

Yi Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4648935/publications.pdf>

Version: 2024-02-01

44
papers

4,120
citations

236925

25
h-index

243625

44
g-index

45
all docs

45
docs citations

45
times ranked

6151
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | MdMADS6 Recruits Histone Deacetylase MdHDA19 to Repress the Expression of the Carotenoid Synthesis-Related Gene MdCCD1 during Fruit Ripening. <i>Plants</i> , 2022, 11, 668. | 3.5 | 7 |
| 2 | Genotyping-by-sequencing to determine the genetic structure of a Tibetan medicinal plant <i>Swertia mussotii</i> Franch.. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 469-484. | 1.6 | 3 |
| 3 | Interpopulation differences of retroduplication variations (RDVs) in rice retrogenes and their phenotypic correlations. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 600-611. | 4.1 | 1 |
| 4 | Venn diagrams in bioinformatics. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 84 |
| 5 | RetroScan: An Easy-to-Use Pipeline for Retrocopy Annotation and Visualization. <i>Frontiers in Genetics</i> , 2021, 12, 719204. | 2.3 | 4 |
| 6 | SilkDB 3.0: visualizing and exploring multiple levels of data for silkworm. <i>Nucleic Acids Research</i> , 2020, 48, D749-D755. | 14.5 | 59 |
| 7 | Synergism of open chromatin regions involved in regulating genes in <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 110, 10-18. | 2.7 | 6 |
| 8 | OrthoVenn2: a web server for whole-genome comparison and annotation of orthologous clusters across multiple species. <i>Nucleic Acids Research</i> , 2019, 47, W52-W58. | 14.5 | 661 |
| 9 | Unprecedented [5.5.5.6]Dioxafenestrane Ring Construction in Fungal Insecticidal Sesquiterpene Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 6569-6573. | 13.8 | 27 |
| 10 | OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 3.0 | 50 |
| 11 | Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4284-E4293. | 7.1 | 391 |
| 12 | Dynamic Evolution of γ -Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat. <i>Scientific Reports</i> , 2018, 8, 5181. | 3.3 | 68 |
| 13 | Gene Duplication and Evolution Dynamics in the Homeologous Regions Harboring Multiple Prolamin and Resistance Gene Families in Hexaploid Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 673. | 3.6 | 84 |
| 14 | Modular assembly of transposable element arrays by microsatellite targeting in the guayule and rice genomes. <i>BMC Genomics</i> , 2018, 19, 271. | 2.8 | 7 |
| 15 | Deep sequencing and transcriptome analyses to identify genes involved in secoiridoid biosynthesis in the Tibetan medicinal plant <i>Swertia mussotii</i> . <i>Scientific Reports</i> , 2017, 7, 43108. | 3.3 | 56 |
| 16 | St ₂ -80: a new FISH marker for <i>St</i> genome and genome analysis in Triticeae. <i>Genome</i> , 2017, 60, 553-563. | 2.0 | 17 |
| 17 | New insights into structural organization and gene duplication in a 1.75 Mb genomic region harboring the γ -gliadin gene family in <i>Aegilops tauschii</i> , the source of wheat D genome. <i>Plant Journal</i> , 2017, 92, 571-583. | 5.7 | 29 |
| 18 | Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502. | 27.8 | 563 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | PIECE 2.0: an update for the plant gene structure comparison and evolution database. <i>Nucleic Acids Research</i> , 2017, 45, 1015-1020. | 14.5 | 24 |
| 20 | Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 51-61. | 3.9 | 25 |
| 21 | PlantRGDB: A Database of Plant Retrocopied Genes. <i>Plant and Cell Physiology</i> , 2017, 58, pcw210. | 3.1 | 6 |
| 22 | A whole-genome, radiation hybrid mapping resource of hexaploid wheat. <i>Plant Journal</i> , 2016, 86, 195-207. | 5.7 | 23 |
| 23 | Rapid evolutionary dynamics in a 2.8-Mb chromosomal region containing multiple prolamin and resistance gene families in <i>Aegilops tauschii</i> . <i>Plant Journal</i> , 2016, 87, 495-506. | 5.7 | 33 |
| 24 | Draft Genome Sequence of <i>Agrobacterium rhizogenes</i> Strain NCPPB2659. <i>Genome Announcements</i> , 2016, 4, . | 0.8 | 11 |
| 25 | MetaCoMET: a web platform for discovery and visualization of the core microbiome. <i>Bioinformatics</i> , 2016, 32, 3469-3470. | 4.1 | 80 |
| 26 | GSP: a web-based platform for designing genome-specific primers in polyploids. <i>Bioinformatics</i> , 2016, 32, 2382-2383. | 4.1 | 30 |
| 27 | Fast-forward genetics by radiation hybrids to saturate the locus regulating nuclear-cytoplasmic compatibility in <i>Triticum</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 1716-1726. | 8.3 | 9 |
| 28 | Radiation hybrid maps of the D-genome of <i>Aegilops tauschii</i> and their application in sequence assembly of large and complex plant genomes. <i>BMC Genomics</i> , 2015, 16, 800. | 2.8 | 31 |
| 29 | OrthoVenn: a web server for genome wide comparison and annotation of orthologous clusters across multiple species. <i>Nucleic Acids Research</i> , 2015, 43, W78-W84. | 14.5 | 612 |
| 30 | Development of a D genome specific marker resource for diploid and hexaploid wheat. <i>BMC Genomics</i> , 2015, 16, 646. | 2.8 | 6 |
| 31 | WheatExp: an RNA-seq expression database for polyploid wheat. <i>BMC Plant Biology</i> , 2015, 15, 299. | 3.6 | 124 |
| 32 | AIM: a comprehensive Arabidopsis interactome module database and related interologs in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau117. | 3.0 | 8 |
| 33 | NetVenn: an integrated network analysis web platform for gene lists. <i>Nucleic Acids Research</i> , 2014, 42, W161-W166. | 14.5 | 29 |
| 34 | A New Tomato NAC (NAM/ATAF1/2/CUC2) Transcription Factor, SINAC4, Functions as a Positive Regulator of Fruit Ripening and Carotenoid Accumulation. <i>Plant and Cell Physiology</i> , 2014, 55, 119-135. | 3.1 | 296 |
| 35 | Constructing regulatory networks to identify biomarkers for insulin resistance. <i>Gene</i> , 2014, 539, 68-74. | 2.2 | 9 |
| 36 | A Tomato MADS-Box Transcription Factor, SIMADS1, Acts as a Negative Regulator of Fruit Ripening. <i>Plant Physiology</i> , 2013, 163, 1026-1036. | 4.8 | 161 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945. | 7.1 | 214 |
| 38 | PIECE: a database for plant gene structure comparison and evolution. <i>Nucleic Acids Research</i> , 2013, 41, D1159-D1166. | 14.5 | 50 |
| 39 | Complete Chloroplast Genome Sequences of Mongolia Medicine <i>Artemisia frigida</i> and Phylogenetic Relationships with Other Plants. <i>PLoS ONE</i> , 2013, 8, e57533. | 2.5 | 122 |
| 40 | Physical mapping resources for large plant genomes: radiation hybrids for wheat D-genome progenitor <i>Aegilops tauschii</i> . <i>BMC Genomics</i> , 2012, 13, 597. | 2.8 | 33 |
| 41 | Exploring the diploid wheat ancestral A genome through sequence comparison at the high-molecular-weight glutenin locus region. <i>Molecular Genetics and Genomics</i> , 2012, 287, 855-866. | 2.1 | 7 |
| 42 | Characterizing the citrus cultivar Carrizo genome through 454 shotgun sequencing. <i>Genome</i> , 2011, 54, 1005-1015. | 2.0 | 3 |
| 43 | Function Annotation of an SBP-box Gene in <i>Arabidopsis</i> Based on Analysis of Co-expression Networks and Promoters. <i>International Journal of Molecular Sciences</i> , 2009, 10, 116-132. | 4.1 | 55 |
| 44 | A systems biology analysis of protein-protein interactions in the APOBEC family. <i>Life Sciences</i> , 2008, 83, 521-530. | 4.3 | 2 |