

# Mohsen Mohammadi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4567292/publications.pdf>

Version: 2024-02-01

31  
papers

787  
citations

623734

14  
h-index

552781

26  
g-index

31  
all docs

31  
docs citations

31  
times ranked

1154  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Genetic Trends in Fusarium Head Blight Resistance from 20 Years of Winter Wheat Breeding and Cooperative Testing in the Northern U.S.A.. <i>Plant Disease</i> , 2022, 106, 364-372.          | 1.4 | 6         |
| 2  | Multi-trait genomic selection can increase selection accuracy for deoxynivalenol accumulation resulting from fusarium head blight in wheat. <i>Plant Genome</i> , 2022, 15, e20188.          | 2.8 | 20        |
| 3  | Genome-Wide Association Studies for Fusarium Head Blight Resistance and Its Trade-Off With Grain Yield in Soft Red Winter Wheat. <i>Plant Disease</i> , 2021, 105, 2435-2444.                | 1.4 | 14        |
| 4  | Using Genomic Selection to Leverage Resources among Breeding Programs: Consortium-Based Breeding. <i>Agronomy</i> , 2021, 11, 1555.  | 3.0 | 6         |
| 5  | Incorporating Multi-Scale, Spectrally Detected Nitrogen Concentrations into Assessing Nitrogen Use Efficiency for Winter Wheat Breeding Populations. <i>Remote Sensing</i> , 2021, 13, 3991. | 4.0 | 4         |
| 6  | Genome-wide association study in historical and contemporary U.S. winter wheats identifies height-reducing loci. <i>Crop Journal</i> , 2020, 8, 243-251.                                     | 5.2 | 8         |
| 7  | High-throughput phenotyping identifies plant growth differences under well-watered and drought treatments. <i>Journal of Integrative Agriculture</i> , 2020, 19, 2429-2438.                  | 3.5 | 10        |
| 8  | A proteomic analysis of grain yield-related traits in wheat. <i>AoB PLANTS</i> , 2020, 12, plaa042.  | 2.3 | 14        |
| 9  | Growth Analysis of Wheat Using Machine Vision: Opportunities and Challenges. <i>Sensors</i> , 2020, 20, 6501.  | 3.8 | 6         |
| 10 | Application of Artificial Neural Network for Modeling and Studying In Vitro Genotype-Independent Shoot Regeneration in Wheat. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 5370.        | 2.5 | 39        |
| 11 | Identification, deployment, and transferability of quantitative trait loci from genome-wide association studies in plants. <i>Current Plant Biology</i> , 2020, 24, 100145.                  | 4.7 | 20        |
| 12 | Registration of durum wheat ( <i>Triticum turgidum</i> ssp . durum ) sources of resistance to Hessian fly. <i>Journal of Plant Registrations</i> , 2020, 14, 445-449.                        | 0.5 | 0         |
| 13 | Identification of regions under selection and loci controlling agronomic traits in a soft red winter wheat population. <i>Plant Genome</i> , 2020, 13, e20031.                               | 2.8 | 12        |
| 14 | Variation in Root and Shoot Growth in Response to Reduced Nitrogen. <i>Plants</i> , 2020, 9, 144.  | 3.5 | 15        |
| 15 | Cultivar, Trait and Management System Selection to Improve Soft-Red Winter Wheat Productivity in the Eastern United States. <i>Frontiers in Plant Science</i> , 2020, 11, 335.               | 3.6 | 6         |
| 16 | Reimagining Maize Inbred Potential: Identifying Breeding Crosses Using Genetic Variance of Simulated Progeny. <i>Crop Science</i> , 2019, 59, 1457-1468.                                     | 1.8 | 6         |
| 17 | Association Analysis of Baking and Milling Quality Traits in an Elite Soft Red Winter Wheat Population. <i>Crop Science</i> , 2019, 59, 1085-1094.   | 1.8 | 9         |
| 18 | Registration of the S2MET Barley Mapping Population for Multi-Environment Genomewide Selection. <i>Journal of Plant Registrations</i> , 2019, 13, 270-280.                                   | 0.5 | 11        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 19 | Loci and candidate genes controlling root traits in wheat seedlingsâ€”a wheat root GWAS. <i>Functional and Integrative Genomics</i> , 2019, 19, 91-107.  | 3.5 | 69        |
| 20 | Association and genome analyses to propose putative candidate genes for malt quality traits. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 2775-2785.                                    | 3.5 | 8         |
| 21 | Genome-wide Association Studies and Candidate Gene Identification for Leaf Scald and Net Blotch in Barley ( <i>Hordeum vulgare</i> L.). <i>Plant Disease</i> , 2019, 103, 880-889.                           | 1.4 | 25        |
| 22 | Phylogenetic analyses and in-seedling expression of ammonium and nitrate transporters in wheat. <i>Scientific Reports</i> , 2018, 8, 7082.   | 3.3 | 26        |
| 23 | Genome-Wide Association Studies to Identify Loci and Candidate Genes Controlling Kernel Weight and Length in a Historical United States Wheat Population. <i>Frontiers in Plant Science</i> , 2018, 9, 1045. | 3.6 | 39        |
| 24 | The Effects of Both Recent and Long-Term Selection and Genetic Drift Are Readily Evident in North American Barley Breeding Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 609-622.              | 1.8 | 21        |
| 25 | The Role of Deleterious Substitutions in Crop Genomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2307-2317.   | 8.9 | 83        |
| 26 | Effectiveness of Genes for Hessian Fly (Diptera: Cecidomyiidae) Resistance in the Southeastern United States. <i>Journal of Economic Entomology</i> , 2016, 109, 399-405.                                    | 1.8 | 19        |
| 27 | PopVar: A Genome-Wide Procedure for Predicting Genetic Variance and Correlated Response in Biparental Breeding Populations. <i>Crop Science</i> , 2015, 55, 2068-2077.                                       | 1.8 | 99        |
| 28 | A genome-wide association study of malting quality across eight U.S. barley breeding programs. <i>Theoretical and Applied Genetics</i> , 2015, 128, 705-721.   | 3.6 | 67        |
| 29 | Predicting genetic variance in bi-parental breeding populations is more accurate when explicitly modeling the segregation of informative genomewide markers. <i>Molecular Breeding</i> , 2015, 35, 1.        | 2.1 | 24        |
| 30 | Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and Î²-glucan in US barley breeding germplasm. <i>Molecular Breeding</i> , 2014, 34, 1229-1243.                 | 2.1 | 35        |
| 31 | Transcriptional profiling of hexaploid wheat ( <i>Triticum aestivum</i> L.) roots identifies novel, dehydration-responsive genes. <i>Plant, Cell and Environment</i> , 2007, 30, 630-645.                    | 5.7 | 66        |