

# Benjamin Stich

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/857289/publications.pdf>

Version: 2024-02-01

63  
papers

3,086  
citations

172207

29  
h-index

168136

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.	4.1	16
2	Improvement of prediction ability by integrating multi-omic datasets in barley. <i>BMC Genomics</i> , 2022, 23, 200.	1.2	5
3	Genetic Divergence of Lineage-Specific Tandemly Duplicated Gene Clusters in Four Diploid Potato Genotypes. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	6
4	Accurate recombination estimation from pooled genotyping and sequencing: a case study on barley. <i>BMC Genomics</i> , 2022, 23, .	1.2	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, .	0.8	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.	2.9	13
7	The maize shoot ionome: Its interaction partners, predictive power, and genetic determinants. <i>Plant, Cell and Environment</i> , 2020, 43, 2095-2111.	2.8	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.	1.6	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.	1.2	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.	1.7	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.	1.7	19
12	Agronomic and Seed Quality Traits Dissected by Genome-Wide Association Mapping in Brassica napus. <i>Frontiers in Plant Science</i> , 2016, 7, 386.	1.7	78
13	A high-density SNP genotyping array for Brassica napus 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.	1.8	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.	1.6	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.	1.8	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.	0.8	33
17	Linkage mapping of Barley yellow dwarf virus resistance in connected populations of maize. <i>BMC Plant Biology</i> , 2015, 15, 29.	1.6	12
18	Seedling development traits in Brassica napus examined by gene expression analysis and association mapping. <i>BMC Plant Biology</i> , 2015, 15, 136.	1.6	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.	1.2	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.	1.7	35
22	The genetic basis of natural variation for iron homeostasis in the maize IBM population. BMC Plant Biology, 2014, 14, 12.	1.6	24
23	Genes involved in barley yellow dwarf virus resistance of maize. Theoretical and Applied Genetics, 2014, 127, 2575-2584.	1.8	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 SolCAP SNP array. Plant Breeding, 2013, 132, 718-724.	1.0	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.	1.6	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.	1.2	1
28	Co-Variation between Seed Dormancy, Growth Rate and Flowering Time Changes with Latitude in Arabidopsis thaliana. PLoS ONE, 2013, 8, e61075.	1.1	130
29	A candidate gene-based association study of tocopherol content and composition in rapeseed (Brassica napus). Frontiers in Plant Science, 2012, 3, 129.	1.7	58
30	QTL detection power of multi-parental RIL populations in Arabidopsis thaliana. Heredity, 2012, 108, 626-632.	1.2	27
31	Seedling development in a Brassica napus diversity set and its relationship to agronomic performance. Theoretical and Applied Genetics, 2012, 125, 1275-1287.	1.8	30
32	High-throughput polymorphism detection and genotyping in Brassica napus using next-generation RAD sequencing. BMC Genomics, 2012, 13, 281.	1.2	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.	1.6	30
34	Genome-wide association mapping of flowering time and northern corn leaf blight (Setosphaeria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	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.	1.8	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.	2.8	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.	0.9	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.	1.2	32
39	Population structure in sorghum accessions from West Africa differing in race and maturity class. <i>Genetica</i> , 2011, 139, 453-463.	0.5	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.	1.8	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.	1.2	5
42	Genome-wide distribution of genetic diversity and linkage disequilibrium in elite sugar beet germplasm. <i>BMC Genomics</i> , 2011, 12, 484.	1.2	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.	1.2	52
44	Detection of epistatic interactions in association mapping populations: an example from tetraploid potato. <i>Heredity</i> , 2011, 107, 537-547.	1.2	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.	1.8	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.	1.8	232
47	Population structure and genetic diversity in elite sugar beet germplasm investigated with SSR markers. <i>Euphytica</i> , 2010, 175, 35-42.	0.6	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.	1.6	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.	2.8	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.	2.8	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.	2.3	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.	1.2	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.	1.2	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.	1.2	45

#	ARTICLE	IF	CITATIONS
55	Multi-trait association mapping in sugar beet ( <i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 947-954.	1.8	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.	1.8	28
57	Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754.	1.2	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.	1.2	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.	1.8	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.	1.0	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.	1.8	33
62	Linkage disequilibrium in European elite maize germplasm investigated with SSRs. <i>Theoretical and Applied Genetics</i> , 2005, 111, 723-730.	1.8	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, , .	1.0	1