

# Benjamin Stich

## List of Publications by Year in descending order

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63  
papers

3,086  
citations

172457

29  
h-index

168389

53  
g-index

66  
all docs

66  
docs citations

66  
times ranked

3656  
citing authors

| #  | ARTICLE                                                                                                                                                                                                                                            | IF  | CITATIONS |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 1  | Genomic prediction of the recombination rate variation in barley “ A route to highly recombinogenic genotypes. <i>Plant Biotechnology Journal</i> , 2022, 20, 676-690.                                                                             | 8.3 | 16        |
| 2  | Improvement of prediction ability by integrating multi-omic datasets in barley. <i>BMC Genomics</i> , 2022, 23, 200.                                                                                                                               | 2.8 | 5         |
| 3  | Genetic Divergence of Lineage-Specific Tandemly Duplicated Gene Clusters in Four Diploid Potato Genotypes. <i>Frontiers in Plant Science</i> , 2022, 13, .                                                                                         | 3.6 | 6         |
| 4  | Accurate recombination estimation from pooled genotyping and sequencing: a case study on barley. <i>BMC Genomics</i> , 2022, 23, .                                                                                                                 | 2.8 | 0         |
| 5  | Chromosome-scale reference genome assembly of a diploid potato clone derived from an elite variety. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .                                                                                              | 1.8 | 12        |
| 6  | Aroma and quality of breads baked from old and modern wheat varieties and their prediction from genomic and flour-based metabolite profiles. <i>Food Research International</i> , 2020, 129, 108748.                                               | 6.2 | 13        |
| 7  | The maize shoot ionome: Its interaction partners, predictive power, and genetic determinants. <i>Plant, Cell and Environment</i> , 2020, 43, 2095-2111.                                                                                            | 5.7 | 10        |
| 8  | QTL mapping and genome-wide prediction of heat tolerance in multiple connected populations of temperate maize. <i>Scientific Reports</i> , 2019, 9, 14418.                                                                                         | 3.3 | 26        |
| 9  | Transcriptomic and presence/absence variation in the barley genome assessed from multi-tissue mRNA sequencing and their power to predict phenotypic traits. <i>BMC Genomics</i> , 2019, 20, 787.                                                   | 2.8 | 16        |
| 10 | Prospects and Potential Uses of Genomic Prediction of Key Performance Traits in Tetraploid Potato. <i>Frontiers in Plant Science</i> , 2018, 9, 159.                                                                                               | 3.6 | 51        |
| 11 | Iron Retention in Root Hemicelluloses Causes Genotypic Variability in the Tolerance to Iron Deficiency-Induced Chlorosis in Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 557.                                                               | 3.6 | 19        |
| 12 | Agronomic and Seed Quality Traits Dissected by Genome-Wide Association Mapping in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 386.                                                                                        | 3.6 | 78        |
| 13 | A high-density SNP genotyping array for <i>Brassica napus</i> and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1887-1899. | 3.6 | 205       |
| 14 | Comparison of statistical models for nested association mapping in rapeseed ( <i>Brassica napus</i> L.) through computer simulations. <i>BMC Plant Biology</i> , 2016, 16, 26.                                                                     | 3.6 | 15        |
| 15 | First steps to understand heat tolerance of temperate maize at adult stage: identification of QTL across multiple environments with connected segregating populations. <i>Theoretical and Applied Genetics</i> , 2016, 129, 945-961.               | 3.6 | 47        |
| 16 | Study on Essential Derivation in Maize: III. Selection and Evaluation of a Panel of Single Nucleotide Polymorphism Loci for Use in European and North American Germplasm. <i>Crop Science</i> , 2015, 55, 1170-1180.                               | 1.8 | 33        |
| 17 | Linkage mapping of Barley yellow dwarf virus resistance in connected populations of maize. <i>BMC Plant Biology</i> , 2015, 15, 29.                                                                                                                | 3.6 | 12        |
| 18 | Seedling development traits in <i>Brassica napus</i> examined by gene expression analysis and association mapping. <i>BMC Plant Biology</i> , 2015, 15, 136.                                                                                       | 3.6 | 28        |

| #  | ARTICLE                                                                                                                                                                                                   | IF  | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Genome-wide association mapping of iron homeostasis in the maize association population. BMC Genetics, 2015, 16, 1.                                                                                       | 2.7 | 104       |
| 20 | Genome-wide expression profiling and phenotypic evaluation of European maize inbreds at seedling stage in response to heat stress. BMC Genomics, 2015, 16, 123.                                           | 2.8 | 83        |
| 21 | Species- and genome-wide dissection of the shoot ironome in Brassica napus and its relationship to seedling development. Frontiers in Plant Science, 2014, 5, 485.                                        | 3.6 | 35        |
| 22 | The genetic basis of natural variation for iron homeostasis in the maize IBM population. BMC Plant Biology, 2014, 14, 12.                                                                                 | 3.6 | 24        |
| 23 | Genes involved in barley yellow dwarf virus resistance of maize. Theoretical and Applied Genetics, 2014, 127, 2575-2584.                                                                                  | 3.6 | 13        |
| 24 | Dissection of Potato Complex Traits by Linkage and Association Genetics as Basis for Developing Molecular Diagnostics in Breeding Programs. , 2014, , 47-85.                                              |     | 7         |
| 25 | Population structure and linkage disequilibrium in diploid and tetraploid potato revealed by genome-wide high-density genotyping using the <sc>SolCAP SNP</sc> array. Plant Breeding, 2013, 132, 718-724. | 1.9 | 55        |
| 26 | Ups and downs of a transcriptional landscape shape iron deficiency associated chlorosis of the maize inbreds B73 and Mo17. BMC Plant Biology, 2013, 13, 213.                                              | 3.6 | 11        |
| 27 | Response to "Controlling type 1 error rates in genome-wide association studies in plants" by Andrew W George. Heredity, 2013, 111, 88-88.                                                                 | 2.6 | 1         |
| 28 | Co-Variation between Seed Dormancy, Growth Rate and Flowering Time Changes with Latitude in Arabidopsis thaliana. PLoS ONE, 2013, 8, e61075.                                                              | 2.5 | 130       |
| 29 | A candidate gene-based association study of tocopherol content and composition in rapeseed (Brassica napus). Frontiers in Plant Science, 2012, 3, 129.                                                    | 3.6 | 58        |
| 30 | QTL detection power of multi-parental RIL populations in Arabidopsis thaliana. Heredity, 2012, 108, 626-632.                                                                                              | 2.6 | 27        |
| 31 | Seedling development in a Brassica napus diversity set and its relationship to agronomic performance. Theoretical and Applied Genetics, 2012, 125, 1275-1287.                                             | 3.6 | 30        |
| 32 | High-throughput polymorphism detection and genotyping in Brassica napus using next-generation RAD sequencing. BMC Genomics, 2012, 13, 281.                                                                | 2.8 | 129       |
| 33 | Association analysis of photoperiodic flowering time genes in west and central African sorghum [Sorghum bicolor (L.) Moench]. BMC Plant Biology, 2012, 12, 32.                                            | 3.6 | 30        |
| 34 | Genome-wide association mapping of flowering time and northern corn leaf blight (Setosphaeria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50                                                                       | 3.6 | 70        |
| 35 | Analysis of Natural Variation of the Potato Tuber Proteome Reveals Novel Candidate Genes for Tuber Bruising. Journal of Proteome Research, 2012, 11, 703-716.                                             | 3.7 | 30        |
| 36 | Tapping natural variation at functional level reveals allele specific molecular characteristics of potato invertase <i>Painâ€1</i>. Plant, Cell and Environment, 2012, 35, 2143-2154.                    | 5.7 | 7         |

| #  | ARTICLE                                                                                                                                                                                                                                             | IF  | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | An analysis of selection on candidate genes for regulation, mobilization, uptake, and transport of iron in maize. <i>Genome</i> , 2011, 54, 674-683.                                                                                                | 2.0 | 9         |
| 38 | A general method for controlling the genome-wide type I error rate in linkage and association mapping experiments in plants. <i>Heredity</i> , 2011, 106, 825-831.                                                                                  | 2.6 | 32        |
| 39 | Population structure in sorghum accessions from West Africa differing in race and maturity class. <i>Genetica</i> , 2011, 139, 453-463.                                                                                                             | 1.1 | 19        |
| 40 | Patterns of molecular variation in a species-wide germplasm set of <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2011, 123, 1413-1423.                                                                                          | 3.6 | 171       |
| 41 | Molecular Diagnostics for Complex Pest and Disease Resistance and Tuber Quality Traits: Concept, Achievements and Perspectives. <i>Potato Research</i> , 2011, 54, 313-318.                                                                         | 2.7 | 5         |
| 42 | Genome-wide distribution of genetic diversity and linkage disequilibrium in elite sugar beet germplasm. <i>BMC Genomics</i> , 2011, 12, 484.                                                                                                        | 2.8 | 18        |
| 43 | Association genetics in <i>Solanum tuberosum</i> provides new insights into potato tuber bruising and enzymatic tissue discoloration. <i>BMC Genomics</i> , 2011, 12, 7.                                                                            | 2.8 | 52        |
| 44 | Detection of epistatic interactions in association mapping populations: an example from tetraploid potato. <i>Heredity</i> , 2011, 107, 537-547.                                                                                                    | 2.6 | 15        |
| 45 | Optimum allocation of resources for QTL detection using a nested association mapping strategy in maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 553-561.                                                                               | 3.6 | 14        |
| 46 | Population structure and genetic diversity in a commercial maize breeding program assessed with SSR and SNP markers. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1289-1299.                                                                | 3.6 | 232       |
| 47 | Population structure and genetic diversity in elite sugar beet germplasm investigated with SSR markers. <i>Euphytica</i> , 2010, 175, 35-42.                                                                                                        | 1.2 | 33        |
| 48 | Patterns of molecular and phenotypic diversity in pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.] from West and Central Africa and their relation to geographical and environmental parameters. <i>BMC Plant Biology</i> , 2010, 10, 216.     | 3.6 | 55        |
| 49 | Relation among plant growth, carbohydrates and flowering time in the <i>Arabidopsis</i> Landsberg <i>erecta</i> Kondara recombinant inbred line population. <i>Plant, Cell and Environment</i> , 2010, 33, 1369-1382.                               | 5.7 | 35        |
| 50 | Physical organization of mixed protease inhibitor gene clusters, coordinated expression and association with resistance to late blight at the <i>StKI</i> locus on potato chromosome III. <i>Plant, Cell and Environment</i> , 2010, 33, 2149-2161. | 5.7 | 26        |
| 51 | Relationships between Growth, Growth Response to Nutrient Supply, and Ion Content Using a Recombinant Inbred Line Population in <i>Arabidopsis</i> [W][OA]. <i>Plant Physiology</i> , 2010, 154, 1361-1371.                                         | 4.8 | 54        |
| 52 | Comparison of mixed-model approaches for association mapping in rapeseed, potato, sugar beet, maize, and <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2009, 10, 94.                                                                                   | 2.8 | 79        |
| 53 | Single Nucleotide Polymorphisms in the Allene Oxide Synthase 2 Gene Are Associated With Field Resistance to Late Blight in Populations of Tetraploid Potato Cultivars. <i>Genetics</i> , 2009, 181, 1115-1127.                                      | 2.9 | 77        |
| 54 | Comparison of Mating Designs for Establishing Nested Association Mapping Populations in Maize and <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009, 183, 1525-1534.                                                                             | 2.9 | 45        |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | Multi-trait association mapping in sugar beet ( <i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 947-954.                                                     | 3.6 | 57        |
| 56 | Association mapping in multiple segregating populations of sugar beet ( <i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 1167-1179.                           | 3.6 | 28        |
| 57 | Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754.                                                                                       | 2.9 | 273       |
| 58 | Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. <i>Genetics</i> , 2007, 176, 563-570.                                              | 2.9 | 43        |
| 59 | Potential causes of linkage disequilibrium in a European maize breeding program investigated with computer simulations. <i>Theoretical and Applied Genetics</i> , 2007, 115, 529-536.       | 3.6 | 20        |
| 60 | Comparison of Linkage Disequilibrium in Elite European Maize Inbred Lines using AFLP and SSR Markers. <i>Molecular Breeding</i> , 2006, 17, 217-226.                                        | 2.1 | 52        |
| 61 | A new test for family-based association mapping with inbred lines from plant breeding programs. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1121-1130.                             | 3.6 | 33        |
| 62 | Linkage disequilibrium in European elite maize germplasm investigated with SSRs. <i>Theoretical and Applied Genetics</i> , 2005, 111, 723-730.                                              | 3.6 | 167       |
| 63 | Development of a near-infrared spectroscopy calibration for Hagberg falling number assessment of barley ( <i>Hordeum vulgare</i> ): A comparison of methods. <i>Plant Breeding</i> , 0, , . | 1.9 | 1         |