

# Sibin Yu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7400211/publications.pdf>

Version: 2024-02-01

72  
papers

8,121  
citations

134610

34  
h-index

97045

71  
g-index

76  
all docs

76  
docs citations

76  
times ranked

7602  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | Dissection of heterotic loci for grain yield using interconnected chromosome segment substitution lines in rice. <i>Crop Journal</i> , 2022, 10, 323-331.                             | 2.3 | 4         |
| 2  | From Green Super Rice to green agriculture: Reaping the promise of functional genomics research. <i>Molecular Plant</i> , 2022, 15, 9-26.   | 3.9 | 44        |
| 3  | Fine Mapping of Two Interacting Loci for Transmission Ratio Distortion in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 866276.                       | 1.7 | 0         |
| 4  | Control of Thousand-Grain Weight by OsMADS56 in Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 125.   | 1.8 | 12        |
| 5  | Verifying the Breeding Value of A Rare Haplotype of Chalk7, GS3, and Chalk5 to Improve Grain Appearance Quality in Rice. <i>Plants</i> , 2022, 11, 1470.                              | 1.6 | 4         |
| 6  | Insights into the Regulation of Rice Seed Storability by Seed Tissue-Specific Transcriptomic and Metabolic Profiling. <i>Plants</i> , 2022, 11, 1570.                                 | 1.6 | 7         |
| 7  | Genetic architecture and key genes controlling the diversity of oil composition in rice grains. <i>Molecular Plant</i> , 2021, 14, 456-469.   | 3.9 | 18        |
| 8  | The origin of <i>Wx<sup>la</sup></i> provides new insights into the improvement of grain quality in rice. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 878-888.            | 4.1 | 43        |
| 9  | Identification of QTLs for Salt Tolerance at the Germination and Seedling Stages in Rice. <i>Plants</i> , 2021, 10, 428.  | 1.6 | 23        |
| 10 | <i>OsGRETCHENHAGEN3-2</i> modulates rice seed storability via accumulation of abscisic acid and protective substances. <i>Plant Physiology</i> , 2021, 186, 469-482.                  | 2.3 | 24        |
| 11 | Rice SPL10 positively regulates trichome development through expression of <i>HL6</i> and auxin-related genes. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1521-1537.     | 4.1 | 21        |
| 12 | Mapping causal genes and genetic interactions for agronomic traits using a large F2 population in rice. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .                             | 0.8 | 5         |
| 13 | Identification of a novel QTL and candidate gene associated with grain size using chromosome segment substitution lines in rice. <i>Scientific Reports</i> , 2021, 11, 189.           | 1.6 | 15        |
| 14 | Identification of Heterotic Loci with Desirable Allelic Interaction to Increase Yield in Rice. <i>Rice</i> , 2021, 14, 97.  | 1.7 | 4         |
| 15 | Genome-wide Dissection of Co-selected UV-B Responsive Pathways in the UV-B Adaptation of Qingke. <i>Molecular Plant</i> , 2020, 13, 112-127.  | 3.9 | 106       |
| 16 | Genomic Breeding of Green Super Rice Varieties and Their Deployment in Asia and Africa. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1427-1442.                               | 1.8 | 53        |
| 17 | Spider Silk Fibroin Protein Heterologously Produced in Rice Seeds Reduce Diabetes and Hypercholesterolemia in Mice. <i>Plants</i> , 2020, 9, 1282.                                    | 1.6 | 3         |
| 18 | Genetic Dissection and Validation of Chromosomal Regions for Transmission Ratio Distortion in Intersubspecific Crosses of Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 563548. | 1.7 | 4         |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | A xylan glucuronosyltransferase gene exhibits pleiotropic effects on cellular composition and leaf development in rice. <i>Scientific Reports</i> , 2020, 10, 3726.   | 1.6 | 8         |
| 20 | Genetic Dissection of Seed Dormancy using Chromosome Segment Substitution Lines in Rice ( <i>Oryza</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 Tf  | 1.8 | 11        |
| 21 | Genetic Dissection of Seed Dormancy in Rice ( <i>Oryza sativa</i> L.) by Using Two Mapping Populations Derived from Common Parents. <i>Rice</i> , 2020, 13, 52.   | 1.7 | 20        |
| 22 | Identification and Validation of Quantitative Trait Loci for Grain Number in Rice ( <i>Oryza sativa</i> L.). <i>Agronomy</i> , 2020, 10, 180.   | 1.3 | 11        |
| 23 | A key variant in the cis-regulatory element of flowering gene <i>Ghd8</i> associated with cold tolerance in rice. <i>Scientific Reports</i> , 2019, 9, 9603.  | 1.6 | 16        |
| 24 | <i>Ghd8</i> controls rice photoperiod sensitivity by forming a complex that interacts with <i>Ghd7</i> . <i>BMC Plant Biology</i> , 2019, 19, 462.  | 1.6 | 28        |
| 25 | Genetic Dissection of Seed Storability and Validation of Candidate Gene Associated with Antioxidant Capability in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4442.                          | 1.8 | 25        |
| 26 | Divergent functions of the <scp>GAGA</scp>-binding transcription factor family in rice. <i>Plant Journal</i> , 2018, 94, 32-47.   | 2.8 | 22        |
| 27 | Genetic dissection and validation of candidate genes for flag leaf size in rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 801-815.  | 1.8 | 49        |
| 28 | Metabolome Analysis of Multi-Connected Biparental Chromosome Segment Substitution Line Populations. <i>Plant Physiology</i> , 2018, 178, 612-625.   | 2.3 | 25        |
| 29 | Genome-wide Association Analyses Reveal the Genetic Basis of Stigma Exsertion in Rice. <i>Molecular Plant</i> , 2017, 10, 634-644.  | 3.9 | 66        |
| 30 | Hairy Leaf 6, an AP2/ERF Transcription Factor, Interacts with OsWOX3B and Regulates Trichome Formation in Rice. <i>Molecular Plant</i> , 2017, 10, 1417-1433.   | 3.9 | 71        |
| 31 | Pedigree-based genome re-sequencing reveals genetic variation patterns of elite backbone varieties during modern rice improvement. <i>Scientific Reports</i> , 2017, 7, 292.  | 1.6 | 8         |
| 32 | Dissection of the qTGW1.1 region into two tightly-linked minor QTLs having stable effects for grain weight in rice. <i>BMC Genetics</i> , 2016, 17, 98.   | 2.7 | 34        |
| 33 | Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71. | 3.3 | 211       |
| 34 | Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.   | 2.4 | 34        |
| 35 | Genome-wide Association Study (GWAS) of mesocotyl elongation based on re-sequencing approach in rice. <i>BMC Plant Biology</i> , 2015, 15, 218.   | 1.6 | 116       |
| 36 | Identification of Genomic Regions and the Isoamylase Gene for Reduced Grain Chalkiness in Rice. <i>PLoS ONE</i> , 2015, 10, e0122013.   | 1.1 | 53        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 37 | Genetic Architecture of Natural Variation in Rice Chlorophyll Content Revealed by a Genome-Wide Association Study. <i>Molecular Plant</i> , 2015, 8, 946-957.   | 3.9 | 106       |
| 38 | Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5411-9.                 | 3.3 | 165       |
| 39 | Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism. <i>Nature Genetics</i> , 2014, 46, 714-721.  | 9.4 | 560       |
| 40 | Mapping of minor quantitative trait loci (<scp>QTL</scp>s) conferring fertility restoration of wild abortive cytoplasmic male sterility and <scp>QTL</scp>s conferring stigma exertion in rice. <i>Plant Breeding</i> , 2014, 133, 722-727. | 1.0 | 7         |
| 41 | Natural variation and artificial selection in four genes determine grain shape in rice. <i>New Phytologist</i> , 2013, 200, 1269-1280.  | 3.5 | 70        |
| 42 | QTL mapping for combining ability in different population-based NCII designs: a simulation study. <i>Journal of Genetics</i> , 2013, 92, 529-543.   | 0.4 | 6         |
| 43 | Natural variation in Ghd7.1 plays an important role in grain yield and adaptation in rice. <i>Cell Research</i> , 2013, 23, 969-971.  | 5.7 | 222       |
| 44 | Three genetic systems controlling growth, development and productivity of rice ( <i>Oryza sativa</i> L.): a reevaluation of the "Green Revolution". <i>Theoretical and Applied Genetics</i> , 2013, 126, 1011-1024.                         | 1.8 | 21        |
| 45 | Genetic analysis of the metabolome exemplified using a rice population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20320-20325.  | 3.3 | 155       |
| 46 | A Novel Integrated Method for Large-Scale Detection, Identification, and Quantification of Widely Targeted Metabolites: Application in the Study of Rice Metabolomics. <i>Molecular Plant</i> , 2013, 6, 1769-1780.                         | 3.9 | 1,107     |
| 47 | Mapping and characterization of the major quantitative trait locus qSS7 associated with increased length and decreased width of rice seeds. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1717-1726.                                 | 1.8 | 62        |
| 48 | Improving rice yield and quality by QTL pyramiding. <i>Molecular Breeding</i> , 2012, 29, 903-913.  | 1.0 | 30        |
| 49 | Clustered QTL for source leaf size and yield traits in rice ( <i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2012, 29, 99-113.  | 1.0 | 72        |
| 50 | QTL Mapping of Combining Ability and Heterosis of Agronomic Traits in Rice Backcross Recombinant Inbred Lines and Hybrid Crosses. <i>PLoS ONE</i> , 2012, 7, e28463.  | 1.1 | 58        |
| 51 | Functional markers developed from multiple loci in GS3 for fine marker-assisted selection of grain length in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 905-913.  | 1.8 | 97        |
| 52 | Identification of quantitative trait loci associated with germination using chromosome segment substitution lines of rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 411-420.                          | 1.8 | 23        |
| 53 | Candidacy of a chitin-inducible gibberellin-responsive gene for a major locus affecting plant height in rice that is closely linked to Green Revolution gene sd1. <i>Theoretical and Applied Genetics</i> , 2011, 123, 705-714.             | 1.8 | 41        |
| 54 | Fine mapping a major QTL for flag leaf size and yield-related traits in rice. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1319-1330.   | 1.8 | 81        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 55 | Diversity and selective sweep in the OsAMT1;1 genomic region of rice. <i>BMC Evolutionary Biology</i> , 2011, 11, 61.  | 3.2 | 20        |
| 56 | A Major QTL, Ghd8, Plays Pleiotropic Roles in Regulating Grain Productivity, Plant Height, and Heading Date in Rice. <i>Molecular Plant</i> , 2011, 4, 319-330.  | 3.9 | 498       |
| 57 | Chromosome Segment Substitution Lines: A Powerful Tool for the Introgression of Valuable Genes from <i>Oryza</i> Wild Species into Cultivated Rice ( <i>O. sativa</i> ). <i>Rice</i> , 2010, 3, 218-234.   | 1.7 | 134       |
| 58 | A global analysis of QTLs for expression variations in rice shoots at the early seedling stage. <i>Plant Journal</i> , 2010, 63, 1063-1074.  | 2.8 | 69        |
| 59 | Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10578-10583.                                     | 3.3 | 299       |
| 60 | Linking differential domain functions of the GS3 protein to natural variation of grain size in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19579-19584.  | 3.3 | 580       |
| 61 | A causal C $\rightarrow$ A mutation in the second exon of GS3 highly associated with rice grain length and validated as a functional marker. <i>Theoretical and Applied Genetics</i> , 2009, 118, 465-472.   | 1.8 | 160       |
| 62 | Population structure and association mapping on chromosome 7 using a diverse panel of Chinese germplasm of rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2009, 119, 459-470.   | 1.8 | 55        |
| 63 | Identification of quantitative trait loci controlling rice mature seed culturability using chromosomal segment substitution lines. <i>Plant Cell Reports</i> , 2009, 28, 247-256.  | 2.8 | 35        |
| 64 | Analysis of Quantitative Trait Loci in Response to Nitrogen and Phosphorus Deficiency in Rice Using Chromosomal Segment Substitution Lines. <i>Acta Agronomica Sinica</i> , 2009, 35, 580-587.   | 0.3 | 14        |
| 65 | Mapping of a Novel Semisterile Pollen QTL in Rice. <i>Acta Agronomica Sinica</i> , 2009, 35, 1584-1589.  | 0.3 | 1         |
| 66 | Mapping QTLs for seedling characteristics under different water supply conditions in rice ( <i>Oryza</i> ). <i>Journal of Agricultural Science</i> , 2009, 143, 107-114.   | 2.6 | 39        |
| 67 | Natural variation in Ghd7 is an important regulator of heading date and yield potential in rice. <i>Nature Genetics</i> , 2008, 40, 761-767.   | 9.4 | 1,666     |
| 68 | Mapping quantitative trait loci (QTLs) for seedling-vigor using recombinant inbred lines of rice ( <i>Oryza</i> ). <i>Journal of Agricultural Science</i> , 2008, 142, 107-114.  | 2.8 | 67        |
| 69 | Molecular Dissection of the Relationships among Tiller Number, Plant Height and Heading Date in Rice. <i>Plant Production Science</i> , 2004, 7, 309-318.  | 0.9 | 28        |
| 70 | Single-locus heterotic effects and dominance by dominance interactions can adequately explain the genetic basis of heterosis in an elite rice hybrid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2574-2579. | 3.3 | 367       |
| 71 | Epistasis plays an important role as genetic basis of heterosis in rice. <i>Science in China Series C: Life Sciences</i> , 1998, 41, 293-302.  | 1.3 | 6         |
| 72 | Dissection of two QTL for grain length linked on the long arm of chromosome 5 in rice. <i>Crop Science</i> , 2000, 40, 107-114.  | 0.8 | 0         |