29	Wild tobacco genomes reveal the evolution of nicotine biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6133-6138.	7.1	160
30	jpHMM: Improving the reliability of recombination prediction in HIV-1. <i>Nucleic Acids Research</i> , 2009, 37, W647-W651.	14.5	145
31	The <i>Chlamydomonas</i> genome project: a decade on. <i>Trends in Plant Science</i> , 2014, 19, 672-680.	8.8	145
32	The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. <i>Nature Communications</i> , 2015, 6, 7822.	12.8	139
33	Scipio: Using protein sequences to determine the precise exon/intron structures of genes and their orthologs in closely related species. <i>BMC Bioinformatics</i> , 2008, 9, 278.	2.6	137
34	Genome sequencing of the lizard parasite <i>Leishmania tarentolae</i> reveals loss of genes associated to the intracellular stage of human pathogenic species. <i>Nucleic Acids Research</i> , 2012, 40, 1131-1147.	14.5	135
35	Large scale RNAi screen in <i>Tribolium</i> reveals novel target genes for pest control and the proteasome as prime target. <i>BMC Genomics</i> , 2015, 16, 674.	2.8	119
36	Tissue-specific transcriptomics, chromosomal localization, and phylogeny of chemosensory and odorant binding proteins from the red flour beetle <i>Tribolium castaneum</i> reveal subgroup specificities for olfaction or more general functions. <i>BMC Genomics</i> , 2014, 15, 1141.	2.8	111

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37	The role of recombination in the emergence of a complex and dynamic HIV epidemic. <i>Retrovirology</i> , 2010, 7, 25.	2.0	110
38	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	5.5	99
39	<i>V</i> erticillium transcription activator of adhesion <i>V</i> ta2 suppresses microsclerotia formation and is required for systemic infection of plant roots. <i>New Phytologist</i> , 2014, 202, 565-581.	7.3	92
40	TSEBRA: transcript selector for BRAKER. <i>BMC Bioinformatics</i> , 2021, 22, 566.	2.6	91
41	Comparative Annotation Toolkit (CAT) simultaneous clade and personal genome annotation. <i>Genome Research</i> , 2018, 28, 1029-1038.	5.5	86
42	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
43	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47.	2.8	84
44	Simultaneous gene finding in multiple genomes. <i>Bioinformatics</i> , 2016, 32, 3388-3395.	4.1	74
45	jpHMM: recombination analysis in viruses with circular genomes such as the hepatitis B virus. <i>Nucleic Acids Research</i> , 2012, 40, W193-W198.	14.5	67
46	House spider genome uncovers evolutionary shifts in the diversity and expression of black widow venom proteins associated with extreme toxicity. <i>BMC Genomics</i> , 2017, 18, 178.	2.8	57
47	jpHMM at GOBICS: a web server to detect genomic recombinations in HIV-1. <i>Nucleic Acids Research</i> , 2006, 34, W463-W465.	14.5	47
48	Multi-Genome Annotation with AUGUSTUS. <i>Methods in Molecular Biology</i> , 2019, 1962, 139-160.	0.9	43
49	Detection of viral sequence fragments of HIV-1 subfamilies yet unknown. <i>BMC Bioinformatics</i> , 2011, 12, 93.	2.6	37
50	The genome of the thermoacidophilic red microalga <i>Galdieria sulphuraria</i> encodes a small family of secreted class III peroxidases that might be involved in cell wall modification. <i>Planta</i> , 2007, 227, 353-362.	3.2	27
51	Current methods for automated annotation of protein-coding genes. <i>Current Opinion in Insect Science</i> , 2015, 7, 8-14.	4.4	23
52	CRF-based models of protein surfaces improve protein-protein interaction site predictions. <i>BMC Bioinformatics</i> , 2014, 15, 277.	2.6	20
53	Design of a tobacco exon array with application to investigate the differential cadmium accumulation property in two tobacco varieties. <i>BMC Genomics</i> , 2012, 13, 674.	2.8	18
54	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021, 31, 1203-1215.	5.5	17

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55	Application of YOLOv4 for Detection and Motion Monitoring of Red Foxes. <i>Animals</i> , 2021, 11, 1723.	2.3	17
56	Concerted action of the new Genomic Peptide Finder and AUGUSTUS allows for automated proteogenomic annotation of the <i>Chlamydomonas reinhardtii</i> genome. <i>Proteomics</i> , 2011, 11, 1814-1823.	2.2	16
57	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
58	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	2.5	14
59	ClassyFlu: Classification of Influenza A Viruses with Discriminatively Trained Profile-HMMs. <i>PLoS ONE</i> , 2014, 9, e84558.	2.5	13
60	VARUS: sampling complementary RNA reads from the sequence read archive. <i>BMC Bioinformatics</i> , 2019, 20, 558.	2.6	10
61	HIV classification using the coalescent theory. <i>Bioinformatics</i> , 2010, 26, 1409-1415.	4.1	9
62	Comparative Genome Annotation. <i>Methods in Molecular Biology</i> , 2018, 1704, 189-212.	0.9	8
63	Effects of adult temperature on gene expression in a butterfly: identifying pathways associated with thermal acclimation. <i>BMC Evolutionary Biology</i> , 2019, 19, 32.	3.2	8
64	<i>Pseudomonas</i> Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of <i>Verticillium</i> spp.. <i>Frontiers in Microbiology</i> , 2021, 12, 652468.	3.5	6
65	A 20 kb lineage-specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 939-953.	4.2	6
66	Combining features in a graphical model to predict protein binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 844-852.	2.6	5
67	Exome Sequencing Discloses Ionizing-radiation-induced DNA Variants in the Genome of Human Gingiva Fibroblasts. <i>Health Physics</i> , 2018, 115, 151-160.	0.5	5
68	jpHMM: improving the reliability of recombination prediction in HIV-1. <i>Nucleic Acids Research</i> , 2010, 38, 1059-1059.	14.5	3
69	Sequential selection of random vectors under a sum constraint. <i>Journal of Applied Probability</i> , 2004, 41, 131-146.	0.7	1
70	Global, highly specific and fast filtering of alignment seeds. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	1
71	Computational Gene Prediction in Eukaryotic Genomes. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , 291-306.	0.3	0
72	End-to-end learning of evolutionary models to find coding regions in genome alignments. <i>Bioinformatics</i> , 2022, 38, 1857-1862.	4.1	0