

Jernej Jakse

List of Publications by Year in descending order

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119
papers

2,375
citations

201674

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276875

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123
all docs

123
docs citations

123
times ranked

2185
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#	ARTICLE	IF	CITATIONS
1	Discovery of microRNA-like Small RNAs in Pathogenic Plant Fungus <i>Verticillium nonalfalfae</i> Using High-Throughput Sequencing and qPCR and RLM-RACE Validation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 900.	4.1	5
2	Virome Status of Preclonal Candidates of Grapevine Varieties (<i>Vitis vinifera</i> L.) From the Slovenian Wine-Growing Region Primorska as Determined by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2022, 13, 830866.	3.5	5
3	Reference-Grade Genome and Large Linear Plasmid of <i>Streptomyces rimosus</i> : Pushing the Limits of Nanopore Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, e0243421.	3.0	5
4	Small RNA Sequencing and Multiplex RT-PCR for Diagnostics of Grapevine Viruses and Virus-like Organisms. <i>Viruses</i> , 2022, 14, 921.	3.3	1
5	The complete chloroplast genome of dalmatian pyrethrum (<i>Tanacetum cinerariifolium</i> (Trevir.) Tj ETQq1 1 0.784314 rgBT /Ov Resources, 2022, 7, 775-777.	0.4	0
6	Development of Microsatellite Markers for <i>Tanacetum cinerariifolium</i> (Trevis.) Sch. Bip., a Plant with a Large and Highly Repetitive Genome. <i>Plants</i> , 2022, 11, 1778.	3.5	3
7	Genetic Structure and Core Collection of Olive Germplasm from Albania Revealed by Microsatellite Markers. <i>Genes</i> , 2021, 12, 256.	2.4	15
8	Core RNA Interference Genes Involved in miRNA and Ta-siRNA Biogenesis in Hops and Their Expression Analysis after Challenging with <i>Verticillium nonalfalfae</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4224.	4.1	2
9	First set of microsatellite markers for immortal (Helichrysum italicum (Roth) G. Don): A step towards the selection of the most promising genotypes for cultivation. <i>Industrial Crops and Products</i> , 2021, 162, 113298.	5.2	12
10	Antennal transcriptome sequencing and identification of candidate chemoreceptor proteins from an invasive pest, the American palm weevil, <i>Rhynchophorus palmarum</i> . <i>Scientific Reports</i> , 2021, 11, 8334.	3.3	17
11	Plant genera <i>Cannabis</i> and <i>Humulus</i> share the same pair of well-differentiated sex chromosomes. <i>New Phytologist</i> , 2021, 231, 1599-1611.	7.3	17
12	Towards the Well-Tempered Chloroplast DNA Sequences. <i>Plants</i> , 2021, 10, 1360.	3.5	7
13	High Genetic Diversity and Low Population Differentiation in Wild Hop (<i>Humulus lupulus</i> L.) from Croatia. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 6484.	2.5	5
14	Identification and characterization of long non-coding RNA and their response against citrus bark cracking viroid infection in <i>Humulus lupulus</i> . <i>Genomics</i> , 2021, 113, 2350-2364.	2.9	6
15	First report of grapevine satellite virus in Slovenia. <i>Journal of Plant Pathology</i> , 2021, 103, 1329-1330.	1.2	5
16	Identification and Characterization of <i>Verticillium nonalfalfae</i> -Responsive MicroRNAs in the Roots of Resistant and Susceptible Hop Cultivars. <i>Plants</i> , 2021, 10, 1883.	3.5	1
17	Studying RNAi in pathogenic hop fungi <i>Verticillium nonalfalfae</i> . <i>Acta Horticulturae</i> , 2021, , 37-46.	0.2	0
18	Phenolic and miRNA response of resistant hop cultivar "Wye Target"™ after inoculation with phytopathogenic fungus <i>Verticillium nonalfalfae</i> . <i>Acta Horticulturae</i> , 2021, , 47-54.	0.2	0

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19	Ampelographic and molecular characterisation of grapevine varieties in the gene bank of the experimental vineyard "Radmilovac"™ " Serbia. <i>Oeno One</i> , 2021, 55, 129-144.	1.4	2
20	Integrated Proteo-Transcriptomic Analyses Reveal Insights into Regulation of Pollen Development Stages and Dynamics of Cellular Response to Apple Fruit Crinkle Viroid (AFCVd)-Infection in <i>Nicotiana tabacum</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 8700.	4.1	3
21	Molecular Study of Selected Taxonomically Critical Taxa of the Genus <i>Iris</i> L. from the Broader Alpine-Dinaric Area. <i>Plants</i> , 2020, 9, 1229.	3.5	1
22	The Potential of HTS Approaches for Accurate Genotyping in Grapevine (<i>Vitis vinifera</i> L.). <i>Genes</i> , 2020, 11, 917.	2.4	4
23	Transporters and Efflux Pumps Are the Main Mechanisms Involved in <i>Staphylococcus epidermidis</i> Adaptation and Tolerance to Didecyldimethylammonium Chloride. <i>Microorganisms</i> , 2020, 8, 344.	3.6	9
24	Dissection of Dynamic Transcriptome Landscape of Leaf, Bract, and Lupulin Gland in Hop (<i>Humulus lupulus</i> L.). <i>Plant Physiology</i> , 2020, 184, 1075-1087.	4.1	19
25	Mapping the Gene Expression Spectrum of Mediator Subunits in Response to Viroid Infection in Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2498.	4.1	10
26	Studying strands polarity of different viroids and their combinations in infected hop plants. <i>Acta Agriculturae Slovenica</i> , 2020, 115, .	0.3	0
27	Traditional and molecular methods for the identification of whitefly (Aleyrodidae) species. <i>Acta Agriculturae Slovenica</i> , 2020, 116, .	0.3	0
28	Morphological and microsatellite analysis of the ancient Montenegrin olive variety "Zlatica"™ revealed different clones. <i>Acta Agriculturae Slovenica</i> , 2020, 116, .	0.3	0
29	First report of powdery mildew of <i>Sonchus oleraceus</i> caused by <i>Golovinomyces sonchicola</i> in Slovenia. <i>Journal of Plant Pathology</i> , 2019, 101, 805-805.	1.2	2
30	Confirming infection of hop plants inoculated with <i>Verticillium nonalfalfae</i> . <i>Data in Brief</i> , 2019, 25, 104355.	1.0	0
31	Temporal and spatial assessment of defence responses in resistant and susceptible hop cultivars during infection with <i>Verticillium nonalfalfae</i> . <i>Journal of Plant Physiology</i> , 2019, 240, 153008.	3.5	7
32	Evaluation of Disease Severity and Global Transcriptome Response Induced by Citrus bark cracking viroid, Hop latent viroid, and Their Co-Infection in Hop (<i>Humulus lupulus</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 3154.	4.1	30
33	New Male Specific Markers for Hop and Application in Breeding Program. <i>Scientific Reports</i> , 2019, 9, 14223.	3.3	15
34	Proposal of a New Hybrid Breeding Method Based on Genotyping, Inter-Pollination, Phenotyping and Paternity Testing of Selected Elite F1 Hybrids. <i>Frontiers in Plant Science</i> , 2019, 10, 1111.	3.6	8
35	First report of powdery mildew of <i>Solidago gigantea</i> caused by <i>Golovinomyces asterum</i> var. <i>solidaginis</i> in Slovenia. <i>Journal of Plant Pathology</i> , 2019, 101, 765-765.	1.2	0
36	RNA interference core components identified and characterised in <i>Verticillium nonalfalfae</i> , a vascular wilt pathogenic plant fungi of hops. <i>Scientific Reports</i> , 2019, 9, 8651.	3.3	16

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37	Global transcriptome profiling and functional analysis reveal that tissue-specific constitutive overexpression of cytochrome P450s confers tolerance to imidacloprid in palm weevils in date palm fields. <i>BMC Genomics</i> , 2019, 20, 440.	2.8	25
38	Revisiting the Role of Transcription Factors in Coordinating the Defense Response Against Citrus Bark Cracking Viroid Infection in Commercial Hop (<i>Humulus lupulus</i> L.). <i>Viruses</i> , 2019, 11, 419.	3.3	22
39	The complete chloroplast genome of <i>Helichrysum italicum</i> (Roth) G. Don (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1036-1037.	0.4	5
40	One-step multiplex RT-PCR for simultaneous detection of four viroids from hop (<i>Humulus lupulus</i> L.). <i>European Journal of Plant Pathology</i> , 2019, 154, 273-286.	1.7	6
41	Occurrence of grapevine yellow speckle viroid 1 in autochthonous grapevines in Slovenia. <i>Journal of Plant Pathology</i> , 2019, 101, 397-397.	1.2	1
42	First Report of White Rust of Rocket (<i>Eruca sativa</i>) Caused by <i>Albugo candida</i> in Montenegro. <i>Plant Disease</i> , 2019, 103, 163-163.	1.4	5
43	Viruses Associated with Fig Mosaic Disease in Different Fig Varieties in Montenegro. <i>Plant Pathology Journal</i> , 2019, 35, 32-40.	1.7	6
44	De novo transcriptome of the pallial gland of the date mussel (<i>Lithophaga lithophaga</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 26, 1-9.	1.0	4
45	Genome Sequence of a Lethal Strain of Xylem-Invading <i>Verticillium nonalfalfae</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	13
46	First report of powdery mildew of <i>Helianthus tuberosus</i> caused by <i>Golovinomyces ambrosiae</i> in Slovenia. <i>Journal of Plant Pathology</i> , 2018, 100, 331-331.	1.2	4
47	First report of powdery mildew of <i>Capsella bursa-pastoris</i> caused by <i>Golovinomyces orontii</i> in Slovenia. <i>Journal of Plant Pathology</i> , 2018, 100, 359-359.	1.2	4
48	Genome-Wide Transcriptomic Analysis Reveals Insights into the Response to Citrus bark cracking viroid (CBCVd) in Hop (<i>Humulus lupulus</i> L.). <i>Viruses</i> , 2018, 10, 570.	3.3	23
49	Genome-wide transcriptome profiling of transgenic hop (<i>Humulus lupulus</i> L.) constitutively overexpressing <i>HWY1</i> and <i>HWDR1</i> transcription factors. <i>BMC Genomics</i> , 2018, 19, 739.	2.8	13
50	Comparative assessment of genetic diversity in Albanian olive (<i>Olea europaea</i> L.) using SSRs from anonymous and transcribed genomic regions. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	15
51	Comprehensive analysis of <i>Verticillium nonalfalfae</i> in silico secretome uncovers putative effector proteins expressed during hop invasion. <i>PLoS ONE</i> , 2018, 13, e0198971.	2.5	51
52	Interlaboratory comparison of fig (<i>Ficus carica</i> L.) microsatellite genotyping data and determination of reference alleles. <i>Acta Agriculturae Slovenica</i> , 2018, 111, .	0.3	2
53	Broad taxonomic characterization of <i>Verticillium</i> wilt resistance genes reveals an ancient origin of the tomato <i>Ve1</i> immune receptor. <i>Molecular Plant Pathology</i> , 2017, 18, 195-209.	4.2	58
54	Propagation and some physiological effects of Citrus bark cracking viroid and Apple fruit crinkle viroid in multiple infected hop (<i>Humulus lupulus</i> L.). <i>Journal of Plant Physiology</i> , 2017, 213, 166-177.	3.5	22

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55	Comparative transcriptional analysis of hop responses to infection with <i>Verticillium nonalfalfae</i> . <i>Plant Cell Reports</i> , 2017, 36, 1599-1613.	5.6	11
56	Diagnostic techniques for viroids. <i>Plant Pathology</i> , 2017, 66, 339-358.	2.4	23
57	Development of hop transcriptome to support research into host-viroid interactions. <i>PLoS ONE</i> , 2017, 12, e0184528.	2.5	26
58	Identification and validation of novel EST-SSR markers in olives. <i>Scientia Agricola</i> , 2017, 74, 215-225.	1.2	38
59	Identification of Novel Virulence-Associated Proteins Secreted to Xylem by <i>Verticillium nonalfalfae</i> During Colonization of Hop Plants. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 362-373.	2.6	14
60	Characterization and defining of a core set of novel microsatellite markers for use in genotyping and diversity study of Adriatic fig (<i>Ficus carica</i> L.) germplasm. <i>Revista Brasileira De Botanica</i> , 2016, 39, 1095-1102.	1.3	6
61	Identification and characterization of microRNAs in <i>Humulus lupulus</i> using high-throughput sequencing and their response to Citrus bark cracking viroid (CBCVd) infection. <i>BMC Genomics</i> , 2016, 17, 919.	2.8	26
62	Identification of the genes involved in odorant reception and detection in the palm weevil <i>Rhynchophorus ferrugineus</i> , an important quarantine pest, by antennal transcriptome analysis. <i>BMC Genomics</i> , 2016, 17, 69.	2.8	102
63	Complete mitochondrial genome of the <i>Verticillium</i> -wilt causing plant pathogen <i>Verticillium nonalfalfae</i> . <i>PLoS ONE</i> , 2016, 11, e0148525.	2.5	19
64	Deep sequencing revealed Citrus bark cracking viroid (CBCVd) as a highly aggressive pathogen on hop. <i>Plant Pathology</i> , 2015, 64, 831-842.	2.4	58
65	Different Gene Expressions of Resistant and Susceptible Hop Cultivars in Response to Infection with a Highly Aggressive Strain of <i>Verticillium albo-atrum</i> . <i>Plant Molecular Biology Reporter</i> , 2015, 33, 689-704.	1.8	28
66	Genes involved in sex pheromone biosynthesis of <i>Ephesia cautella</i> , an important food storage pest, are determined by transcriptome sequencing. <i>BMC Genomics</i> , 2015, 16, 532.	2.8	38
67	Vegetative propagation: linear barriers and somatic mutation affect the genetic structure of <i>Prunus avium</i> L. stand. <i>Forestry</i> , 2015, 88, 612-621.	2.3	14
68	New Microsatellite Markers for <i>Campanula pyramidalis</i> (Campanulaceae) and Cross-Amplification in Closely Related Species. <i>Applications in Plant Sciences</i> , 2015, 3, 1400117.	2.1	5
69	Paternity Analysis of the Olive Variety 'Celstrska Belica' and Identification of Pollen Donors by Microsatellite Markers. <i>Scientific World Journal</i> , The, 2014, 2014, 1-6.	2.1	19
70	Development of novel EST-derived resistance gene markers in hop (<i>Humulus lupulus</i> L.). <i>Molecular Breeding</i> , 2014, 33, 61-74.	2.1	6
71	Development and characterization of new polymorphic microsatellite markers for <i>Degenia velebitica</i> (Degen) Hayek (Brassicaceae). <i>Conservation Genetics Resources</i> , 2014, 6, 409-411.	0.8	1
72	First Report of Downy Mildew Caused by <i>Hyaloperonospora camelinae</i> on <i>Camelina sativa</i> in Slovenia. <i>Plant Disease</i> , 2014, 98, 1439-1439.	1.4	1

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73	Quantitative trait loci in hop (<i>Humulus lupulus</i> L.) reveal complex genetic architecture underlying variation in sex, yield and cone chemistry. <i>BMC Genomics</i> , 2013, 14, 360.	2.8	39
74	Identification of quantitative trait loci for resistance to <i>Verticillium</i> wilt and yield parameters in hop (<i>Humulus lupulus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1431-1443.	3.6	29
75	The relationship between molecular variation and variation in the wing shape of three aphid parasitoid species: <i>Aphidius uzbekistanicus</i> Luzhetzki, <i>Aphidius rhopalosiphii</i> De Stefani Perez and <i>Aphidius avenaphis</i> (Fitch) (Hymenoptera: Braconidae: Aphidiinae). <i>Zoologischer Anzeiger</i> , 2013, 252, 41-47.	0.9	21
76	Validation of candidate reference genes in RT-qPCR studies of developing olive fruit and expression analysis of four genes involved in fatty acids metabolism. <i>Molecular Breeding</i> , 2013, 32, 211-222.	2.1	18
77	Application of Microsatellite Markers in Grapevine and Olives. , 2013, , .		5
78	First Report of <i>Hop stunt viroid</i> Infecting Hop in Slovenia. <i>Plant Disease</i> , 2012, 96, 592-592.	1.4	23
79	Genotypic variation in sulfur assimilation and metabolism of onion (<i>Allium cepa</i> L.) III. Characterization of sulfite reductase. <i>Phytochemistry</i> , 2012, 83, 34-42.	2.9	10
80	Development of New Microsatellite Markers for <i>Salvia officinalis</i> L. and Its Potential Use in Conservation-Genetic Studies of Narrow Endemic <i>Salvia brachyodon</i> Vandas. <i>International Journal of Molecular Sciences</i> , 2012, 13, 12082-12093.	4.1	32
81	Ploidy and sex expression in monoecious hop (<i>Humulus lupulus</i>). <i>Botany</i> , 2012, 90, 617-626.	1.0	6
82	First Report of Powdery Mildew Caused by <i>Golovinomyces biocellatus</i> on Common Sage (<i>Salvia officinalis</i>) in Slovenia. <i>Plant Disease</i> , 2012, 96, 1065-1065.	1.4	3
83	On the Identity of Cereal Aphid Parasitoid Wasps <i>Aphidius uzbekistanicus</i> , <i>Aphidius rhopalosiphii</i> , and <i>Aphidius avenaphis</i> (Hymenoptera: Braconidae: Aphidiinae) by Examination of COI Mitochondrial Gene, Geometric Morphometrics, and Morphology. <i>Annals of the Entomological Society of America</i> , 2011, 104, 1221-1232.	2.5	30
84	Development of transcript-associated microsatellite markers for diversity and linkage mapping studies in hop (<i>Humulus lupulus</i> L.). <i>Molecular Breeding</i> , 2011, 28, 227-239.	2.1	15
85	High-throughput genotyping of hop (<i>Humulus lupulus</i> L.) utilising diversity arrays technology (DArT). <i>Theoretical and Applied Genetics</i> , 2011, 122, 1265-1280.	3.6	30
86	New microsatellite markers for <i>Salvia officinalis</i> (Lamiaceae) and cross-amplification in closely related species. <i>American Journal of Botany</i> , 2011, 98, e316-8.	1.7	32
87	Fluorescent AFLP fingerprinting of <i>Monilinia fructicola</i> . <i>Journal of Plant Diseases and Protection</i> , 2010, 117, 168-172.	2.9	8
88	Origins of <i>Allium ampeloprasum</i> horticultural groups and a molecular phylogeny of the section <i>Allium</i> (<i>Allium</i> : Alliaceae). <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 488-497.	2.7	64
89	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2009–30 November 2009. <i>Molecular Ecology Resources</i> , 2010, 10, 404-408.	4.8	84
90	Identification of QTLs for alpha acid content and yield in hop (<i>Humulus Lupulus</i> L.). <i>Euphytica</i> , 2009, 170, 141-154.	1.2	17

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91	Occurrence of <i>Cercospora cantuariensis</i> on hop in Austria and Slovenia. <i>Plant Pathology</i> , 2009, 58, 400-400.	2.4	4
92	Identification of a phytoplasma from the aster yellows group infecting purple coneflower (<i>Echinacea purpurea</i>) in Slovenia. <i>Plant Pathology</i> , 2009, 58, 392-392.	2.4	8
93	Isolation and sequence analysis of NBS-LRR disease resistance gene analogues from hop <i>Humulus lupulus</i> L.. <i>Plant Science</i> , 2009, 176, 775-782.	3.6	12
94	Densitometric DNA analysis in agarose electrophoretic gels. <i>Journal of Planar Chromatography - Modern TLC</i> , 2009, 22, 167-170.	1.2	3
95	Trinucleotide microsatellite repeat is tightly linked to male sex in hop (<i>Humulus lupulus</i> L.). <i>Molecular Breeding</i> , 2008, 21, 139-148.	2.1	29
96	The oldest macroremains of <i>Vitis</i> from Slovenia. <i>Vegetation History and Archaeobotany</i> , 2008, 17, 93-102.	2.1	8
97	Pilot sequencing of onion genomic DNA reveals fragments of transposable elements, low gene densities, and significant gene enrichment after methyl filtration. <i>Molecular Genetics and Genomics</i> , 2008, 280, 287-92.	2.1	48
98	First report of <i>Phoma exigua</i> as a pathogen of hop in Slovenia. <i>Plant Pathology</i> , 2008, 57, 381-381.	2.4	3
99	DNA fingerprinting of olive varieties in Istria (Croatia) by microsatellite markers. <i>Scientia Horticulturae</i> , 2008, 115, 223-230.	3.6	52
100	New polymorphic dinucleotide and trinucleotide microsatellite loci for hop <i>Humulus lupulus</i> L.. <i>Molecular Ecology Resources</i> , 2008, 8, 769-772.	4.8	18
101	AFLP Analysis of Intraspecific Variation Between <i>Monilinia laxa</i> Isolates from Different Hosts. <i>Plant Disease</i> , 2008, 92, 1616-1624.	1.4	27
102	Segregations for Onion Bulb Colors Reveal That Red Is Controlled by at Least Three Loci. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 42-47.	1.0	34
103	Production and genetic evaluation of interspecific hybrids within the genus <i>Sambucus</i> . <i>Plant Breeding</i> , 2007, 126, 628-633.	1.9	20
104	Development of microsatellite markers in the common fig, <i>Ficus carica</i> L.. <i>Molecular Ecology Notes</i> , 2007, 7, 1311-1314.	1.7	28
105	Genetic mapping of sulfur assimilation genes reveals a QTL for onion bulb pungency. <i>Theoretical and Applied Genetics</i> , 2007, 114, 815-822.	3.6	57
106	Microsatellite Marker for Homozygosity Testing of Putative Doubled Haploids and Characterization of <i>Mimulus</i> Species Derived by a Cross-genera Approach. <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 659-663.	1.0	8
107	Genetic variability and virulence among <i>Verticillium albo-atrum</i> isolates from hop. <i>European Journal of Plant Pathology</i> , 2006, 116, 301-314.	1.7	44
108	Comparative sequence and genetic analyses of asparagus BACs reveal no microsynteny with onion or rice. <i>Theoretical and Applied Genetics</i> , 2006, 114, 31-39.	3.6	13

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109	Genetic mapping of expressed sequences in onion and in silico comparisons with rice show scant colinearity. <i>Molecular Genetics and Genomics</i> , 2005, 274, 197-204.	2.1	110
110	The isolation and characterisation of microsatellites in hop (<i>Humulus lupulus</i> L.). <i>Plant Science</i> , 2005, 168, 213-221.	3.6	49
111	Single Nucleotide Polymorphisms, Indels, and Simple Sequence Repeats for Onion Cultivar Identification. <i>Journal of the American Society for Horticultural Science</i> , 2005, 130, 912-917.	1.0	50
112	Identification and Differentiation of Hop Varieties Using Simple Sequence Repeat Markers. <i>Journal of the American Society of Brewing Chemists</i> , 2004, 62, 1-7.	1.1	20
113	Assessment of genetic variability of olive varieties by microsatellite and AFLP markers. <i>Euphytica</i> , 2004, 136, 93-102.	1.2	79
114	Microsatellite variability among wild and cultivated hops (<i>Humulus lupulus</i> L.). <i>Genome</i> , 2004, 47, 889-899.	2.0	38
115	Development of Pathotype-Specific SCAR Markers for Detection of <i>Verticillium albo-atrum</i> Isolates from Hop. <i>Plant Disease</i> , 2004, 88, 1115-1122.	1.4	32
116	Characterization of <i>Verticillium albo-atrum</i> Field Isolates Using Pathogenicity Data and AFLP Analysis. <i>Plant Disease</i> , 2003, 87, 633-638.	1.4	44
117	Eleven new microsatellites for hop (<i>Humulus lupulus</i> L.). <i>Molecular Ecology Notes</i> , 2002, 2, 544-546.	1.7	36
118	High throughput isolation of microsatellites in hop (<i>Humulus lupulus</i> L.). <i>Plant Molecular Biology Reporter</i> , 2001, 19, 217-226.	1.8	20
119	Assessment of genetic variation and differentiation of hop genotypes by microsatellite and AFLP markers. <i>Genome</i> , 2001, 44, 773-782.	2.0	68