Mario Stanke

List of Publications by Year
in descending order

72 papers	**23,071** citations	57681 **46** h-index	100535 **70** g-index
90 all docs	**90** docs citations	**90** times ranked	**32684** citing authors

#	Article	IF	Citations
1	End-to-end learning of evolutionary models to find coding regions in genome alignments. Bioinformatics, 2022, 38, 1857-1862.	1.8	0
2	Global, highly specific and fast filtering of alignment seeds. BMC Bioinformatics, 2022, 23, .	1.2	1
3	Pseudomonas Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of Verticillium spp.. Frontiers in Microbiology, 2021, 12, 652468.	1.5	6
4	A 20â€‘kb lineageâ€‘specific genomic region tames virulence in pathogenic amphidiploid Verticillium longisporum. Molecular Plant Pathology, 2021, 22, 939-953.	2.0	6
5	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	2.4	17
6	Application of YOLOv4 for Detection and Motion Monitoring of Red Foxes. Animals, 2021, 11, 1723.	1.0	17
7	BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database. NAR Genomics and Bioinformatics, 2021, 3, lqaa108.	1.5	803
8	TSEBRA: transcript selector for BRAKER. BMC Bioinformatics, 2021, 22, 566.	1.2	91
9	Enhanced genome assembly and a new official gene set for Tribolium castaneum. BMC Genomics, 2020, 21, 47.	1.2	84
10	Predicting Genes in Single Genomes with AUGUSTUS. Current Protocols in Bioinformatics, 2019, 65, e57.	25.8	225
11	Effects of adult temperature on gene expression in a butterfly: identifying pathways associated with thermal acclimation. BMC Evolutionary Biology, 2019, 19, 32.	3.2	8
12	Whole-Genome Annotation with BRAKER. Methods in Molecular Biology, 2019, 1962, 65-95.	0.4	461
13	Multi-Genome Annotation with AUGUSTUS. Methods in Molecular Biology, 2019, 1962, 139-160.	0.4	43
14	VARUS: sampling complementary RNA reads from the sequence read archive. BMC Bioinformatics, 2019, 20, 558.	1.2	10
15	Comparative Genome Annotation. Methods in Molecular Biology, 2018, 1704, 189-212.	0.4	8
16	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. Genome Research, 2018, 28, 448-459.	2.4	99
17	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
18	Exome Sequencing Discloses Ionizing-radiation-induced DNA Variants in the Genome of Human Gingiva Fibroblasts. Health Physics, 2018, 115, 151-160.	0.3	5

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19	Comparative Annotation Toolkit (CAT)â€"simultaneous clade and personal genome annotation. Genome Research, 2018, 28, 1029-1038.	2.4	86
20	Wild tobacco genomes reveal the evolution of nicotine biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6133-6138.	3.3	160
21	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	1.1	14
22	House spider genome uncovers evolutionary shifts in the diversity and expression of black widow venom proteins associated with extreme toxicity. BMC Genomics, 2017, 18, 178.	1.2	57
23	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC Biology, 2017, 15, 62.	1.7	286
24	Simultaneous gene finding in multiple genomes. Bioinformatics, 2016, 32, 3388-3395.	1.8	74
25	BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS. Bioinformatics, 2016, 32, 767-769.	1.8	918
26	Large scale RNAi screen in Tribolium reveals novel target genes for pest control and the proteasome as prime target. BMC Genomics, 2015, 16, 674.	1.2	119
27	Combining features in a graphical model to predict protein binding sites. Proteins: Structure, Function and Bioinformatics, 2015, 83, 844-852.	1.5	5
28	The iBeetle large-scale RNAi screen reveals gene functions for insect development and physiology. Nature Communications, 2015, 6, 7822.	5.8	139
29	Current methods for automated annotation of protein-coding genes. Current Opinion in Insect Science, 2015, 7, 8-14.	2.2	23
30	ClassyFlu: Classification of Influenza A Viruses with Discriminatively Trained Profile-HMMs. PLoS ONE, 2014, 9, e84558.	1.1	13
31	Tissue-specific transcriptomics, chromosomal localization, and phylogeny of chemosensory and odorant binding proteins from the red flour beetle Tribolium castaneum reveal subgroup specificities for olfaction or more general functions. BMC Genomics, 2014, 15, 1141.	1.2	111
32	<i><scp>V</scp>erticillium</i> transcription activator of adhesion <scp>V</scp>ta2 suppresses microsclerotia formation and is required for systemic infection of plant roots. New Phytologist, 2014, 202, 565-581.	3.5	92
33	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	1.2	375
34	CRF-based models of protein surfaces improve protein-protein interaction site predictions. BMC Bioinformatics, 2014, 15, 277.	1.2	20
35	The Chlamydomonas genome project: a decade on. Trends in Plant Science, 2014, 19, 672-680.	4.3	145
36	WebAUGUSTUS--a web service for training AUGUSTUS and predicting genes in eukaryotes. Nucleic Acids Research, 2013, 41, W123-W128.	6.5	253

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37	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. Science, 2013, 339, 1207-1210.	6.0	439
38	Genome sequencing of the lizard parasite Leishmania tarentolae reveals loss of genes associated to the intracellular stage of human pathogenic species. Nucleic Acids Research, 2012, 40, 1131-1147.	6.5	135
39	jpHMM: recombination analysis in viruses with circular genomes such as the hepatitis B virus. Nucleic Acids Research, 2012, 40, W193-W198.	6.5	67
40	Design of a tobacco exon array with application to investigate the differential cadmium accumulation property in two tobacco varieties. BMC Genomics, 2012, 13, 674.	1.2	18
41	Detection of viral sequence fragments of HIV-1 subfamilies yet unknown. BMC Bioinformatics, 2011, 12, 93.	1.2	37
42	Concerted action of the new Genomic Peptide Finder and AUGUSTUS allows for automated proteogenomic annotation of the <i>Chlamydomonas reinhardtii</i> genome. Proteomics, 2011, 11, 1814-1823.	1.3	16
43	A novel hybrid gene prediction method employing protein multiple sequence alignments. Bioinformatics, 2011, 27, 757-763.	1.8	468
44	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	6.0	424
45	The role of recombination in the emergence of a complex and dynamic HIV epidemic. Retrovirology, 2010, 7, 25.	0.9	110
46	The Amphimedon queenslandica genome and the evolution of animal complexity. Nature, 2010, 466, 720-726.	13.7	917
47	Draft genome sequence of the oilseed species Ricinus communis. Nature Biotechnology, 2010, 28, 951-956.	9.4	449
48	jpHMM: improving the reliability of recombination prediction in HIV-1. Nucleic Acids Research, 2010, 38, 1059-1059.	6.5	3
49	HIV classification using the coalescent theory. Bioinformatics, 2010, 26, 1409-1415.	1.8	9
50	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	2.6	913
51	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11889-11894.	3.3	389
52	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. Science, 2010, 327, 343-348.	6.0	808
53	Computational Gene Prediction in Eukaryotic Genomes. Cellular Origin and Life in Extreme Habitats, 2010, , 291-306.	0.3	0
54	jpHMM: Improving the reliability of recombination prediction in HIV-1. Nucleic Acids Research, 2009, 37, W647-W651.	6.5	145

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55	The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358.	13.7	945
56	AUGUSTUS at MediGRID: Adaption of a bioinformatics application to grid computing for efficient genome analysis. Future Generation Computer Systems, 2009, 25, 337-345.	4.9	15
57	The genome of the model beetle and pest Tribolium castaneum. Nature, 2008, 452, 949-955.	13.7	1,255
58	Scipio: Using protein sequences to determine the precise exon/intron structures of genes and their orthologs in closely related species. BMC Bioinformatics, 2008, 9, 278.	1.2	137
59	Discovery and revision of *Arabidopsis* genes by proteogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 21034-21038.	3.3	268
60	Using native and syntenically mapped cDNA alignments to improve *de novo* gene finding. Bioinformatics, 2008, 24, 637-644.	1.8	1,618
61	Draft Genome of the Filarial Nematode Parasite *Brugia malayi*. Science, 2007, 317, 1756-1760.	6.0	571
62	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	6.0	1,025
63	The genome of the thermoacidophilic red microalga Galdieria sulphuraria encodes a small family of secreted class III peroxidases that might be involved in cell wall modification. Planta, 2007, 227, 353-362.	1.6	27
64	AUGUSTUS at EGASP: using EST, protein and genomic alignments for improved gene prediction in the human genome. Genome Biology, 2006, 7, S11.	13.9	263
65	A jumping profile Hidden Markov Model and applications to recombination sites in HIV and HCV genomes. BMC Bioinformatics, 2006, 7, 265.	1.2	85
66	Gene prediction in eukaryotes with a generalized hidden Markov model that uses hints from external sources. BMC Bioinformatics, 2006, 7, 62.	1.2	968
67	AUGUSTUS: ab initio prediction of alternative transcripts. Nucleic Acids Research, 2006, 34, W435-W439.	6.5	1,851
68	jpHMM at GOBICS: a web server to detect genomic recombinations in HIV-1. Nucleic Acids Research, 2006, 34, W463-W465.	6.5	47
69	AUGUSTUS: a web server for gene prediction in eukaryotes that allows user-defined constraints. Nucleic Acids Research, 2005, 33, W465-W467.	6.5	1,286
70	AUGUSTUS: a web server for gene finding in eukaryotes. Nucleic Acids Research, 2004, 32, W309-W312.	6.5	1,068
71	Sequential selection of random vectors under a sum constraint. Journal of Applied Probability, 2004, 41, 131-146.	0.4	1
72	Gene prediction with a hidden Markov model and a new intron submodel. Bioinformatics, 2003, 19, ii215-ii225.	1.8	1,294