Chris-Carolin SchÃ¶n

List of Publications by Year
in descending order

93 papers	6,237 citations	71102 41 h-index	74163 75 g-index
100 all docs	100 docs citations	100 times ranked	5435 citing authors

#	Article	IF	Citations
1	High-resolution association mapping with libraries of immortalized lines from ancestral landraces. Theoretical and Applied Genetics, 2022, 135, 243-256.	3.6	5
2	Genetic diversity of European maize landraces: Dataset on the molecular and phenotypic variation of derived doubled-haploid populations. Data in Brief, 2022, 42, 108164.	1.0	4
3	Theoretical and experimental assessment of genome-based prediction in landraces of allogamous crops. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121797119.	7.1	4
4	Natural alleles of the abscisic acid catabolism gene *ZmAbh4* modulate water use efficiency and carbon isotope discrimination in maize. Plant Cell, 2022, 34, 3860-3872.	6.6	5
5	Exploiting genetic diversity in two European maize landraces for improving Gibberella ear rot resistance using genomic tools. Theoretical and Applied Genetics, 2021, 134, 793-805.	3.6	18
6	The carbon isotopic signature of C4 crops and its applicability in breeding for climate resilience. Theoretical and Applied Genetics, 2021, 134, 1663-1675.	3.6	8
7	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	2.6	4
8	Accounting for epistasis improves genomic prediction of phenotypes with univariate and bivariate models across environments. Theoretical and Applied Genetics, 2021, 134, 2913-2930.	3.6	5
9	Calibration and validation of predicted genomic breeding values in an advanced cycle maize population. Theoretical and Applied Genetics, 2021, 134, 3069-3081.	3.6	12
10	Increasing calling accuracy, coverage, and read-depth in sequence data by the use of haplotype blocks. PLoS Genetics, 2021, 17, e1009944.	3.5	5
11	Improving Imputation Quality in BEAGLE for Crop and Livestock Data. G3: Genes, Genomes, Genetics, 2020, 10, 177-188.	1.8	43
12	Inferring trait-specific similarity among individuals from molecular markers and phenotypes with Bayesian regression. Theoretical Population Biology, 2020, 132, 47-59.	1.1	9
13	Discovery of beneficial haplotypes for complex traits in maize landraces. Nature Communications, 2020, 11, 4954.	12.8	38
14	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	21.4	84
15	Transcriptomic diversity in seedling roots of European flint maize in response to cold. BMC Genomics, 2020, 21, 300.	2.8	14
16	European maize landraces made accessible for plant breeding and genome-based studies. Theoretical and Applied Genetics, 2019, 132, 3333-3345.	3.6	52
17	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. Theoretical and Applied Genetics, 2019, 132, 1897-1908.	3.6	28
18	Carbon isotope composition, water use efficiency, and drought sensitivity are controlled by a common genomic segment in maize. Theoretical and Applied Genetics, 2019, 132, 53-63.	3.6	26

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19	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. Genetics, 2018, 210, 1185-1196.	2.9	18
20	Generating Plants with Improved Water Use Efficiency. Agronomy, 2018, 8, 194.	3.0	51
21	Assay for abscisic acid 8′-hydroxylase activity of cloned plant cytochrome P450 oxidases in Saccharomyces cerevisiae. Analytical Biochemistry, 2018, 553, 24-27.	2.4	6
22	Prediction of Complex Traits: Robust Alternatives to Best Linear Unbiased Prediction. Frontiers in Genetics, 2018, 9, 195.	2.3	29
23	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. Genetics, 2017, 206, 1611-1619.	2.9	24
24	Genetic Gain Increases by Applying the Usefulness Criterion with Improved Variance Prediction in Selection of Crosses. Genetics, 2017, 207, 1651-1661.	2.9	65
25	Exploring new alleles for frost tolerance in winter rye. Theoretical and Applied Genetics, 2017, 130, 2151-2164.	3.6	20
26	Is there an optimum level of diversity in utilization of genetic resources?. Theoretical and Applied Genetics, 2017, 130, 2283-2295.	3.6	25
27	Bayesian Networks Illustrate Genomic and Residual Trait Connections in Maize (*Zea mays* L.). G3: Genes, Genomes, Genetics, 2017, 7, 2779-2789.	1.8	16
28	Towards a whole‐genome sequence for rye (*Secale cereale* L.). Plant Journal, 2017, 89, 853-869.	5.7	238
29	Geography and end use drive the diversification of worldwide winter rye populations. Molecular Ecology, 2016, 25, 500-514.	3.9	17
30	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. Genome Biology, 2016, 17, 137.	8.8	51
31	Association mapping for cold tolerance in two large maize inbred panels. BMC Plant Biology, 2016, 16, 127.	3.6	73
32	Model training across multiple breeding cycles significantly improves genomic prediction accuracy in rye (Secale cereale L.). Theoretical and Applied Genetics, 2016, 129, 2043-2053.	3.6	84
33	Oligogenic control of resistance to soil‐borne viruses SBCMV and WSSMV in rye (*Secale cereale* L.). Plant Breeding, 2016, 135, 552-559.	1.9	6
34	Cross-Validation Without Doing Cross-Validation in Genome-Enabled Prediction. G3: Genes, Genomes, Genetics, 2016, 6, 3107-3128.	1.8	50
35	Genome-Wide Association Studies with a Genomic Relationship Matrix: A Case Study with Wheat and *Arabidopsis*. G3: Genes, Genomes, Genetics, 2016, 6, 3241-3256.	1.8	32
36	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. Genetics, 2016, 202, 1267-1276.	2.9	61

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37	Choice of models for QTL mapping with multiple families and design of the training set for prediction of Fusarium resistance traits in maize. Theoretical and Applied Genetics, 2016, 129, 431-444.	3.6	30
38	Diversity analysis and genomic prediction of Sclerotinia resistance in sunflower using a new 25ÂK SNP genotyping array. Theoretical and Applied Genetics, 2016, 129, 317-329.	3.6	22
39	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav046.	3.0	62
40	Prolonged expression of the BX1 signature enzyme is associated with a recombination hotspot in the benzoxazinoid gene cluster in Zea mays. Journal of Experimental Botany, 2015, 66, 3917-3930.	4.8	53
41	Resemblance between two relatives â€" animal and plant breeding. Journal of Animal Breeding and Genetics, 2015, 132, 1-2.	2.0	9
42	Do Molecular Markers Inform About Pleiotropy?. Genetics, 2015, 201, 23-29.	2.9	53
43	Forecasting the accuracy of genomic prediction with different selection targets in the training and prediction set as well as truncation selection. Theoretical and Applied Genetics, 2015, 128, 2189-2201.	3.6	7
44	Improving resistance to the European corn borer: a comprehensive study in elite maize using QTL mapping and genome-wide prediction. Theoretical and Applied Genetics, 2015, 128, 875-891.	3.6	37
45	Assessment of Genetic Heterogeneity in Structured Plant Populations Using Multivariate Whole-Genome Regression Models. Genetics, 2015, 201, 323-337.	2.9	58
46	Enhancing Genome-Enabled Prediction by Bagging Genomic BLUP. PLoS ONE, 2014, 9, e91693.	2.5	41
47	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. Crop Science, 2014, 54, 1981-1991.	1.8	30
48	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. Genetics, 2014, 198, 1717-1734.	2.9	89
49	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. BMC Genomics, 2014, 15, 823.	2.8	242
50	Stable Carbon Isotope Discrimination Is under Genetic Control in the C4 Species Maize with Several Genomic Regions Influencing Trait Expression Â. Plant Physiology, 2014, 164, 131-143.	4.8	34
51	Genome-based prediction of maize hybrid performance across genetic groups, testers, locations, and years. Theoretical and Applied Genetics, 2014, 127, 1375-1386.	3.6	90
52	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. Theoretical and Applied Genetics, 2014, 127, 2313-2331.	3.6	41
53	The importance of phenotypic data analysis for genomic prediction - a case study comparing different spatial models in rye. BMC Genomics, 2014, 15, 646.	2.8	51
54	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	2.9	114

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55	Statistical Models for the Prediction of Genetic Values. , 2014, , 183-205.		0
56	Genome-Wide Prediction of Traits with Different Genetic Architecture Through Efficient Variable Selection. Genetics, 2013, 195, 573-587.	2.9	129
57	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	9.6	176
58	BSTA: a targeted approach combines bulked segregant analysis with next- generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. BMC Genomics, 2013, 14, 628.	2.8	43
59	Reticulate Evolution of the Rye Genome. Plant Cell, 2013, 25, 3685-3698.	6.6	194
60	Sensitivity to prior specification in Bayesian genome-based prediction models. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 375-91.	0.6	27
61	synbreed: a framework for the analysis of genomic prediction data using R. Bioinformatics, 2012, 28, 2086-2087.	4.1	296
62	The genetics of environmental variation of dry matter grain yield in maize. Genetical Research, 2012, 94, 113-119.	0.9	4
63	Maximizing the Reliability of Genomic Selection by Optimizing the Calibration Set of Reference Individuals: Comparison of Methods in Two Diverse Groups of Maize Inbreds (<i>Zea mays</i> L.). Genetics, 2012, 192, 715-728.	2.9	258
64	QTL mapping under truncation selection in homozygous lines derived from biparental crosses. Theoretical and Applied Genetics, 2012, 124, 543-553.	3.6	5
65	Genome-based prediction of testcross values in maize. Theoretical and Applied Genetics, 2011, 123, 339-350.	3.6	268
66	From RNA-seq to large-scale genotyping - genomics resources for rye (Secale cereale L.). BMC Plant Biology, 2011, 11, 131.	3.6	109
67	Association analysis of frost tolerance in rye using candidate genes and phenotypic data from controlled, semi-controlled, and field phenotyping platforms. BMC Plant Biology, 2011, 11, 146.	3.6	47
68	High levels of nucleotide diversity and fast decline of linkage disequilibrium in rye (Secale cerealeL.) genes involved in frost response. BMC Plant Biology, 2011, 11, 6.	3.6	55
69	A Large Maize (Zea mays L.) SNP Genotyping Array: Development and Germplasm Genotyping, and Genetic Mapping to Compare with the B73 Reference Genome. PLoS ONE, 2011, 6, e28334.	2.5	523
70	High congruency of QTL positions for heterosis of grain yield in three crosses of maize. Theoretical and Applied Genetics, 2010, 120, 321-332.	3.6	75
71	Fine mapping of the sunflower resistance locus Pl ARG introduced from the wild species Helianthus argophyllus. Theoretical and Applied Genetics, 2010, 121, 1633-1644.	3.6	41
72	Development of Heterotic Groups in Triticale. Crop Science, 2010, 50, 584-590.	1.8	76

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73	Impact of Genetic Divergence on the Ratio of Variance Due to Specific vs. General Combining Ability in Winter Triticale. Crop Science, 2009, 49, 2119-2122.	1.8	14
74	Unraveling Epistasis With Triple Testcross Progenies of Near-Isogenic Lines. Genetics, 2009, 181, 247-257.	2.9	28
75	Revealing the genetic architecture of FHB resistance in hexaploid wheat (Triticum aestivum L.) by QTL meta-analysis. Molecular Breeding, 2009, 23, 473-488.	2.1	203
76	Marker selection for Fusarium head blight resistance based on quantitative trait loci (QTL) from two European sources compared to phenotypic selection in winter wheat. Euphytica, 2009, 166, 219-227.	1.2	41
77	Marker-based introduction of three quantitative-trait loci conferring resistance to Fusarium head blight into an independent elite winter wheat breeding population. Theoretical and Applied Genetics, 2008, 117, 29-35.	3.6	41
78	Trends in genetic variance components during 30 years of hybrid maize breeding at the University of Hohenheim. Plant Breeding, 2008, 127, 446-451.	1.9	44
79	Genetic Expectations of Quantitative Trait Loci Main and Interaction Effects Obtained With the Triple Testcross Design and Their Relevance for the Analysis of Heterosis. Genetics, 2008, 178, 2265-2274.	2.9	30
80	The Role of Epistasis in the Manifestation of Heterosis: A Systems-Oriented Approach. Genetics, 2007, 177, 1815-1825.	2.9	125
81	Heterosis for Biomass-Related Traits in Arabidopsis Investigated by Quantitative Trait Loci Analysis of the Triple Testcross Design With Recombinant Inbred Lines. Genetics, 2007, 177, 1839-1850.	2.9	55
82	Prospects for hybrid breeding in winter triticale: II. Relationship between parental genetic distance and specific combining ability. Plant Breeding, 2006, 125, 331-336.	1.9	24
83	Effect of population size on the estimation of QTL: a test using resistance to barley stripe rust. Theoretical and Applied Genetics, 2005, 111, 1260-1270.	3.6	185
84	QTL mapping of resistance to Sclerotinia midstalk rot in RIL of sunflower population NDBLOSsel×CM625. Theoretical and Applied Genetics, 2005, 110, 1490-1498.	3.6	39
85	Identification and validation of QTL for Sclerotinia midstalk rot resistance in sunflower by selective genotyping. Theoretical and Applied Genetics, 2005, 111, 233-242.	3.6	36
86	Quantitative Trait Locus Mapping Based on Resampling in a Vast Maize Testcross Experiment and Its Relevance to Quantitative Genetics for Complex Traits. Genetics, 2004, 167, 485-498.	2.9	231
87	QTL analyses of complex traits with cross validation, bootstrapping and other biometric methods. Euphytica, 2004, 137, 1-11.	1.2	48
88	Hybrid performance and AFLP- based genetic similarity in faba bean. Euphytica, 2004, 139, 207-216.	1.2	14
89	QTL mapping of Sclerotinia midstalk-rot resistance in sunflower. Theoretical and Applied Genetics, 2004, 109, 1474-1484.	3.6	44
90	Genetic diversity in recent elite faba bean lines using AFLP markers. Theoretical and Applied Genetics, 2003, 107, 1304-1314.	3.6	78

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91	RFLP Mapping in Maize: Quantitative Trait Loci Affecting Testcross Performance of Elite European Flint Lines. Crop Science, 1994, 34, 378-389.	1.8	147
92	Influence of barley variety mixtures on severity of scald and net blotch and on yield *. Plant Pathology, 1994, 43, 356-361.	2.4	34
93	Mapping and characterization of quantitative trait loci affecting resistance against second-generation European corn borer in maize with the aid of RFLPs. Heredity, 1993, 70, 648-659.	2.6	135

RFLP Mapping in Maize: Quantitative Trait Loci Affecting Testcross Performance of Elite European Flint Lines. Crop Science, 1994, 34, 378-389.