

Volker P Brendel

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

4,608
citations

117625

34
h-index

118850

62
g-index

68
all docs

68
docs citations

68
times ranked

6694
citing authors

#	ARTICLE	IF	CITATIONS
1	Tools and applications for integrative analysis of DNA methylation in social insects. <i>Molecular Ecology Resources</i> , 2022, 22, 1656-1674.	4.8	4
2	iLoc: robust evaluation of genome content and organization for provisional and mature genome assemblies. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac013.	3.2	0
3	Flexible analysis of TSS mapping data and detection of TSS shifts with TSRexploreR. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab051.	3.2	11
4	The Xa7 resistance gene guards the rice susceptibility gene SWEET14 against exploitation by the bacterial blight pathogen. <i>Plant Communications</i> , 2021, 2, 100164.	7.7	30
5	Simple and efficient profiling of transcription initiation and transcript levels with STRIPE-seq. <i>Genome Research</i> , 2020, 30, 910-923.	5.5	23
6	SRAssembler: Selective Recursive local Assembly of homologous genomic regions. <i>BMC Bioinformatics</i> , 2019, 20, 371.	2.6	8
7	Changes in gene DNA methylation and expression networks accompany caste specialization and age-related physiological changes in a social insect. <i>Molecular Ecology</i> , 2019, 28, 1975-1993.	3.9	30
8	Using RAMPAGE to Identify and Annotate Promoters in Insect Genomes. <i>Methods in Molecular Biology</i> , 2019, 1858, 99-116.	0.9	3
9	From small RNA discoveries to a new paradigm in computational genomics?. <i>New Phytologist</i> , 2018, 220, 659-660.	7.3	3
10	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	4.8	11
11	xGDBvm: A Web GUI-Driven Workflow for Annotating Eukaryotic Genomes in the Cloud. <i>Plant Cell</i> , 2016, 28, 840-854.	6.6	2
12	Genome, transcriptome and methylome sequencing of a primitively eusocial wasp reveal a greatly reduced DNA methylation system in a social insect. <i>Molecular Ecology</i> , 2016, 25, 1769-1784.	3.9	148
13	Promoter Architecture and Sex-Specific Gene Expression in <i>Daphnia pulex</i> . <i>Genetics</i> , 2016, 204, 593-612.	2.9	20
14	Discovery and Expression Analysis of Alternative Splicing Events Conserved among Plant SR Proteins. <i>Molecular Biology and Evolution</i> , 2014, 31, 605-613.	8.9	40
15	Single Nucleotide Polymorphisms of Human STING Can Affect Innate Immune Response to Cyclic Dinucleotides. <i>PLoS ONE</i> , 2013, 8, e77846.	2.5	209
16	ParsEval: parallel comparison and analysis of gene structure annotations. <i>BMC Bioinformatics</i> , 2012, 13, 187.	2.6	24
17	TAL Effector-Nucleotide Targeter (TALE-NT) 2.0: tools for TAL effector design and target prediction. <i>Nucleic Acids Research</i> , 2012, 40, W117-W122.	14.5	549
18	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	2.2	189

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19	Genome-Wide Distribution of Transposed <i>Dissociation</i> Elements in Maize <i>Â</i> . <i>Plant Cell</i> , 2010, 22, 1667-1685.	6.6	123
20	Common introns within orthologous genes: software and application to plants. <i>Briefings in Bioinformatics</i> , 2009, 10, 631-644.	6.5	29
21	Expression and evolution of the phosphoinositide-specific phospholipase C gene family in <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2008, 46, 627-637.	5.8	106
22	Cross-species EST alignments reveal novel and conserved alternative splicing events in legumes. <i>BMC Plant Biology</i> , 2008, 8, 17.	3.6	49
23	Pairwise statistical significance and empirical determination of effective gap opening penalties for protein local sequence alignment. <i>International Journal of Computational Biology and Drug Design</i> , 2008, 1, 347.	0.3	16
24	Acquisition and Evolution of Plant Pathogenesis-Associated Gene Clusters and Candidate Determinants of Tissue-Specificity in <i>Xanthomonas</i> . <i>PLoS ONE</i> , 2008, 3, e3828.	2.5	89
25	PlantGDB: a resource for comparative plant genomics. <i>Nucleic Acids Research</i> , 2007, 36, D959-D965.	14.5	246
26	Tracempler <i>â</i> software for in-silico chromosome walking in unassembled genomes. <i>BMC Bioinformatics</i> , 2007, 8, 151.	2.6	12
27	Gene Structure Annotation at PlantGDB. , 2007, 406, 521-533.		4
28	xGDB: open-source computational infrastructure for the integrated evaluation and analysis of genome features. <i>Genome Biology</i> , 2006, 7, R111.	9.6	17
29	yrGATE: a web-based gene-structure annotation tool for the identification and dissemination of eukaryotic genes. <i>Genome Biology</i> , 2006, 7, R58.	9.6	21
30	Genomewide comparative analysis of alternative splicing in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7175-7180.	7.1	481
31	Molecular Characterization and Phylogeny of U2AF35 Homologs in Plants. <i>Plant Physiology</i> , 2006, 140, 624-636.	4.8	46
32	Engineering a software tool for gene structure prediction in higher organisms. <i>Information and Software Technology</i> , 2005, 47, 965-978.	4.4	251
33	Comparative EST Analyses in Plant Systems. <i>Methods in Enzymology</i> , 2005, 395, 400-418.	1.0	22
34	Comparative Plant Genomics Resources at PlantGDB. <i>Plant Physiology</i> , 2005, 139, 610-618.	4.8	95
35	The Maize Genetics and Genomics Database. The Community Resource for Access to Diverse Maize Data. <i>Plant Physiology</i> , 2005, 138, 55-58.	4.8	59
36	Community-based gene structure annotation. <i>Trends in Plant Science</i> , 2005, 10, 9-14.	8.8	24

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37	Gene structure prediction from consensus spliced alignment of multiple ESTs matching the same genomic locus. <i>Bioinformatics</i> , 2004, 20, 1157-1169.	4.1	97
38	Refined Annotation of the Arabidopsis Genome by Complete Expressed Sequence Tag Mapping. <i>Plant Physiology</i> , 2003, 132, 469-484.	4.8	111
39	Identification, characterization and molecular phylogeny of U12-dependent introns in the Arabidopsis thaliana genome. <i>Nucleic Acids Research</i> , 2003, 31, 4561-4572.	14.5	61
40	GeneSeqer@PlantGDB: gene structure prediction in plant genomes. <i>Nucleic Acids Research</i> , 2003, 31, 3597-3600.	14.5	59
41	The Maize Genome Contains a Helitron Insertion. <i>Plant Cell</i> , 2003, 15, 381-391.	6.6	115
42	Efficient clustering of large EST data sets on parallel computers. <i>Nucleic Acids Research</i> , 2003, 31, 2963-2974.	14.5	69
43	ZmDB, an integrated database for maize genome research. <i>Nucleic Acids Research</i> , 2003, 31, 244-247.	14.5	33
44	The Maize Genome Sequencing Project. <i>Plant Physiology</i> , 2002, 130, 1594-1597.	4.8	69
45	Comparison of RNA Expression Profiles Based on Maize Expressed Sequence Tag Frequency Analysis and Micro-Array Hybridization. <i>Plant Physiology</i> , 2002, 128, 896-910.	4.8	96
46	Computational modeling of gene structure in Arabidopsis thaliana. <i>Plant Molecular Biology</i> , 2002, 48, 49-58.	3.9	8
47	Gene structure prediction by spliced alignment of genomic DNA with protein sequences: increased accuracy by differential splice site scoring ¹¹ Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 2000, 297, 1075-1085.	4.2	59
48	Test of the combinatorial model of intron recognition in a native maize gene. <i>Plant Molecular Biology</i> , 1999, 41, 637-644.	3.9	15
49	Identification of Biased Amino Acid Substitution Patterns in Human Immunodeficiency Virus Type 1 Isolates from Patients Treated with Protease Inhibitors. <i>Journal of Virology</i> , 1999, 73, 6197-6202.	3.4	65
50	U-richness is a defining feature of plant introns and may function as an intron recognition signal in maize. <i>Plant Molecular Biology</i> , 1998, 36, 573-583.	3.9	65
51	Prediction of splice sites in plant pre-mRNA from sequence properties. <i>Journal of Molecular Biology</i> , 1998, 276, 85-104.	4.2	28
52	Evolutionary Comparisons of RecA-Like Proteins Across All Major Kingdoms of Living Organisms. <i>Journal of Molecular Evolution</i> , 1997, 44, 528-541.	1.8	125
53	A combinatorial role for exon, intron and splice site sequences in splicing in maize. <i>Plant Journal</i> , 1997, 11, 1253-1263.	5.7	39
54	A comparative analysis of distinctive features of yeast protein sequences. <i>Yeast</i> , 1993, 9, 1287-1298.	1.7	10

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55	Quantitative Model of ColE1 Plasmid Copy Number Control. <i>Journal of Molecular Biology</i> , 1993, 229, 860-872.	4.2	46
56	PROSETâ€”a fast procedure to create non-redundant sets of protein sequences. <i>Mathematical and Computer Modelling</i> , 1992, 16, 37-43.	2.0	37
57	Too many leucine zippers?. <i>Nature</i> , 1989, 341, 574-575.	27.8	35
58	A method to identify distinctive charge configurations in protein sequences, with application to human herpesvirus polypeptides. <i>Journal of Molecular Biology</i> , 1989, 205, 165-177.	4.2	41
59	Kinetics of complementary RNA-RNA interaction involved in plasmid ColE1 copy number control. <i>Journal of Molecular Biology</i> , 1989, 208, 245-255.	4.2	21
60	Kinetic Analysis of Adsorption Processes. <i>SIAM Journal on Applied Mathematics</i> , 1987, 47, 1306-1319.	1.8	11
61	On modes of recombination, replication, and segregation of the higher plant mitochondrial genome. <i>Journal of Theoretical Biology</i> , 1987, 125, 163-176.	1.7	4
62	Intervening Sequences Exhibit Distinct Vocabulary. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 391-400.	3.5	31
63	Terminators of Transcription with RNA Polymerase from <i>Escherichia coli</i> : What They Look Like and How to Find Them. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 3, 705-723.	3.5	118
64	Linguistics of Nucleotide Sequences: Morphology and Comparison of Vocabularies. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 11-21.	3.5	146