

Genlou Sun

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1985644/publications.pdf>

Version: 2024-02-01

72
papers

1,208
citations

361413

20
h-index

454955

30
g-index

72
all docs

72
docs citations

72
times ranked

1046
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular prospective on the wheat grain development. <i>Critical Reviews in Biotechnology</i> , 2023, 43, 38-49.	9.0	5
2	Transcriptome and Metabolite Insights into Domestication Process of Cultivated Barley in China. <i>Plants</i> , 2022, 11, 209.	3.5	3
3	N6-Methyladenosine dynamic changes and differential methylation in wheat grain development. <i>Planta</i> , 2022, 255, 125.	3.2	2
4	MiR396 regulatory network and its expression during grain development in wheat. <i>Protoplasma</i> , 2021, 258, 103-113.	2.1	17
5	Molecular regulatory mechanisms underlying the adaptability of polyploid plants. <i>Biological Reviews</i> , 2021, 96, 394-407.	10.4	16
6	Origins and chromosome differentiation of <i>Thinopyrum elongatum</i> revealed by <i>PepC</i> and <i>Pgk1</i> genes and ND-FISH. <i>Genome</i> , 2021, 64, 901-913.	2.0	6
7	Genome-Wide Identification of <i>Triticum aestivum</i> Xylanase Inhibitor Gene Family and Inhibitory Effects of XI-2 Subfamily Proteins on <i>Fusarium graminearum</i> GH11 Xylanase. <i>Frontiers in Plant Science</i> , 2021, 12, 665501.	3.6	2
8	Cloning, expression analysis and molecular marker development of cinnamyl alcohol dehydrogenase gene in common wheat. <i>Protoplasma</i> , 2021, 258, 881-889.	2.1	7
9	MicroRNA-mediated responses to colchicine treatment in barley. <i>Planta</i> , 2020, 251, 44.	3.2	4
10	Demographic history and genetic differentiation of an endemic and endangered <i>Ulmus lamellosa</i> (<i>Ulmus</i>). <i>BMC Plant Biology</i> , 2020, 20, 526.	3.6	7
11	Physiological and transcriptional response to heat stress in heat-resistant and heat-sensitive maize (<i>Zea mays</i> L.) inbred lines at seedling stage. <i>Protoplasma</i> , 2020, 257, 1615-1637.	2.1	19
12	Population genetic variation characterization of the boreal tree <i>Acer ginnala</i> in Northern China. <i>Scientific Reports</i> , 2020, 10, 13515.	3.3	1
13	Phylogenetic analysis of two single-copy nuclear genes revealed origin of tetraploid barley <i>Hordeum marinum</i> . <i>PLoS ONE</i> , 2020, 15, e0235475.	2.5	2
14	Insights into the N ⁶ -methyladenosine mechanism and its functionality: progress and questions. <i>Critical Reviews in Biotechnology</i> , 2020, 40, 639-652.	9.0	15
15	Nucleotide diversity patterns at the DREB1 transcriptional factor gene in the genome donor species of wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2019, 14, e0217081.	2.5	2
16	Evolutionary mechanism of genome duplication enhancing natural autotetraploid sea barley adaptability to drought stress. <i>Environmental and Experimental Botany</i> , 2019, 159, 44-54.	4.2	12
17	Genome constitution and evolution of <i>Elytrigia lolioides</i> inferred from <i>Acc1</i> , <i>EF-G</i> , <i>ITS</i> , <i>TrnL-F</i> sequences and <i>GISH</i> . <i>BMC Plant Biology</i> , 2019, 19, 158.	3.6	6
18	Identification of QTL underlying the leaf length and area of different leaves in barley. <i>Scientific Reports</i> , 2019, 9, 4431.	3.3	18

#	ARTICLE	IF	CITATIONS
19	Transcriptome and miRNAs analyses enhance our understanding of the evolutionary advantages of polyploidy. <i>Critical Reviews in Biotechnology</i> , 2019, 39, 173-180.	9.0	12
20	Phylogenetic analysis of two single-copy nuclear genes revealed origin and complex relationships of polyploid species of <i>Hordeum</i> in Triticeae (Poaceae). <i>Genome</i> , 2017, 60, 518-529.	2.0	1
21	micro<scp>RNA</scp>s contribute to enhanced salt adaptation of the autopolyploid <i>Hordeum bulbosum</i> compared with its diploid ancestor. <i>Plant Journal</i> , 2017, 91, 57-69.	5.7	44
22	Detection of QTLs for seedling characteristics in barley (<i>Hordeum vulgare</i> L.) grown under hydroponic culture condition. <i>BMC Genetics</i> , 2017, 18, 94.	2.7	18
23	Transcriptome analysis reveals plant response to colchicine treatment during on chromosome doubling. <i>Scientific Reports</i> , 2017, 7, 8503.	3.3	17
24	QTL underlying some agronomic traits in barley detected by SNP markers. <i>BMC Genetics</i> , 2016, 17, 103.	2.7	46
25	Molecular evidence of RNA polymerase II gene reveals the origin of worldwide cultivated barley. <i>Scientific Reports</i> , 2016, 6, 36122.	3.3	9
26	Molecular evolution of <i>Wcor15</i> gene enhanced our understanding of the origin of A, B and D genomes in <i>Triticum aestivum</i> . <i>Scientific Reports</i> , 2016, 6, 31706.	3.3	4
27	Comparison of gene flow among species that occur within the same geographic locations versus gene flow among populations within species reveals introgression among several <i>Elymus</i> species. <i>Journal of Systematics and Evolution</i> , 2016, 54, 152-161.	3.1	3
28	Origin and Evolution of Allopolyploid Wheatgrass <i>Elymus fibrosus</i> (Schrenk) Tzvelev (Poaceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38	2.5	5
29	Genetic Divergence in Domesticated and Non-Domesticated Gene Regions of Barley Chromosomes. <i>PLoS ONE</i> , 2015, 10, e0121106.	2.5	6
30	Origin and Reticulate Evolutionary Process of Wheatgrass <i>Elymus trachycaulus</i> (Triticeae: Poaceae). <i>PLoS ONE</i> , 2015, 10, e0125417.	2.5	3
31	Identification of a Novel Allele of <i>TaCKX6a02</i> Associated with Grain Size, Filling Rate and Weight of Common Wheat. <i>PLoS ONE</i> , 2015, 10, e0144765.	2.5	38
32	Copy Number Variation of Cytokinin Oxidase Gene <i>Tackx4</i> Associated with Grain Weight and Chlorophyll Content of Flag Leaf in Common Wheat. <i>PLoS ONE</i> , 2015, 10, e0145970.	2.5	57
33	Origin of worldwide cultivated barley revealed by <i>NAM-1</i> gene and grain protein content. <i>Frontiers in Plant Science</i> , 2015, 6, 803.	3.6	28
34	Molecular phylogeny revealed distinct origin of the Y and St genome in <i>Elymus longearistatus</i> (Triticeae: Poaceae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 141-149.	2.7	8
35	Identification of QTL underlying physiological and morphological traits of flag leaf in barley. <i>BMC Genetics</i> , 2015, 16, 29.	2.7	43
36	Phylogenetic analysis of the genus <i>Pseudoroegneria</i> and the Triticeae tribe using the <i>rbcl</i> gene. <i>Biochemical Systematics and Ecology</i> , 2015, 62, 73-81.	1.3	9

#	ARTICLE	IF	CITATIONS
37	Cloning and Characterization of Low-Molecular-Weight Glutenin Subunit Alleles from Chinese Wheat Landraces (<i>Triticum aestivum</i>). <i>Scientific World Journal</i> , The, 2014, 2014, 1-6.	2.1	4
38	Nuclear and chloroplast DNA phylogeny reveals complex evolutionary history of <i>Elymus pendulinus</i> . <i>Genome</i> , 2014, 57, 97-109.	2.0	6
39	Effects of nitrogen spraying on the post-anthesis stage of winter wheat under waterlogging stress. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 207-216.	2.1	33
40	Molecular phylogeny revealed complex evolutionary process in <i>Elymus</i> species. <i>Journal of Systematics and Evolution</i> , 2014, 52, 706-711.	3.1	16
41	Molecular evolution and nucleotide diversity of nuclear plastid phosphoglycerate kinase (PGK) gene in Triticeae (Poaceae). <i>Gene</i> , 2014, 533, 142-148.	2.2	11
42	Comparison of Acetyl-CoA carboxylase 1 (Acc-1) gene diversity among different Triticeae genomes. <i>Gene</i> , 2014, 546, 11-15.	2.2	2
43	Identification of active VQ motif-containing genes and the expression patterns under low nitrogen treatment in soybean. <i>Gene</i> , 2014, 543, 237-243.	2.2	40
44	A Comprehensive Analysis of the Cupin Gene Family in Soybean (<i>Glycine max</i>). <i>PLoS ONE</i> , 2014, 9, e110092.	2.5	20
45	Phylogenetic analysis revealed reticulate evolution of allotetraploid <i>Elymus ciliaris</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 805-813.	2.7	9
46	Tibet as a Potential Domestication Center of Cultivated Barley of China. <i>PLoS ONE</i> , 2013, 8, e62700.	2.5	30
47	Multiple origins of allopolyploid wheatgrass <i>Elymus caninus</i> revealed by RPB2, PepC and TrnD/T genes. <i>Molecular Phylogenetics and Evolution</i> , 2012, 64, 441-451.	2.7	23
48	Untangling Nucleotide Diversity and Evolution of the H Genome in Polyploid <i>Hordeum</i> and <i>Elymus</i> Species Based on the Single Copy of Nuclear Gene DMC1. <i>PLoS ONE</i> , 2012, 7, e50369.	2.5	9
49	Molecular phylogeny of diploid <i>Hordeum</i> species and incongruence between chloroplast and nuclear datasets. <i>Genome</i> , 2011, 54, 986-992.	2.0	7
50	Distinct Origin of the Y and St Genome in <i>Elymus</i> Species: Evidence from the Analysis of a Large Sample of St Genome Species Using Two Nuclear Genes. <i>PLoS ONE</i> , 2011, 6, e26853.	2.5	34
51	Nucleotide divergence and genetic relationships of <i>Pseudoroegneria</i> species. <i>Biochemical Systematics and Ecology</i> , 2011, 39, 309-319.	1.3	12
52	Origin of the H genome in StH-genomic <i>Elymus</i> species based on the single-copy nuclear gene <i>DMC1</i> . <i>Genome</i> , 2011, 54, 655-662.	2.0	7
53	Molecular phylogeny and reticulate origins of several American polyploid <i>Hordeum</i> species. <i>Botany</i> , 2011, 89, 405-415.	1.0	6
54	Genomic constitution and phylogenetic position of several New Zealand Triticeae species revealed by two single copy nuclear genes. <i>Australian Journal of Botany</i> , 2011, 59, 1.	0.6	3

#	ARTICLE	IF	CITATIONS
55	RPB2 sequences reveal a close phylogenetic relationship between tetraploid <i>Hordelymus</i> and diploid <i>Hordeum</i> species in Triticeae (Poaceae). <i>Biochemical Systematics and Ecology</i> , 2010, 38, 789-795.	1.3	2
56	Inheritance and identification of molecular markers associated with a novel dwarfing gene in barley. <i>BMC Genetics</i> , 2010, 11, 89.	2.7	29
57	Origin of the Y genome in <i>Elymus</i> and its relationship to other genomes in Triticeae based on evidence from elongation factor G (EF-G) gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 727-733.	2.7	38
58	Phylogenetic analysis of the maternal genome of tetraploid StStYY <i>Elymus</i> (Triticeae: Poaceae) species and the monogenomic Triticeae based on rps16 sequence data. <i>Plant Science</i> , 2010, 178, 463-468.	3.6	16
59	Molecular evolution and phylogeny of the RPB2 gene in the genus <i>Hordeum</i> . <i>Annals of Botany</i> , 2009, 103, 975-983.	2.9	33
60	Nucleotide diversity and minisatellite in chloroplast Asp(GUC)â€“Thr(GGU) region in <i>Elymus trachycaulus</i> complex, <i>Elymus alaskanus</i> and <i>Elymus caninus</i> . <i>Biochemical Systematics and Ecology</i> , 2009, 37, 67-75.	1.3	5
61	Inheritance of genes controlling supernumerary spikelet in wheat line 51885. <i>Euphytica</i> , 2009, 167, 173-179.	1.2	8
62	Molecular evolution and origin of tetraploid <i>Elymus</i> species. <i>Breeding Science</i> , 2009, 59, 487-491.	1.9	20
63	Molecular phylogeny of RPB2 gene reveals multiple origin, geographic differentiation of H genome, and the relationship of the Y genome to other genomes in <i>Elymus</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 897-907.	2.7	76
64	Microsatellite variability and heterozygote excess in <i>Elymus trachycaulus</i> populations from British Columbia in Canada. <i>Biochemical Systematics and Ecology</i> , 2007, 35, 725-736.	1.3	26
65	Molecular evolution and genome divergence at RPB2 gene of the St and H genome in <i>Elymus</i> species. <i>Plant Molecular Biology</i> , 2007, 64, 645-655.	3.9	50
66	Genetic diversity of rbcL gene in <i>Elymus trachycaulus</i> complex and their phylogenetic relationships to several Triticeae species. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 1737-1746.	1.6	11
67	Molecular diversity and relationships among <i>Elymus trachycaulus</i> , <i>E. subsecundus</i> , <i>E. â€“virescens</i> , <i>E. â€“violaceus</i> , and <i>E. â€“hyperarcticus</i> (Poaceae: Triticeae) as determined by amplified fragment length polymorphism. <i>Genome</i> , 2006, 49, 1160-1169.	2.0	7
68	Molecular diversity and relationships of North American <i>Elymus trachycaulus</i> and the Eurasian <i>E. caninus</i> species. <i>Genetica</i> , 2006, 127, 55-64.	1.1	7
69	Identification of <i>Pseudomonas aeruginosa</i> -induced genes in human mast cells using suppression subtractive hybridization: up-regulation of IL-8 and CCL4 production. <i>Clinical and Experimental Immunology</i> , 2005, 142, 199-205.	2.6	13
70	Genetic relationships of tetraploid <i>Elymus</i> species and their genomic donor species inferred from polymerase chain reaction-restriction length polymorphism analysis of chloroplast gene regions. <i>Theoretical and Applied Genetics</i> , 2004, 108, 535-542.	3.6	38
71	Microsatellite variability and heterozygote deficiency in the arcticâ€“alpine Alaskan wheatgrass (<i>Elymus</i>) Tj ETQq1 1.0,784314 rgBT /Ove	2.0	40
72	Interspecific polymorphism at non-coding regions of chloroplast, mitochondrial DNA and rRNA IGS region in <i>Elymus</i> species. <i>Hereditas</i> , 2002, 137, 119-124.	1.4	22