

Jasper Rees

List of Publications by Year in descending order

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71
papers

5,729
citations

186265

28
h-index

106344

65
g-index

71
all docs

71
docs citations

71
times ranked

6863
citing authors

#	ARTICLE	IF	CITATIONS
1	First report of maize yellow mosaic virus (MaYMV) on maize (<i>Zea mays</i>) in Tanzania. <i>Journal of Plant Pathology</i> , 2019, 101, 203-203.	1.2	13
2	Molecular characterization of Morogoro maize-associated virus, a nucleorhabdovirus detected in maize (<i>Zea mays</i>) in Tanzania. <i>Archives of Virology</i> , 2019, 164, 1711-1715.	2.1	8
3	Diversity and distribution of Maize-associated totivirus strains from Tanzania. <i>Virus Genes</i> , 2019, 55, 429-432.	1.6	6
4	Characterization and detection of maize-associated pteridovirus (MaPV), infecting maize (<i>Zea mays</i>) in the Arusha region of Tanzania. <i>European Journal of Plant Pathology</i> , 2019, 154, 1165-1170.	1.7	3
5	Application of Chloroplast Phylogenomics to Resolve Species Relationships Within the Plant Genus <i>Amaranthus</i> . <i>Journal of Molecular Evolution</i> , 2018, 86, 216-239.	1.8	25
6	The early transcriptome response of cassava (<i>Manihot esculenta</i> Crantz) to mealybug (<i>Phenacoccus</i>) Tj ETQq0 0 0 BT /Overlock 10 Tf	2.5	20
7	Whole genome sequencing and identification of <i>Bacillus endophyticus</i> and <i>B. anthracis</i> isolated from anthrax outbreaks in South Africa. <i>BMC Microbiology</i> , 2018, 18, 67.	3.3	11
8	Viral metagenomics reveals sweet potato virus diversity in the Eastern and Western Cape provinces of South Africa. <i>South African Journal of Botany</i> , 2018, 117, 256-267.	2.5	13
9	First Report of Sweet potato badnavirus A and Sweet potato badnavirus B in South Africa. <i>Plant Disease</i> , 2018, 102, 1865-1865.	1.4	4
10	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	21.4	693
11	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. <i>Nature Communications</i> , 2017, 8, 2062.	12.8	88
12	Genome-wide association analysis of agronomic traits in wheat under drought-stressed and non-stressed conditions. <i>PLoS ONE</i> , 2017, 12, e0171692.	2.5	138
13	Sialotranscriptomics of <i>Rhipicephalus zambeziensis</i> reveals intricate expression profiles of secretory proteins and suggests tight temporal transcriptional regulation during blood-feeding. <i>Parasites and Vectors</i> , 2017, 10, 384.	2.5	28
14	A draft genome sequence of the rose black spot fungus <i>Diplocarpon rosae</i> reveals a high degree of genome duplication. <i>PLoS ONE</i> , 2017, 12, e0185310.	2.5	8
15	Significant up-regulation of 1-ACBP, B-ACBP and PBR genes in immune cells within the oesophageal malignant tissue and a possible link in carcinogenic angiogenesis. <i>Histology and Histopathology</i> , 2017, 32, 561-570.	0.7	2
16	The Critical Role Of VP1 In Forming The Necessary Cavities For Receptor-mediated Entry Of FMDV To The Host Cell. <i>Scientific Reports</i> , 2016, 6, 27140.	3.3	10
17	Tropically adapted cattle of Africa: perspectives on potential role of copy number variations. <i>Animal Genetics</i> , 2016, 47, 154-164.	1.7	11
18	De novo assembly and annotation of the salivary gland transcriptome of <i>Rhipicephalus appendiculatus</i> male and female ticks during blood feeding. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 536-548.	2.7	55

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19	A Comprehensive Study of Molecular Evolution at the Self-Incompatibility Locus of Rosaceae. <i>Journal of Molecular Evolution</i> , 2016, 82, 128-145.	1.8	19
20	Polyphasic characterization of <i>Bacillus</i> species from anthrax outbreaks in animals from South Africa and Lesotho. <i>Journal of Infection in Developing Countries</i> , 2016, 10, 814-823.	1.2	4
21	A simple, high-throughput modeling approach reveals insights into the mechanism of gametophytic self-incompatibility. <i>Scientific Reports</i> , 2016, 6, 34732.	3.3	0
22	Draft Genome Sequences of Two South African <i>Bacillus anthracis</i> Strains. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
23	Heteroditopic P,N ligands in gold(I) complexes: Synthesis, structure and cytotoxicity. <i>Journal of Inorganic Biochemistry</i> , 2015, 145, 108-120.	3.5	10
24	In vitro cytotoxic and pro-apoptotic effects of water extracts of <i>Tulbaghia violacea</i> leaves and bulbs. <i>Journal of Ethnopharmacology</i> , 2015, 164, 203-209.	4.1	15
25	Complete Genome Sequence of <i>Mannheimia haemolytica</i> Strain Mh10517, Isolated from Sheep in South Africa. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
26	Extending the sRNAome of Apple by Next-Generation Sequencing. <i>PLoS ONE</i> , 2014, 9, e95782.	2.5	17
27	A glance at quality score: implication for de novo transcriptome reconstruction of Illumina reads. <i>Frontiers in Genetics</i> , 2014, 5, 17.	2.3	36
28	Draft Genome Sequence of the Antarctic Polyextremophile <i>Nesterenkonia</i> sp. Strain AN1. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
29	High-throughput sequencing reveals small RNAs involved in ASGV infection. <i>BMC Genomics</i> , 2014, 15, 568.	2.8	39
30	METAGENOMIC DEEP-SEQUENCING: A PROMISING TOOL TO ELUCIDATE ETIOLOGY. <i>Acta Horticulturae</i> , 2014, , 335-340.	0.2	0
31	Solution Structure of RING Finger-like Domain of Retinoblastoma-binding Protein-6 (RBBP6) Suggests It Functions as a U-box. <i>Journal of Biological Chemistry</i> , 2012, 287, 7146-7158.	3.4	18
32	Full genomic sequence of an African Avian Paramyxovirus Type 4 strain isolated from a wild duck. <i>Virus Genes</i> , 2012, 45, 537-41.	1.6	22
33	A genetic linkage map of an apple rootstock progeny anchored to the <i>Malus</i> genome sequence. <i>Tree Genetics and Genomes</i> , 2012, 8, 991-1002.	1.6	17
34	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. <i>PLoS ONE</i> , 2012, 7, e31745.	2.5	249
35	De-regulation of the RBBP6 isoform 3/DWNN in human cancers. <i>Molecular and Cellular Biochemistry</i> , 2012, 362, 249-262.	3.1	29
36	Diversity arrays technology (DArT) markers in apple for genetic linkage maps. <i>Molecular Breeding</i> , 2012, 29, 645-660.	2.1	41

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37	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	21.4	1,091
38	Inheritance of Flowering Time in Apricot (<i>Prunus armeniaca</i> L.) and Analysis of Linked Quantitative Trait Loci (QTLs) using Simple Sequence Repeat (SSR) Markers. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 404-410.	1.8	72
39	Identification of a major QTL for time of initial vegetative budbreak in apple (<i>Malus x domestica</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.6 63	1.6	63
40	Developing Microsatellite Multiplex and Megaplex PCR Systems for High-Throughput Characterization of Breeding Progenies and Linkage Maps Spanning the Apricot (<i>Prunus armeniaca</i> L.) Genome. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 560-568.	1.8	20
41	Deep sequencing analysis of viruses infecting grapevines: Virome of a vineyard. <i>Virology</i> , 2010, 400, 157-163.	2.4	248
42	Genome-wide SNP identification by high-throughput sequencing and selective mapping allows sequence assembly positioning using a framework genetic linkage map. <i>BMC Biology</i> , 2010, 8, 155.	3.8	19
43	WHOLE-GENOME SNP SEQUENCING OF SELECTED PROGENY INDIVIDUALS ALLOWS ANCHORING OF DRAFT GENOME SEQUENCE TO A LINKAGE MAP FOR THE APPLE SCAB PATHOGEN <i>VENTURIA INAEQUALIS</i> . <i>Acta Horticulturae</i> , 2010, , 295-300.	0.2	1
44	Abstract 1085: RbBP6 isoform 3/DWNN is essential for arsenic trioxide-induced G2/M arrest in cancer cell lines. , 2010, , .		0
45	Abstract 1265: RbBP6 Isoform 3 (DWNN) is a p53 stabilizer in arsenic trioxide-induced apoptosis in human cancer cell lines. , 2010, , .		0
46	GENETIC LINKAGE MAP CONSTRUCTION AND IDENTIFICATION OF QTLs AFFECTING TIME OF INITIAL VEGETATIVE BUDBREAK IN APPLE (<i>MALUS X DOMESTICA</i> BORKH.). <i>Acta Horticulturae</i> , 2009, , 585-590.	0.2	1
47	BIN MAPPING OF EST-SSRS IN APPLE (<i>MALUS X DOMESTICA</i> BORKH.). <i>Acta Horticulturae</i> , 2009, , 681-688.	0.2	1
48	In vitro evaluation of dichloro-bis(pyrazole)palladium(II) and dichloro-bis(pyrazole)platinum(II) complexes as anticancer agents. <i>Cancer Chemotherapy and Pharmacology</i> , 2008, 63, 127-138.	2.3	62
49	RBBP6 Interacts with Multifunctional Protein YB-1 through Its RING Finger Domain, Leading to Ubiquitination and Proteosomal Degradation of YB-1. <i>Journal of Molecular Biology</i> , 2008, 384, 908-916.	4.2	66
50	A low-cost flow cytometric assay for the detection and quantification of apoptosis using an anionic halogenated fluorescein dye. <i>BioTechniques</i> , 2008, 45, 317-320.	1.8	24
51	INVESTIGATING THE MOLECULAR MECHANISM OF ANTHOCYANIN PRODUCTION IN 'BON ROUGE' <i>PYRUS COMMUNIS</i> L.. <i>Acta Horticulturae</i> , 2008, , 383-390.	0.2	1
52	DWNN, a novel ubiquitin-like domain, implicates RBBP6 in mRNA processing and ubiquitin-like pathways. <i>BMC Structural Biology</i> , 2006, 6, 1.	2.3	68
53	MOLECULAR GENETIC STUDIES ON PEARS (<i>PYRUS</i> SPP.) IN THE WESTERN CAPE. <i>Acta Horticulturae</i> , 2005, , 259-265.	0.2	2
54	MOLECULAR TYPING OF RED AND GREEN PHENOTYPES OF 'BON ROUGE'™ PEAR TREES, WITH THE USE OF MICROSATELLITES. <i>Acta Horticulturae</i> , 2005, , 293-297.	0.2	5

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55	STRESS INDUCED DIFFERENTIAL GENE EXPRESSION PATTERNS FOR RED AND GREEN PHENOTYPES OF 'BON ROUGE' PEAR TREES (PYRUS COMMUNIS). <i>Acta Horticulturae</i> , 2005, , 299-305.	0.2	1
56	DIFFERENTIAL GENE EXPRESSION PATTERNS FOR RED AND GREEN PHENOTYPES OF 'BON ROUGE' PEAR TREES, PYRUS COMMUNIS L.. <i>Acta Horticulturae</i> , 2004, , 337-340.	0.2	0
57	PRE-SCREENING FOR MILDEW RESISTANCE IN APPLES: DEVELOPMENT OF A MARKER-ASSISTED SELECTION TECHNIQUE. <i>Acta Horticulturae</i> , 2000, , 597-600.	0.2	1
58	The Talin Head Domain Binds to Integrin β 2 Subunit Cytoplasmic Tails and Regulates Integrin Activation. <i>Journal of Biological Chemistry</i> , 1999, 274, 28071-28074.	3.4	617
59	Sequence analysis of rat integrin β 1 and β 2 subunits: Tissue expression reveals phenotypic similarities between intraepithelial lymphocytes and dendritic cells in lymph. <i>European Journal of Immunology</i> , 1997, 27, 3070-3079.	2.9	34
60	Isolation and sequence analysis of a cDNA encoding the c subunit of a vacuolar-type H ⁺ -ATPase from the CAM plant <i>Kalanchoe daigremontiana</i> . <i>Plant Molecular Biology</i> , 1996, 31, 435-442.	3.9	12
61	Analysis of Repeated Motifs in the Talin Rod. <i>Journal of Molecular Biology</i> , 1994, 235, 1278-1290.	4.2	42
62	The cytoskeletal protein talin contains at least two distinct vinculin binding domains. <i>Journal of Cell Biology</i> , 1993, 122, 337-347.	5.2	79
63	Sequence and domain structure of talin. <i>Nature</i> , 1990, 347, 685-689.	27.8	302
64	An ancient, highly conserved family of cysteine-rich protein domains revealed by cloning type I and type II murine macrophage scavenger receptors.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 8810-8814.	7.1	291
65	sevenless: Seven found?. <i>Cell</i> , 1990, 61, 15-16.	28.9	39
66	DETECTION OF POLYMORPHISMS AT CYTOSINE PHOSPHOGUANADINE DINUCLEOTIDES AND DIAGNOSIS OF HAEMOPHILIA B CARRIERS. <i>Lancet</i> , The, 1989, 333, 631-634.	13.7	67
67	Randomly picked cosmid clones overlap the <i>pyrB</i> and <i>oriC</i> gap in the physical map of the <i>E.coli</i> chromosome. <i>Nucleic Acids Research</i> , 1988, 16, 2601-2612.	14.5	46
68	Defective propeptide processing of blood clotting factor IX caused by mutation of arginine to glutamine at position 4. <i>Cell</i> , 1986, 45, 343-348.	28.9	191
69	Haemophilia B caused by a point mutation in a donor splice junction of the human factor IX gene. <i>Nature</i> , 1985, 316, 643-645.	27.8	85
70	Gene deletions in patients with haemophilia B and anti-factor IX antibodies. <i>Nature</i> , 1983, 303, 181-182.	27.8	221
71	Molecular cloning of the gene for human anti-haemophilic factor IX. <i>Nature</i> , 1982, 299, 178-180.	27.8	296