

Kevin P Smith

List of Publications by Year in descending order

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97
papers

3,969
citations

136740

32
h-index

138251

58
g-index

107
all docs

107
docs citations

107
times ranked

3386
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Selection in Plant Breeding. <i>Advances in Agronomy</i> , 2011, 110, 77-123.	2.4	395
2	A high-density consensus map of barley linking DArT markers to SSR, RFLP and STS loci and agricultural traits. <i>BMC Genomics</i> , 2006, 7, 206.	1.2	305
3	HOST VARIATION FOR INTERACTIONS WITH BENEFICIAL PLANT-ASSOCIATED MICROBES. <i>Annual Review of Phytopathology</i> , 1999, 37, 473-491.	3.5	195
4	Association mapping of spot blotch resistance in wild barley. <i>Molecular Breeding</i> , 2010, 26, 243-256.	1.0	151
5	Adding Genetically Distant Individuals to Training Populations Reduces Genomic Prediction Accuracy in Barley. <i>Crop Science</i> , 2015, 55, 2657-2667.	0.8	150
6	Genome-wide association mapping of Fusarium head blight resistance in contemporary barley breeding germplasm. <i>Molecular Breeding</i> , 2011, 27, 439-454.	1.0	142
7	Assessing Genomic Selection Prediction Accuracy in a Dynamic Barley Breeding Population. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.05.0020.	1.6	130
8	Quantitative trait loci associated with resistance to Fusarium head blight and kernel discoloration in barley. <i>Theoretical and Applied Genetics</i> , 1999, 99, 561-569.	1.8	129
9	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. <i>Crop Science</i> , 2010, 50, 556-566.	0.8	106
10	PopVar: A Genome-Wide Procedure for Predicting Genetic Variance and Correlated Response in Biparental Breeding Populations. <i>Crop Science</i> , 2015, 55, 2068-2077.	0.8	99
11	Quantitative Trait Loci for Multiple Disease Resistance in Wild Barley. <i>Crop Science</i> , 2005, 45, 2563-2572.	0.8	85
12	The Role of Deleterious Substitutions in Crop Genomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2307-2317.	3.5	83
13	Genome-wide SNPs and re-sequencing of growth habit and inflorescence genes in barley: implications for association mapping in germplasm arrays varying in size and structure. <i>BMC Genomics</i> , 2010, 11, 707.	1.2	81
14	Quantitative Trait Loci for Fusarium Head Blight Resistance in Barley Detected in a Two-Rowed by Six-Rowed Population. <i>Crop Science</i> , 2003, 43, 307-318.	0.8	78
15	Effect of population size and unbalanced data sets on QTL detection using genome-wide association mapping in barley breeding germplasm. <i>Theoretical and Applied Genetics</i> , 2012, 124, 111-124.	1.8	77
16	Development and Genetic Characterization of an Advanced Backcross-Nested Association Mapping (AB-NAM) Population of Wild – Cultivated Barley. <i>Genetics</i> , 2016, 203, 1453-1467.	1.2	73
17	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.	1.8	67
18	Genetic architecture of quantitative trait loci associated with morphological and agronomic trait differences in a wild by cultivated barley cross. <i>Genome</i> , 2007, 50, 714-723.	0.9	66

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19	Transpiration increases under high temperature stress: Potential mechanisms, trade-offs and prospects for crop resilience in a warming world. <i>Plant, Cell and Environment</i> , 2021, 44, 2102-2116.	2.8	65
20	Differential transcriptomic responses to <i>Fusarium graminearum</i> infection in two barley quantitative trait loci associated with <i>Fusarium</i> head blight resistance. <i>BMC Genomics</i> , 2016, 17, 387.	1.2	64
21	Association Mapping of Agronomic QTLs in U.S. Spring Barley Breeding Germplasm. <i>Plant Genome</i> , 2014, 7, plantgenome2013.11.0037.	1.6	63
22	The Genetics of Winterhardiness in Barley: Perspectives from Genome-Wide Association Mapping. <i>Plant Genome</i> , 2011, 4, .	1.6	62
23	Accelerating <i>Silphium</i> Domestication: An Opportunity to Develop New Crop Ideotypes and Breeding Strategies Informed by Multiple Disciplines. <i>Crop Science</i> , 2017, 57, 1274-1284.	0.8	61
24	Validation of Quantitative Trait Loci for Multiple Disease Resistance in Barley Using Advanced Backcross Lines Developed with a Wild Barley. <i>Crop Science</i> , 2006, 46, 1179-1186.	0.8	47
25	Evaluating Methods of Updating Training Data in Long-Term Genomewide Selection. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1499-1510.	0.8	44
26	Quantitative Trait Loci for <i>Fusarium</i> Head Blight Resistance in Barley Detected in a Two-Rowed by Six-Rowed Population. <i>Crop Science</i> , 2003, 43, 307.	0.8	44
27	Genomic Selection Performs Similarly to Phenotypic Selection in Barley. <i>Crop Science</i> , 2016, 56, 2871-2881.	0.8	39
28	Genetic Relationship between Kernel Discoloration and Grain Protein Concentration in Barley. <i>Crop Science</i> , 2003, 43, 1671-1679.	0.8	38
29	Two Genomic Regions Contribute Disproportionately to Geographic Differentiation in Wild Barley. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1193-1203.	0.8	38
30	Mapping Agronomic Traits in a Wild Barley Advanced Backcross-Nested Association Mapping Population. <i>Crop Science</i> , 2017, 57, 1199-1210.	0.8	38
31	QTL Mapping of <i>Fusarium</i> Head Blight and Correlated Agromorphological Traits in an Elite Barley Cultivar Rasmusson. <i>Frontiers in Plant Science</i> , 2018, 9, 1260.	1.7	37
32	Effect of Advanced Cycle Breeding on Genetic Diversity in Barley Breeding Germplasm. <i>Crop Science</i> , 2008, 48, 1027-1036.	0.8	36
33	Analysis of the chromosome 2(2H) region of barley associated with the correlated traits <i>Fusarium</i> head blight resistance and heading date. <i>Theoretical and Applied Genetics</i> , 2007, 115, 561-570.	1.8	35
34	The <i>Hordeum</i> Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012, 5, 81-91.	1.6	35
35	Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and β -glucan in US barley breeding germplasm. <i>Molecular Breeding</i> , 2014, 34, 1229-1243.	1.0	35
36	Evaluation and retrospective optimization of genomic selection for yield and disease resistance in spring barley. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	34

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37	Multi-trait Improvement by Predicting Genetic Correlations in Breeding Crosses. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3153-3165.	0.8	34
38	Transcriptome analysis of a barley breeding program examines gene expression diversity and reveals target genes for malting quality improvement. <i>BMC Genomics</i> , 2010, 11, 653.	1.2	29
39	Validation of quantitative trait loci for Fusarium head blight and kernel discoloration in barley. <i>Molecular Breeding</i> , 2004, 14, 91-104.	1.0	27
40	Host Genetic Effect on Deoxynivalenol Accumulation in Fusarium Head Blight of Barley. <i>Phytopathology</i> , 2004, 94, 766-771.	1.1	27
41	Genome-wide association mapping of agronomic traits in relevant barley germplasm in Uruguay. <i>Molecular Breeding</i> , 2013, 31, 631-654.	1.0	25
42	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.	1.0	24
43	Development of a Multiparent Population for Genetic Mapping and Allele Discovery in Six-Row Barley. <i>Genetics</i> , 2019, 213, 595-613.	1.2	23
44	Registration of "Quest"™ Spring Malting Barley with Improved Resistance to Fusarium Head Blight. <i>Journal of Plant Registrations</i> , 2013, 7, 125-129.	0.4	23
45	Genome-Wide Association Study of Spot Form of Net Blotch Resistance in the Upper Midwest Barley Breeding Programs. <i>Phytopathology</i> , 2017, 107, 100-108.	1.1	22
46	Haplotype diversity and population structure in cultivated and wild barley evaluated for Fusarium head blight responses. <i>Theoretical and Applied Genetics</i> , 2013, 126, 619-636.	1.8	21
47	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.	0.8	21
48	Validating Genomewide Predictions of Genetic Variance in a Contemporary Breeding Program. <i>Crop Science</i> , 2019, 59, 1062-1072.	0.8	21
49	Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. <i>Theoretical and Applied Genetics</i> , 2021, 134, 4043-4054.	1.8	20
50	Using near-isogenic barley lines to validate deoxynivalenol (DON) QTL previously identified through association analysis. <i>Theoretical and Applied Genetics</i> , 2014, 127, 633-645.	1.8	19
51	Perspectives on Low Temperature Tolerance and Vernalization Sensitivity in Barley: Prospects for Facultative Growth Habit. <i>Frontiers in Plant Science</i> , 2020, 11, 585927.	1.7	19
52	Exploiting selective genotyping to study genetic diversity of resistance to Fusarium head blight in barley. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1160-1168.	1.8	18
53	Variation in Kernel Hardness and Associated Traits in U.S. Barley Breeding Lines. <i>Cereal Chemistry</i> , 2010, 87, 461-466.	1.1	17
54	Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat (<i>Avena sativa</i> L.). <i>Genetics</i> , 2021, 217, .	1.2	17

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55	Effect of Advanced Cycle Breeding on Genetic Gain and Phenotypic Diversity in Barley Breeding Germplasm. <i>Crop Science</i> , 2009, 49, 1751-1761.	0.8	15
56	Identification of quantitative trait loci for net form net blotch resistance in contemporary barley breeding germplasm from the USA using genome-wide association mapping. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1019-1037.	1.8	15
57	Registration of "Rasmusson"™ Barley. <i>Journal of Plant Registrations</i> , 2010, 4, 167-170.	0.4	14
58	Genome-wide association for Î ² -glucan content, population structure, and linkage disequilibrium in elite oat germplasm adapted to subtropical environments. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	14
59	Improving Genomic Prediction for Seed Quality Traits in Oat (<i>Avena sativa</i> L.) Using Trait-Specific Relationship Matrices. <i>Frontiers in Genetics</i> , 2021, 12, 643733.	1.1	14
60	Genetic loci mediating circadian clock output plasticity and crop productivity under barley domestication. <i>New Phytologist</i> , 2021, 230, 1787-1801.	3.5	14
61	Quantitative Trait Loci Associated with the Tocochromanol (Vitamin E) Pathway in Barley. <i>PLoS ONE</i> , 2015, 10, e0133767.	1.1	14
62	Quantitative trait loci conferring resistance to <i>Fusarium</i> head blight in barley respond differentially to <i>Fusarium graminearum</i> infection. <i>Functional and Integrative Genomics</i> , 2011, 11, 95-102.	1.4	12
63	TCAP FACâ€WIN6 Elite Barley GWAS Panel QTL. I. Barley Stripe Rust Resistance QTL in Facultative and Winter Sixâ€Rowed Malt Barley Breeding Programs Identified via GWAS. <i>Crop Science</i> , 2018, 58, 103-119.	0.8	12
64	The Fate of Deleterious Variants in a Barley Genomic Prediction Population. <i>Genetics</i> , 2019, 213, 1531-1544.	1.2	12
65	Comparative Analyses Identify the Contributions of Exotic Donors to Disease Resistance in a Barley Experimental Population. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1945-1953.	0.8	11
66	Registration of the S2MET Barley Mapping Population for Multiâ€Environment Genomewide Selection. <i>Journal of Plant Registrations</i> , 2019, 13, 270-280.	0.4	11
67	Multiscale characterization and micromechanical modeling of crop stem materials. <i>Biomechanics and Modeling in Mechanobiology</i> , 2021, 20, 69-91.	1.4	11
68	Genotype by environment interactions (GEIs) for barley grain yield under salt stress condition. <i>Journal of Crop Science and Biotechnology</i> , 2017, 20, 193-204.	0.7	10
69	Variation in Lignin, Cell Wall-Bound <i>p</i> -Coumaric, and Ferulic Acid in the Nodes and Internodes of Cereals and Their Impact on Lodging. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 12569-12576.	2.4	10
70	Assessment of Winter Barley in Minnesota: Relationships among Cultivar, Fall Seeding Date, Winter Survival, and Grain Yield. <i>Crop, Forage and Turfgrass Management</i> , 2019, 5, 190055.	0.2	9
71	Silflower seed and biomass responses to plant density and nitrogenâ€fertilization. , 2020, 3, e20118.		9
72	Selection for seed size has uneven effects on specialized metabolite abundance in oat (<i>Avena</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	9

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73	Comparison of ELISA for Fusarium, Visual Screening, and Deoxynivalenol Analysis of Fusarium Head Blight for Barley Field Nurseries. <i>Crop Science</i> , 2008, 48, 1389-1398.	0.8	8
74	Mapping crown rust resistance at multiple time points in elite oat germplasm. <i>Plant Genome</i> , 2020, 13, e20007.	1.6	8
75	Generalizable approaches for genomic prediction of metabolites in plants. <i>Plant Genome</i> , 2022, 15, e20205.	1.6	8
76	Natural Genetic Variation Underlying Tiller Development in Barley (<i>Hordeum vulgare</i> L). G3: Genes, Genomes, Genetics, 2020, 10, 1197-1212.	0.8	7
77	Optimizing the choice of test locations for multitrait genotypic evaluation. <i>Crop Science</i> , 2022, 62, 192-202.	0.8	7
78	Measurements of lethal and nonlethal inbreeding depression inform the de novo domestication of <i>Silphium integrifolium</i> . <i>American Journal of Botany</i> , 2021, 108, 980-992.	0.8	6
79	Inexpensive, High Throughput Microplate Format for Plant Nucleic Acid Extraction: Suitable for Multiplex Southern Analyses of Transgenes. <i>Crop Science</i> , 2005, 45, 1985-1989.	0.8	5
80	Genomics-Based Barley Breeding. <i>Compendium of Plant Genomes</i> , 2018, , 287-315.	0.3	5
81	Quantifying cereal crop movement through hemispherical video analysis of agricultural plots. <i>Plant Methods</i> , 2019, 15, 55.	1.9	5
82	Cereal Stem Stress: In Situ Biomechanical Characterization of Stem Elasticity. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 7965.	1.3	5
83	Using environmental similarities to design training sets for genomewide selection. <i>Crop Science</i> , 2021, 61, 396-409.	0.8	5
84	Genetic dissection of a pericentromeric region of barley chromosome 6H associated with Fusarium head blight resistance, grain protein content and agronomic traits. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3963-3981.	1.8	5
85	Genetic characterization of agronomic traits and grain threshability for organic naked barley in the northern United States. <i>Crop Science</i> , 2022, 62, 690-703.	0.8	5
86	Cold Conditioned: Discovery of Novel Alleles for Low-Temperature Tolerance in the Vavilov Barley Collection. <i>Frontiers in Plant Science</i> , 2021, 12, 800284.	1.7	5
87	TCAP FACWIN6 Elite Barley GWAS Panel QTL. II. Malting Quality QTL in Elite North American Facultative and Winter Six-Rowed Barley Identified via GWAS. <i>Crop Science</i> , 2018, 58, 120-132.	0.8	4
88	Mapping QTLs for Grain Protein Concentration and Agronomic Traits under Different Nitrogen Levels in Barley. <i>Crop Science</i> , 2019, 59, 68-83.	0.8	4
89	Genome-wide association mapping for kernel shape and its association with β -glucan content in oats. <i>Crop Science</i> , 2021, 61, 3986-3999.	0.8	4
90	Development of first linkage map for <i>Silphium integrifolium</i> (Asteraceae) enables identification of sporophytic self-incompatibility locus. <i>Heredity</i> , 2022, 128, 304-312.	1.2	4

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91	Mapping malting quality and yield characteristics in a north American two-rowed malting barley Ã— wild barley advanced backcross population. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	3
92	Assessing phenotypic diversity in silflower (<i>Silphium integrifolium</i> Michx.) to identify traits of interest for domestication selection. <i>Crop Science</i> , 2022, 62, 1443-1460.	0.8	3
93	The evolutionary patterns of barley pericentromeric chromosome regions, as shaped by linkage disequilibrium and domestication. <i>Plant Journal</i> , 0, , .	2.8	3
94	Oat Crown Rust Disease Severity Estimated at Many Time Points Using Multispectral Aerial Photos. <i>Phytopathology</i> , 2022, 112, 682-690.	1.1	2
95	Reverse introduction of twoâ€•and sixâ€•rowed barley lines from the United States into Egypt. <i>Crop Science</i> , 2020, 60, 812-829.	0.8	1
96	Capturing High Resolution Plant Movement in the Field. <i>Integrative and Comparative Biology</i> , 0, , .	0.9	1
97	Association between xylem vasculature size and freezing survival in winter barley. <i>Journal of Agronomy and Crop Science</i> , 0, , .	1.7	0