

# Benjamin Stich

## List of Publications by Year in descending order

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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	Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754.	1.2	273
2	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
3	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.	1.8	205
4	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
5	Linkage disequilibrium in European elite maize germplasm investigated with SSRs. <i>Theoretical and Applied Genetics</i> , 2005, 111, 723-730.	1.8	167
6	Co-Variation between Seed Dormancy, Growth Rate and Flowering Time Changes with Latitude in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2013, 8, e61075.	1.1	130
7	High-throughput polymorphism detection and genotyping in <i>Brassica napus</i> using next-generation RAD sequencing. <i>BMC Genomics</i> , 2012, 13, 281.	1.2	129
8	Genome-wide association mapping of iron homeostasis in the maize association population. <i>BMC Genetics</i> , 2015, 16, 1.	2.7	104
9	Genome-wide expression profiling and phenotypic evaluation of European maize inbreds at seedling stage in response to heat stress. <i>BMC Genomics</i> , 2015, 16, 123.	1.2	83
10	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
11	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.	1.7	78
12	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
13	Genome-wide association mapping of flowering time and northern corn leaf blight ( <i>Setosphaeria</i> ) Tj ETQq1 1 0.784314 rgBT /Overloc 1.6 70		
14	A candidate gene-based association study of tocopherol content and composition in rapeseed ( <i>Brassica napus</i> ). <i>Frontiers in Plant Science</i> , 2012, 3, 129.	1.7	58
15	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
16	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
17	Population structure and linkage disequilibrium in diploid and tetraploid potato revealed by genome-wide high-density genotyping using the <sc>SolCAP SNP</sc> array. <i>Plant Breeding</i> , 2013, 132, 718-724.	1.0	55
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	Relation among plant growth, carbohydrates and flowering time in the <i>Arabidopsis Landsberg erecta</i> — <i>Kondara</i> recombinant inbred line population. <i>Plant, Cell and Environment</i> , 2010, 33, 1369-1382.	2.8	35
26	Species- and genome-wide dissection of the shoot ionome in <i>Brassica napus</i> and its relationship to seedling development. <i>Frontiers in Plant Science</i> , 2014, 5, 485.	1.7	35
27	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
28	Population structure and genetic diversity in elite sugar beet germplasm investigated with SSR markers. <i>Euphytica</i> , 2010, 175, 35-42.	0.6	33
29	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
30	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
31	Seedling development in a <i>Brassica napus</i> diversity set and its relationship to agronomic performance. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1275-1287.	1.8	30
32	Association analysis of photoperiodic flowering time genes in west and central African sorghum [ <i>Sorghum bicolor</i> (L.) Moench]. <i>BMC Plant Biology</i> , 2012, 12, 32.	1.6	30
33	Analysis of Natural Variation of the Potato Tuber Proteome Reveals Novel Candidate Genes for Tuber Bruising. <i>Journal of Proteome Research</i> , 2012, 11, 703-716.	1.8	30
34	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
35	Seedling development traits in <i>Brassica napus</i> examined by gene expression analysis and association mapping. <i>BMC Plant Biology</i> , 2015, 15, 136.	1.6	28
36	QTL detection power of multi-parental RIL populations in <i>Arabidopsis thaliana</i> . <i>Heredity</i> , 2012, 108, 626-632.	1.2	27

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37	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
38	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
39	The genetic basis of natural variation for iron homeostasis in the maize IBM population. <i>BMC Plant Biology</i> , 2014, 14, 12.	1.6	24
40	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
41	Population structure in sorghum accessions from West Africa differing in race and maturity class. <i>Genetica</i> , 2011, 139, 453-463.	0.5	19
42	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
43	Genome-wide distribution of genetic diversity and linkage disequilibrium in elite sugar beet germplasm. <i>BMC Genomics</i> , 2011, 12, 484.	1.2	18
44	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
45	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
46	Detection of epistatic interactions in association mapping populations: an example from tetraploid potato. <i>Heredity</i> , 2011, 107, 537-547.	1.2	15
47	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
48	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
49	Genes involved in barley yellow dwarf virus resistance of maize. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2575-2584.	1.8	13
50	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
51	Linkage mapping of Barley yellow dwarf virus resistance in connected populations of maize. <i>BMC Plant Biology</i> , 2015, 15, 29.	1.6	12
52	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
53	Ups and downs of a transcriptional landscape shape iron deficiency associated chlorosis of the maize inbreds B73 and Mo17. <i>BMC Plant Biology</i> , 2013, 13, 213.	1.6	11
54	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

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55	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
56	Tapping natural variation at functional level reveals allele specific molecular characteristics of potato invertase ( <i>Painâ€1</i> ). <i>Plant, Cell and Environment</i> , 2012, 35, 2143-2154.	2.8	7
57	Dissection of Potato Complex Traits by Linkage and Association Genetics as Basis for Developing Molecular Diagnostics in Breeding Programs. , 2014, , 47-85.		7
58	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
59	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
60	Improvement of prediction ability by integrating multi-omic datasets in barley. <i>BMC Genomics</i> , 2022, 23, 200.	1.2	5
61	Response to â€Controlling type 1 error rates in genome-wide association studies in plantsâ€™ by Andrew W George. <i>Heredity</i> , 2013, 111, 88-88.	1.2	1
62	Development of a nearâ€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
63	Accurate recombination estimation from pooled genotyping and sequencing: a case study on barley. <i>BMC Genomics</i> , 2022, 23, .	1.2	0