

Sithichoke Tangphatsornruang

List of Publications by Year in descending order

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116
papers

3,683
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126708

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155451

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g-index

116
all docs

116
docs citations

116
times ranked

4442
citing authors

#	ARTICLE	IF	CITATIONS
1	Rice height QTLs in KDML105 chromosome segment substitution lines. <i>Genomics</i> , 2022, 114, 482-487.	1.3	7
2	Genetic diversity of the dengue virus population in dengue fever and dengue hemorrhagic fever patients. <i>Asian Pacific Journal of Allergy and Immunology</i> , 2022, , .	0.2	1
3	A chromosome-scale reference genome assembly of yellow mangrove (<i>Bruguiera parviflora</i>) reveals a whole genome duplication event associated with the Rhizophoraceae lineage. <i>Molecular Ecology Resources</i> , 2022, 22, 1939-1953.	2.2	13
4	A <i>de novo</i> reference assembly of the yellow mangrove <i>Ceriops zippeliana</i> genome. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
5	De Novo Reference Assembly of the Upriver Orange Mangrove (<i>Bruguiera sexangula</i>) Genome. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	8
6	Comparative Analysis and Phylogenetic Relationships of <i>Ceriops</i> Species (Rhizophoraceae) and <i>Avicennia lanata</i> (Acanthaceae): Insight into the Chloroplast Genome Evolution between Middle and Seaward Zones of Mangrove Forests. <i>Biology</i> , 2022, 11, 383.	1.3	10
7	The First Genetic Linkage Map of Winged Bean [<i>Psophocarpus tetragonolobus</i> (L.) DC.] and QTL Mapping for Flower-, Pod-, and Seed-Related Traits. <i>Plants</i> , 2022, 11, 500.	1.6	5
8	A SNP variation in an expansin (<i>EgExp4</i>) gene affects height in oil palm. <i>PeerJ</i> , 2022, 10, e13046.	0.9	4
9	Quantitative analysis of methoxyflavones discriminates between the two types of <i>Kaempferia parviflora</i> . <i>Phytochemical Analysis</i> , 2022, 33, 670-677.	1.2	3
10	The Fungus <i>Metarhizium</i> sp. BCC 4849 Is an Effective and Safe Mycoinsecticide for the Management of Spider Mites and Other Insect Pests. <i>Insects</i> , 2022, 13, 42.	1.0	5
11	Assembly of a hybrid mangrove, <i>Bruguiera hainesii</i> , and its two ancestral contributors, <i>Bruguiera cylindrica</i> and <i>Bruguiera gymnorhiza</i> . <i>Genomics</i> , 2022, 114, 110382.	1.3	5
12	The complete mitochondrial genome sequence of the karst-dwelling crab, <i>Terrapoton thungwa</i> (Crustacea: Brachyura: Potamidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 769-771.	0.2	1
13	Chromosome-level genome assembly of Indian mangrove (<i>Ceriops tagal</i>) revealed a genome-wide duplication event predating the divergence of Rhizophoraceae mangrove species. <i>Plant Genome</i> , 2022, 15, .	1.6	8
14	A chromosome-scale assembly of the black gram (<i>Vigna mungo</i>) genome. <i>Molecular Ecology Resources</i> , 2021, 21, 238-250.	2.2	33
15	De novo assemblies of <i>Luffa acutangula</i> and <i>Luffa cylindrica</i> genomes reveal an expansion associated with substantial accumulation of transposable elements. <i>Molecular Ecology Resources</i> , 2021, 21, 212-225.	2.2	23
16	Candidate gene association of gene expression data in sugarcane contrasting for sucrose content. <i>Genomics</i> , 2021, 113, 229-237.	1.3	9
17	Nanopore sequencing in agricultural and food applications. , 2021, , 443-459.		2
18	The complete mitochondrial genome sequence of the mountain crab <i>Indochinamon bhumibol</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 634-635.	0.2	1

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19	Multi-scale comparative transcriptome analysis reveals key genes and metabolic reprogramming processes associated with oil palm fruit abscission. <i>BMC Plant Biology</i> , 2021, 21, 92.	1.6	5
20	Metagenomics of Antimicrobial and Heavy Metal Resistance in the Cecal Microbiome of Fattening Pigs Raised without Antibiotics. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	15
21	De novo chromosome-level assembly of the <i>Centella asiatica</i> genome. <i>Genomics</i> , 2021, 113, 2221-2228.	1.3	14
22	Taxonomic profiling of Symbiodiniaceae and bacterial communities associated with Indo-Pacific corals in the Gulf of Thailand using PacBio sequencing of full-length ITS and 16S rRNA genes. <i>Genomics</i> , 2021, 113, 2717-2729.	1.3	14
23	Identification of Candidate Gene-Based Markers for Girth Growth in Rubber Trees. <i>Plants</i> , 2021, 10, 1440.	1.6	3
24	Complete chloroplast genome sequences of five <i>Bruguiera</i> species (Rhizophoraceae): comparative analysis and phylogenetic relationships. <i>PeerJ</i> , 2021, 9, e12268.	0.9	13
25	De novo Assembly of the Brain Coral <i>Platygyra sinensis</i> Genome. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
26	Iron homeostasis in the absence of ferricrocin and its consequences in fungal development and insect virulence in <i>Beauveria bassiana</i> . <i>Scientific Reports</i> , 2021, 11, 19624.	1.6	4
27	Establishment of Human-Induced Pluripotent Stem Cell-Derived Neurons – A Promising In Vitro Model for a Molecular Study of Rabies Virus and Host Interaction. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11986.	1.8	8
28	Transcriptome sequencing revealed the influence of blue light on the expression levels of light-stress response genes in <i>Centella asiatica</i> . <i>PLoS ONE</i> , 2021, 16, e0260468.	1.1	6
29	The Genome and Transcriptome Analysis of the <i>Vigna mungo</i> Chloroplast. <i>Plants</i> , 2020, 9, 1247.	1.6	6
30	Assembly of the durian chloroplast genome using long PacBio reads. <i>Scientific Reports</i> , 2020, 10, 15980.	1.6	12
31	Chloroplast genome data of <i>Luffa acutangula</i> and <i>Luffa aegyptiaca</i> and their phylogenetic relationships. <i>Data in Brief</i> , 2020, 33, 106470.	0.5	5
32	The complete mitochondrial genome of <i>Luffa acutangula</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3208-3209.	0.2	2
33	High Quality <i>Aspergillus aculeatus</i> Genomes and Transcriptomes: A Platform for Cellulase Activity Optimization Toward Industrial Applications. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 607176.	2.0	4
34	The BPM 24 Rubber Tree Genome, Organellar Genomes and Synteny Within the Family Euphorbiaceae. <i>Compendium of Plant Genomes</i> , 2020, , 55-66.	0.3	3
35	Development of Molecular Markers in <i>Hevea brasiliensis</i> for Marker-Assisted Breeding. <i>Compendium of Plant Genomes</i> , 2020, , 67-79.	0.3	7
36	Differential expression between drought-tolerant and drought-sensitive sugarcane under mild and moderate water stress as revealed by a comparative analysis of leaf transcriptome. <i>PeerJ</i> , 2020, 8, e9608.	0.9	22

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37	Genome-wide association mapping of virulence gene in rice blast fungus <i>Magnaporthe oryzae</i> using a genotyping by sequencing approach. <i>Genomics</i> , 2019, 111, 661-668.	1.3	25
38	Shotgun metagenomic sequencing from Manao-Pee cave, Thailand, reveals insight into the microbial community structure and its metabolic potential. <i>BMC Microbiology</i> , 2019, 19, 144.	1.3	49
39	Heat-induced shift in coral microbiome reveals several members of the Rhodobacteraceae family as indicator species for thermal stress in <i>Porites lutea</i> . <i>MicrobiologyOpen</i> , 2019, 8, e935.	1.2	76
40	Unraveling vascular development-related genes in laticifer-containing tissue of rubber tree by high-throughput transcriptome sequencing. <i>Current Plant Biology</i> , 2019, 19, 100112.	2.3	9
41	Complete Genome Sequences of Four Serotypes of Dengue Virus Prototype Continuously Maintained in the Laboratory. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
42	Dynamics of biogenic amines and bacterial communities in a Thai fermented pork product Nham. <i>Food Research International</i> , 2019, 119, 110-118.	2.9	32
43	Comparative analysis of bacterial communities associated with healthy and diseased corals in the Indonesian sea. <i>PeerJ</i> , 2019, 7, e8137.	0.9	17
44	Bacterial Diversity and Phylogenetic Analysis of Type II Polyketide Synthase Gene from Manao-Pee Cave, Thailand. <i>Geomicrobiology Journal</i> , 2018, 35, 518-527.	1.0	8
45	Dynamics of coral-associated microbiomes during a thermal bleaching event. <i>MicrobiologyOpen</i> , 2018, 7, e00604.	1.2	41
46	Probing the Phylogenomics and Putative Pathogenicity Genes of <i>Pythium insidiosum</i> by Oomycete Genome Analyses. <i>Scientific Reports</i> , 2018, 8, 4135.	1.6	35
47	Transcriptome-based discovery of pathways and genes related to reproduction of the black tiger shrimp (<i>Penaeus monodon</i>). <i>Marine Genomics</i> , 2018, 37, 69-73.	0.4	31
48	Structural and metabolic adaptation of cellulolytic microcosm in co-digested Napier grass-swine manure and its application in enhancing thermophilic biogas production. <i>RSC Advances</i> , 2018, 8, 29806-29815.	1.7	10
49	Development of a Novel Reference Transcriptome for Scleractinian Coral <i>Porites lutea</i> Using Single-Molecule Long-Read Isoform Sequencing (Iso-Seq). <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	7
50	Characterization of cellulolytic microbial consortium enriched on Napier grass using metagenomic approaches. <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 439-447.	1.1	33
51	Uncovering full-length transcript isoforms of sugarcane cultivar Khon Kaen 3 using single-molecule long-read sequencing. <i>PeerJ</i> , 2018, 6, e5818.	0.9	21
52	Transcriptome analysis of oil palm inflorescences revealed candidate genes for an auxin signaling pathway involved in parthenocarpy. <i>PeerJ</i> , 2018, 6, e5975.	0.9	7
53	Effect of freeze-thaw process on physical properties, microbial activities and population structures of anaerobic sludge. <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 474-481.	1.1	22
54	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in <i>Hevea</i> species. <i>Scientific Reports</i> , 2017, 7, 41457.	1.6	95

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55	Targeted disruption of the polyketide synthase gene <i>pks15</i> affects virulence against insects and phagocytic survival in the fungus <i>Beauveria bassiana</i> . <i>Fungal Biology</i> , 2017, 121, 664-675.	1.1	18
56	Genome-wide association mapping of latex yield and girth in Amazonian accessions of <i>Hevea brasiliensis</i> grown in a suboptimal climate zone. <i>Genomics</i> , 2017, 109, 475-484.	1.3	30
57	Brown rice and retrograded brown rice alleviate inflammatory response in dextran sulfate sodium (DSS)-induced colitis mice. <i>Food and Function</i> , 2017, 8, 4630-4643.	2.1	30
58	High resolution profiling of coral-associated bacterial communities using full-length 16S rRNA sequence data from PacBio SMRT sequencing system. <i>Scientific Reports</i> , 2017, 7, 2774.	1.6	106
59	Microbial communities in the reef water at Kham Island, lower Gulf of Thailand. <i>PeerJ</i> , 2017, 5, e3625.	0.9	9
60	The two chromosomes of the mitochondrial genome of a sugarcane cultivar: assembly and recombination analysis using long PacBio reads. <i>Scientific Reports</i> , 2016, 6, 31533.	1.6	55
61	A phenotypic test for delay of abscission and non-abscission oil palm fruit and validation by abscission marker gene expression analysis. <i>Acta Horticulturae</i> , 2016, , 97-104.	0.1	7
62	Effects of methylation-sensitive enzymes on the enrichment of genic SNPs and the degree of genome complexity reduction in a two-enzyme genotyping-by-sequencing (GBS) approach: a case study in oil palm (<i>Elaeis guineensis</i>). <i>Molecular Breeding</i> , 2016, 36, 154.	1.0	35
63	Differentially expressed transcripts in stomach of <i>Penaeus monodon</i> in response to AHPND infection. <i>Developmental and Comparative Immunology</i> , 2016, 65, 53-63.	1.0	54
64	Comparative Study of Bacterial Communities in <i>Nepenthes</i> Pitchers and Their Correlation to Species and Fluid Acidity. <i>Microbial Ecology</i> , 2016, 72, 381-393.	1.4	13
65	Plasmid metagenomics reveals multiple antibiotic resistance gene classes among the gut microbiomes of hospitalised patients. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 6, 57-66.	0.9	13
66	De novo Transcriptome Analysis of Apical Meristem of <i>Jatropha</i> spp. Using 454 Pyrosequencing Platform, and Identification of SNP and EST-SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 786-793.	1.0	9
67	Isolation of cellulolytic microcosms from bagasse compost in co-digested fibrous substrates. <i>Biomass Conversion and Biorefinery</i> , 2016, 6, 421-426.	2.9	2
68	ACC oxidase and miRNA 159a, and their involvement in fresh fruit bunch yield (FFB) via sex ratio determination in oil palm. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1243-1257.	1.0	7
69	Comparative mitochondrial genome analysis of <i>Pythium insidiosum</i> and related oomycete species provides new insights into genetic variation and phylogenetic relationships. <i>Gene</i> , 2016, 575, 34-41.	1.0	11
70	Draft Genome Sequence of the Pathogenic Oomycete <i>Pythium insidiosum</i> Strain Pi-S, Isolated from a Patient with Pythiosis. <i>Genome Announcements</i> , 2015, 3, .	0.8	47
71	Insights from the genome of <i>Ophiocordyceps polyrhachis-furcata</i> to pathogenicity and host specificity in insect fungi. <i>BMC Genomics</i> , 2015, 16, 881.	1.2	34
72	The AKR gene family and modifying sex ratios in palms through abiotic stress responsiveness. <i>Functional and Integrative Genomics</i> , 2015, 15, 349-362.	1.4	5

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73	Genome-wide SNP discovery and identification of QTL associated with agronomic traits in oil palm using genotyping-by-sequencing (GBS). <i>Genomics</i> , 2015, 105, 288-295.	1.3	132
74	Construction of a high-density integrated genetic linkage map of rubber tree (<i>Hevea brasiliensis</i>) using genotyping-by-sequencing (GBS). <i>Frontiers in Plant Science</i> , 2015, 6, 367.	1.7	102
75	A single base substitution in BADH/AMADH is responsible for fragrance in cucumber (<i>Cucumis sativus</i>) Tj ETQq1 1881-1892.	0.784314 1.8	rgBT /Ov 38
76	Comparative analysis of sugarcane bagasse metagenome reveals unique and conserved biomass-degrading enzymes among lignocellulolytic microbial communities. <i>Biotechnology for Biofuels</i> , 2015, 8, 16.	6.2	92
77	SNP Identification from RNA Sequencing and Linkage Map Construction of Rubber Tree for Anchoring the Draft Genome. <i>PLoS ONE</i> , 2015, 10, e0121961.	1.1	44
78	Survey of Microbial Diversity in Flood Areas during Thailand 2011 Flood Crisis Using High-Throughput Tagged Amplicon Pyrosequencing. <i>PLoS ONE</i> , 2015, 10, e0128043.	1.1	20
79	Elucidation of the molecular responses to waterlogging in <i>Jatropha</i> roots by transcriptome profiling. <i>Frontiers in Plant Science</i> , 2014, 5, 658.	1.7	51
80	Structural and functional diversity of free-living microorganisms in reef surface, Kra island, Thailand. <i>BMC Genomics</i> , 2014, 15, 607.	1.2	25
81	Transcriptome analysis reveals pathogenicity and evolutionary history of the pathogenic oomycete <i>Pythium insidiosum</i> . <i>Fungal Biology</i> , 2014, 118, 640-653.	1.1	38
82	Assembly and analysis of a male sterile rubber tree mitochondrial genome reveals DNA rearrangement events and a novel transcript. <i>BMC Plant Biology</i> , 2014, 14, 45.	1.6	53
83	Oil palm (<i>Elaeis guineensis</i> Jacq.) linkage map, and quantitative trait locus analysis for sex ratio and related traits. <i>Molecular Breeding</i> , 2014, 33, 415-424.	1.0	29
84	Characterization of rubber tree microRNA in phytohormone response using large genomic DNA libraries, promoter sequence and gene expression analysis. <i>Molecular Genetics and Genomics</i> , 2014, 289, 921-933.	1.0	12
85	Quantitative trait loci and candidate genes associated with starch pasting viscosity characteristics in cassava (<i>Manihot esculenta</i> Crantz). <i>Plant Biology</i> , 2014, 16, 197-207.	1.8	21
86	Microbial Ecology of Thailand Tsunami and Non-Tsunami Affected Terrestrials. <i>PLoS ONE</i> , 2014, 9, e94236.	1.1	19
87	Large-Scale SNP Discovery through RNA Sequencing and SNP Genotyping by Targeted Enrichment Sequencing in Cassava (<i>Manihot esculenta</i> Crantz). <i>PLoS ONE</i> , 2014, 9, e116028.	1.1	58
88	Determination of the Half-Life of Chloroplast Transcripts in Tobacco Leaves. <i>Methods in Molecular Biology</i> , 2014, 1132, 221-234.	0.4	0
89	Phylogenetic Analysis and Metabolic Potential of Microbial Communities in an Industrial Bagasse Collection Site. <i>Microbial Ecology</i> , 2013, 66, 322-334.	1.4	24
90	Comparative metagenomic analysis of microcosm structures and lignocellulolytic enzyme systems of symbiotic biomass-degrading consortia. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8941-8954.	1.7	59

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91	Comparative Analysis of Microbial Profiles in Cow Rumen Fed with Different Dietary Fiber by Tagged 16S rRNA Gene Pyrosequencing. <i>Current Microbiology</i> , 2013, 67, 130-137.	1.0	184
92	Gene discovery and functional marker development for fragrance in sorghum (<i>Sorghum bicolor</i> (L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	36
93	Development and characterization of single nucleotide polymorphism markers from 454 transcriptome sequences in oil palm (<i>Elaeis guineensis</i>). <i>Plant Breeding</i> , 2013, 132, 711-717.	1.0	12
94	Transcriptome analysis of normal and mantled developing oil palm flower and fruit. <i>Genomics</i> , 2013, 101, 306-312.	1.3	36
95	Bacterial Population in Intestines of the Black Tiger Shrimp (<i>Penaeus monodon</i>) under Different Growth Stages. <i>PLoS ONE</i> , 2013, 8, e60802.	1.1	130
96	Transcriptome Assembly and Expression Data from Normal and Mantled Oil Palm Fruit. <i>Dataset Papers in Biology</i> , 2013, 2013, 1-7.	0.5	4
97	Draft genome sequence of <i>Arthrospira platensis</i> C1 (PCC9438). <i>Standards in Genomic Sciences</i> , 2012, 6, 43-53.	1.5	47
98	Characterization of the chloroplast genome sequence of oil palm (<i>Elaeis guineensis</i> Jacq.). <i>Gene</i> , 2012, 500, 172-180.	1.0	48
99	Feasibility of using 454 pyrosequencing for studying quasispecies of the whole dengue viral genome. <i>BMC Genomics</i> , 2012, 13, S7.	1.2	15
100	Metagenomic profiles of free-living archaea, bacteria and small eukaryotes in coastal areas of Sichang island, Thailand. <i>BMC Genomics</i> , 2012, 13, S29.	1.2	47
101	Development of genomic-derived simple sequence repeat markers in <i>Hevea brasiliensis</i> from 454 genome shotgun sequences. <i>Plant Breeding</i> , 2012, 131, 555-562.	1.0	13
102	Sequencing and analysis of three plasmids from <i>Lactobacillus casei</i> TISTR1341 and development of plasmid-derived <i>Escherichia coli</i> L. casei shuttle vectors. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 261-272.	1.7	15
103	Characterization of the complete chloroplast genome of <i>Hevea brasiliensis</i> reveals genome rearrangement, RNA editing sites and phylogenetic relationships. <i>Gene</i> , 2011, 475, 104-112.	1.0	92
104	The effect of different 3' untranslated regions on the accumulation and stability of transcripts of a <i>gfp</i> transgene in chloroplasts of transplastomic tobacco. <i>Plant Molecular Biology</i> , 2011, 76, 385-396.	2.0	32
105	Construction of a genetic linkage map using simple sequence repeat markers from expressed sequence tags for cassava (<i>Manihot esculenta</i> Crantz). <i>Molecular Breeding</i> , 2011, 27, 67-75.	1.0	32
106	SSR and EST-SSR-based genetic linkage map of cassava (<i>Manihot esculenta</i> Crantz). <i>Theoretical and Applied Genetics</i> , 2011, 122, 1161-1170.	1.8	70
107	Insights into the Phylogeny and Metabolic Potential of a Primary Tropical Peat Swamp Forest Microbial Community by Metagenomic Analysis. <i>Microbial Ecology</i> , 2011, 61, 518-528.	1.4	136
108	A genome scan for quantitative trait loci affecting cyanogenic potential of cassava root in an outbred population. <i>BMC Genomics</i> , 2011, 12, 266.	1.2	40

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109	Transcriptome Sequencing of <i>Hevea brasiliensis</i> for Development of Microsatellite Markers and Construction of a Genetic Linkage Map. <i>DNA Research</i> , 2011, 18, 471-482.	1.5	117
110	Single nucleotide polymorphism marker development in the rubber tree, <i>Hevea brasiliensis</i> (Euphorbiaceae). <i>American Journal of Botany</i> , 2011, 98, e337-8.	0.8	39
111	Genetic linkage map of cassava (<i>Manihot esculenta</i> Crantz) based on AFLP and SSR markers. <i>Plant Breeding</i> , 2010, 129, 112-115.	1.0	38
112	The Chloroplast Genome Sequence of Mungbean (<i>Vigna radiata</i>) Determined by High-throughput Pyrosequencing: Structural Organization and Phylogenetic Relationships. <i>DNA Research</i> , 2010, 17, 11-22.	1.5	198
113	Characterization of microsatellites and gene contents from genome shotgun sequences of mungbean (<i>Vigna radiata</i> (L.) Wilczek). <i>BMC Plant Biology</i> , 2009, 9, 137.	1.6	128
114	Development of polymorphic markers from expressed sequence tags of <i>Manihot esculenta</i> Crantz. <i>Molecular Ecology Resources</i> , 2008, 8, 682-685.	2.2	24
115	Development of simple sequence repeat markers from expressed sequence tags of the black tiger shrimp (<i>Penaeus monodon</i>). <i>Molecular Ecology Resources</i> , 2008, 8, 1494-1496.	2.2	2
116	Isolation and characterization of an α -amylase gene in cassava (<i>Manihot esculenta</i>). <i>Plant Physiology and Biochemistry</i> , 2005, 43, 821-827.	2.8	31