

Genlou Sun

List of Publications by Year in descending order

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72
papers

1,208
citations

361296

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454834

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72
all docs

72
docs citations

72
times ranked

1046
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 1 | Molecular phylogeny of RPB2 gene reveals multiple origin, geographic differentiation of H genome, and the relationship of the Y genome to other genomes in Elymus species. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 897-907. | 1.2 | 76 |
| 2 | Copy Number Variation of Cytokinin Oxidase Gene Tackx4 Associated with Grain Weight and Chlorophyll Content of Flag Leaf in Common Wheat. <i>PLoS ONE</i> , 2015, 10, e0145970. | 1.1 | 57 |
| 3 | Molecular evolution and genome divergence at RPB2 gene of the St and H genome in Elymus species. <i>Plant Molecular Biology</i> , 2007, 64, 645-655. | 2.0 | 50 |
| 4 | QTL underlying some agronomic traits in barley detected by SNP markers. <i>BMC Genetics</i> , 2016, 17, 103. | 2.7 | 46 |
| 5 | 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. | 2.8 | 44 |
| 6 | Identification of QTL underlying physiological and morphological traits of flag leaf in barley. <i>BMC Genetics</i> , 2015, 16, 29. | 2.7 | 43 |
| 7 | Microsatellite variability and heterozygote deficiency in the arctic–alpine Alaskan wheatgrass (<i>Elymus</i>) Tj ETQq1 1,0,784314 rgBT /Ove | 0.9 | 40 |
| 8 | Identification of active VQ motif-containing genes and the expression patterns under low nitrogen treatment in soybean. <i>Gene</i> , 2014, 543, 237-243. | 1.0 | 40 |
| 9 | Genetic relationships of tetraploid Elymus 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. | 1.8 | 38 |
| 10 | Origin of the Y genome in Elymus 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. | 1.2 | 38 |
| 11 | Identification of a Novel Allele of TaCKX6a02 Associated with Grain Size, Filling Rate and Weight of Common Wheat. <i>PLoS ONE</i> , 2015, 10, e0144765. | 1.1 | 38 |
| 12 | Distinct Origin of the Y and St Genome in Elymus Species: Evidence from the Analysis of a Large Sample of St Genome Species Using Two Nuclear Genes. <i>PLoS ONE</i> , 2011, 6, e26853. | 1.1 | 34 |
| 13 | Molecular evolution and phylogeny of the RPB2 gene in the genus <i>Hordeum</i> . <i>Annals of Botany</i> , 2009, 103, 975-983. | 1.4 | 33 |
| 14 | Effects of nitrogen spraying on the post-anthesis stage of winter wheat under waterlogging stress. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 207-216. | 1.0 | 33 |
| 15 | Tibet as a Potential Domestication Center of Cultivated Barley of China. <i>PLoS ONE</i> , 2013, 8, e62700. | 1.1 | 30 |
| 16 | Inheritance and identification of molecular markers associated with a novel dwarfing gene in barley. <i>BMC Genetics</i> , 2010, 11, 89. | 2.7 | 29 |
| 17 | Origin of worldwide cultivated barley revealed by NAM-1 gene and grain protein content. <i>Frontiers in Plant Science</i> , 2015, 6, 803. | 1.7 | 28 |
| 18 | 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. | 0.6 | 26 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | 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. | 1.2 | 23 |
| 20 | 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. | 0.5 | 22 |
| 21 | Molecular evolution and origin of tetraploid <i>Elymus</i> species. <i>Breeding Science</i> , 2009, 59, 487-491. | 0.9 | 20 |
| 22 | A Comprehensive Analysis of the Cupin Gene Family in Soybean (<i>Glycine max</i>). <i>PLoS ONE</i> , 2014, 9, e110092. | 1.1 | 20 |
| 23 | 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. | 1.0 | 19 |
| 24 | 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 |
| 25 | Identification of QTL underlying the leaf length and area of different leaves in barley. <i>Scientific Reports</i> , 2019, 9, 4431. | 1.6 | 18 |
| 26 | Transcriptome analysis reveals plant response to colchicine treatment during on chromosome doubling. <i>Scientific Reports</i> , 2017, 7, 8503. | 1.6 | 17 |
| 27 | MiR396 regulatory network and its expression during grain development in wheat. <i>Protoplasma</i> , 2021, 258, 103-113. | 1.0 | 17 |
| 28 | 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. | 1.7 | 16 |
| 29 | Molecular phylogeny revealed complex evolutionary process in <i>Elymus</i> species. <i>Journal of Systematics and Evolution</i> , 2014, 52, 706-711. | 1.6 | 16 |
| 30 | Molecular regulatory mechanisms underlying the adaptability of polyploid plants. <i>Biological Reviews</i> , 2021, 96, 394-407. | 4.7 | 16 |
| 31 | Insights into the N ⁶ -methyladenosine mechanism and its functionality: progress and questions. <i>Critical Reviews in Biotechnology</i> , 2020, 40, 639-652. | 5.1 | 15 |
| 32 | 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. | 1.1 | 13 |
| 33 | Nucleotide divergence and genetic relationships of <i>Pseudoroegneria</i> species. <i>Biochemical Systematics and Ecology</i> , 2011, 39, 309-319. | 0.6 | 12 |
| 34 | Evolutionary mechanism of genome duplication enhancing natural autotetraploid sea barley adaptability to drought stress. <i>Environmental and Experimental Botany</i> , 2019, 159, 44-54. | 2.0 | 12 |
| 35 | Transcriptome and miRNAs analyses enhance our understanding of the evolutionary advantages of polyploidy. <i>Critical Reviews in Biotechnology</i> , 2019, 39, 173-180. | 5.1 | 12 |
| 36 | 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. | 0.8 | 11 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Molecular evolution and nucleotide diversity of nuclear plastid phosphoglycerate kinase (PCK) gene in Triticeae (Poaceae). <i>Gene</i> , 2014, 533, 142-148. | 1.0 | 11 |
| 38 | 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. | 1.1 | 9 |
| 39 | Phylogenetic analysis revealed reticulate evolution of allotetraploid <i>Elymus ciliaris</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 805-813. | 1.2 | 9 |
| 40 | 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. | 0.6 | 9 |
| 41 | Molecular evidence of RNA polymerase II gene reveals the origin of worldwide cultivated barley. <i>Scientific Reports</i> , 2016, 6, 36122. | 1.6 | 9 |
| 42 | Inheritance of genes controlling supernumerary spikelet in wheat line 51885. <i>Euphytica</i> , 2009, 167, 173-179. | 0.6 | 8 |
| 43 | 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. | 1.2 | 8 |
| 44 | Molecular diversity and relationships among <i>Elymus trachycaulus</i> , <i>E. subsecundus</i> , <i>E. virescens</i> , <i>E. violaceus</i> , and <i>E. hyperarcticus</i> (Poaceae: Triticeae) as determined by amplified fragment length polymorphism. <i>Genome</i> , 2006, 49, 1160-1169. | 0.9 | 7 |
| 45 | 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. | 0.5 | 7 |
| 46 | Molecular phylogeny of diploid <i>Hordeum</i> species and incongruence between chloroplast and nuclear datasets. <i>Genome</i> , 2011, 54, 986-992. | 0.9 | 7 |
| 47 | 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. | 0.9 | 7 |
| 48 | 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. | 1.6 | 7 |
| 49 | Cloning, expression analysis and molecular marker development of cinnamyl alcohol dehydrogenase gene in common wheat. <i>Protoplasma</i> , 2021, 258, 881-889. | 1.0 | 7 |
| 50 | Molecular phylogeny and reticulate origins of several American polyploid <i>Hordeum</i> species. <i>Botany</i> , 2011, 89, 405-415. | 0.5 | 6 |
| 51 | Nuclear and chloroplast DNA phylogeny reveals complex evolutionary history of <i>Elymus pendulinus</i> . <i>Genome</i> , 2014, 57, 97-109. | 0.9 | 6 |
| 52 | Genetic Divergence in Domesticated and Non-Domesticated Gene Regions of Barley Chromosomes. <i>PLoS ONE</i> , 2015, 10, e0121106. | 1.1 | 6 |
| 53 | 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. | 1.6 | 6 |
| 54 | 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. | 0.9 | 6 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | 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. | 0.6 | 5 |
| 56 | Origin and Evolution of Allopolyploid Wheatgrass <i>Elymus fibrosus</i> (Schrenk) Tzvelev (Poaceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70 | 1.1 | 5 |
| 57 | Molecular prospective on the wheat grain development. <i>Critical Reviews in Biotechnology</i> , 2023, 43, 38-49. | 5.1 | 5 |
| 58 | Cloning and Characterization of Low-Molecular-Weight Glutenin Subunit Alleles from Chinese Wheat Landraces (<i>Triticum aestivum</i> L.). <i>Scientific World Journal</i> , The, 2014, 2014, 1-6. | 0.8 | 4 |
| 59 | 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. | 1.6 | 4 |
| 60 | MicroRNA-mediated responses to colchicine treatment in barley. <i>Planta</i> , 2020, 251, 44. | 1.6 | 4 |
| 61 | Origin and Reticulate Evolutionary Process of Wheatgrass <i>Elymus trachycaulus</i> (Triticeae: Poaceae). <i>PLoS ONE</i> , 2015, 10, e0125417. | 1.1 | 3 |
| 62 | 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. | 1.6 | 3 |
| 63 | 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. | 0.3 | 3 |
| 64 | Transcriptome and Metabolite Insights into Domestication Process of Cultivated Barley in China. <i>Plants</i> , 2022, 11, 209. | 1.6 | 3 |
| 65 | 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. | 0.6 | 2 |
| 66 | Comparison of Acetyl-CoA carboxylase 1 (Acc-1) gene diversity among different Triticeae genomes. <i>Gene</i> , 2014, 546, 11-15. | 1.0 | 2 |
| 67 | 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. | 1.1 | 2 |
| 68 | Phylogenetic analysis of two single-copy nuclear genes revealed origin of tetraploid barley <i>Hordeum marinum</i> . <i>PLoS ONE</i> , 2020, 15, e0235475. | 1.1 | 2 |
| 69 | 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. | 1.7 | 2 |
| 70 | N6-Methyladenosine dynamic changes and differential methylation in wheat grain development. <i>Planta</i> , 2022, 255, 125. | 1.6 | 2 |
| 71 | 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. | 0.9 | 1 |
| 72 | Population genetic variation characterization of the boreal tree <i>Acer ginnala</i> in Northern China. <i>Scientific Reports</i> , 2020, 10, 13515. | 1.6 | 1 |