

Chris-Carolin Schön

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/510856/publications.pdf>

Version: 2024-02-01

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	A Large Maize (<i>Zea mays</i> L.) SNP Genotyping Array: Development and Germplasm Genotyping, and Genetic Mapping to Compare with the B73 Reference Genome. <i>PLoS ONE</i> , 2011, 6, e28334.	2.5	523
2	synbreed: a framework for the analysis of genomic prediction data using R. <i>Bioinformatics</i> , 2012, 28, 2086-2087.	4.1	296
3	Genome-based prediction of testcross values in maize. <i>Theoretical and Applied Genetics</i> , 2011, 123, 339-350.	3.6	268
4	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.). <i>Genetics</i> , 2012, 192, 715-728.	2.9	258
5	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. <i>BMC Genomics</i> , 2014, 15, 823.	2.8	242
6	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	5.7	238
7	Quantitative Trait Locus Mapping Based on Resampling in a Vast Maize Testcross Experiment and Its Relevance to Quantitative Genetics for Complex Traits. <i>Genetics</i> , 2004, 167, 485-498.	2.9	231
8	Revealing the genetic architecture of FHB resistance in hexaploid wheat (<i>Triticum aestivum</i> L.) by QTL meta-analysis. <i>Molecular Breeding</i> , 2009, 23, 473-488.	2.1	203
9	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	6.6	194
10	Effect of population size on the estimation of QTL: a test using resistance to barley stripe rust. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1260-1270.	3.6	185
11	Intraspecific variation of recombination rate in maize. <i>Genome Biology</i> , 2013, 14, R103.	9.6	176
12	RFLP Mapping in Maize: Quantitative Trait Loci Affecting Testcross Performance of Elite European Flint Lines. <i>Crop Science</i> , 1994, 34, 378-389.	1.8	147
13	Mapping and characterization of quantitative trait loci affecting resistance against second-generation European corn borer in maize with the aid of RFLPs. <i>Heredity</i> , 1993, 70, 648-659.	2.6	135
14	Genome-Wide Prediction of Traits with Different Genetic Architecture Through Efficient Variable Selection. <i>Genetics</i> , 2013, 195, 573-587.	2.9	129
15	The Role of Epistasis in the Manifestation of Heterosis: A Systems-Oriented Approach. <i>Genetics</i> , 2007, 177, 1815-1825.	2.9	125
16	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. <i>Genetics</i> , 2014, 198, 3-16.	2.9	114
17	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	3.6	109
18	Genome-based prediction of maize hybrid performance across genetic groups, testers, locations, and years. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1375-1386.	3.6	90

#	ARTICLE	IF	CITATIONS
19	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. <i>Genetics</i> , 2014, 198, 1717-1734.	2.9	89
20	Model training across multiple breeding cycles significantly improves genomic prediction accuracy in rye (<i>Secale cereale</i> L.). <i>Theoretical and Applied Genetics</i> , 2016, 129, 2043-2053.	3.6	84
21	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020, 52, 950-957.	21.4	84
22	Genetic diversity in recent elite faba bean lines using AFLP markers. <i>Theoretical and Applied Genetics</i> , 2003, 107, 1304-1314.	3.6	78
23	Development of Heterotic Groups in Triticale. <i>Crop Science</i> , 2010, 50, 584-590.	1.8	76
24	High congruency of QTL positions for heterosis of grain yield in three crosses of maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 321-332.	3.6	75
25	Association mapping for cold tolerance in two large maize inbred panels. <i>BMC Plant Biology</i> , 2016, 16, 127.	3.6	73
26	Genetic Gain Increases by Applying the Usefulness Criterion with Improved Variance Prediction in Selection of Crosses. <i>Genetics</i> , 2017, 207, 1651-1661.	2.9	65
27	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav046.	3.0	62
28	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. <i>Genetics</i> , 2016, 202, 1267-1276.	2.9	61
29	Assessment of Genetic Heterogeneity in Structured Plant Populations Using Multivariate Whole-Genome Regression Models. <i>Genetics</i> , 2015, 201, 323-337.	2.9	58
30	Heterosis for Biomass-Related Traits in Arabidopsis Investigated by Quantitative Trait Loci Analysis of the Triple Testcross Design With Recombinant Inbred Lines. <i>Genetics</i> , 2007, 177, 1839-1850.	2.9	55
31	High levels of nucleotide diversity and fast decline of linkage disequilibrium in rye (<i>Secale cereale</i> L.) genes involved in frost response. <i>BMC Plant Biology</i> , 2011, 11, 6.	3.6	55
32	Prolonged expression of the BX1 signature enzyme is associated with a recombination hotspot in the benzoxazinoid gene cluster in <i>Zea mays</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 3917-3930.	4.8	53
33	Do Molecular Markers Inform About Pleiotropy?. <i>Genetics</i> , 2015, 201, 23-29.	2.9	53
34	European maize landraces made accessible for plant breeding and genome-based studies. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3333-3345.	3.6	52
35	The importance of phenotypic data analysis for genomic prediction - a case study comparing different spatial models in rye. <i>BMC Genomics</i> , 2014, 15, 646.	2.8	51
36	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016, 17, 137.	8.8	51

#	ARTICLE	IF	CITATIONS
37	Generating Plants with Improved Water Use Efficiency. <i>Agronomy</i> , 2018, 8, 194.	3.0	51
38	Cross-Validation Without Doing Cross-Validation in Genome-Enabled Prediction. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3107-3128.	1.8	50
39	QTL analyses of complex traits with cross validation, bootstrapping and other biometric methods. <i>Euphytica</i> , 2004, 137, 1-11.	1.2	48
40	Association analysis of frost tolerance in rye using candidate genes and phenotypic data from controlled, semi-controlled, and field phenotyping platforms. <i>BMC Plant Biology</i> , 2011, 11, 146.	3.6	47
41	QTL mapping of Sclerotinia midstalk-rot resistance in sunflower. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1474-1484.	3.6	44
42	Trends in genetic variance components during 30 years of hybrid maize breeding at the University of Hohenheim. <i>Plant Breeding</i> , 2008, 127, 446-451.	1.9	44
43	BSTA: a targeted approach combines bulked segregant analysis with next-generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. <i>BMC Genomics</i> , 2013, 14, 628.	2.8	43
44	Improving Imputation Quality in BEAGLE for Crop and Livestock Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 177-188.	1.8	43
45	Marker-based introduction of three quantitative-trait loci conferring resistance to Fusarium head blight into an independent elite winter wheat breeding population. <i>Theoretical and Applied Genetics</i> , 2008, 117, 29-35.	3.6	41
46	Marker selection for Fusarium head blight resistance based on quantitative trait loci (QTL) from two European sources compared to phenotypic selection in winter wheat. <i>Euphytica</i> , 2009, 166, 219-227.	1.2	41
47	Fine mapping of the sunflower resistance locus PI ARG introduced from the wild species <i>Helianthus argophyllus</i> . <i>Theoretical and Applied Genetics</i> , 2010, 121, 1633-1644.	3.6	41
48	Enhancing Genome-Enabled Prediction by Bagging Genomic BLUP. <i>PLoS ONE</i> , 2014, 9, e91693.	2.5	41
49	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2313-2331.	3.6	41
50	QTL mapping of resistance to Sclerotinia midstalk rot in RIL of sunflower population NDBLOSSelAACM625. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1490-1498.	3.6	39
51	Discovery of beneficial haplotypes for complex traits in maize landraces. <i>Nature Communications</i> , 2020, 11, 4954.	12.8	38
52	Improving resistance to the European corn borer: a comprehensive study in elite maize using QTL mapping and genome-wide prediction. <i>Theoretical and Applied Genetics</i> , 2015, 128, 875-891.	3.6	37
53	Identification and validation of QTL for Sclerotinia midstalk rot resistance in sunflower by selective genotyping. <i>Theoretical and Applied Genetics</i> , 2005, 111, 233-242.	3.6	36
54	Influence of barley variety mixtures on severity of scald and net blotch and on yield *. <i>Plant Pathology</i> , 1994, 43, 356-361.	2.4	34

#	ARTICLE	IF	CITATIONS
55	Stable Carbon Isotope Discrimination Is under Genetic Control in the C4 Species Maize with Several Genomic Regions Influencing Trait Expression. <i>Plant Physiology</i> , 2014, 164, 131-143.	4.8	34
56	Genome-Wide Association Studies with a Genomic Relationship Matrix: A Case Study with Wheat and <i>Arabidopsis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3241-3256.	1.8	32
57	Genetic Expectations of Quantitative Trait Loci Main and Interaction Effects Obtained With the Triple Testcross Design and Their Relevance for the Analysis of Heterosis. <i>Genetics</i> , 2008, 178, 2265-2274.	2.9	30
58	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. <i>Crop Science</i> , 2014, 54, 1981-1991.	1.8	30
59	Choice of models for QTL mapping with multiple families and design of the training set for prediction of Fusarium resistance traits in maize. <i>Theoretical and Applied Genetics</i> , 2016, 129, 431-444.	3.6	30
60	Prediction of Complex Traits: Robust Alternatives to Best Linear Unbiased Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 195.	2.3	29
61	Unraveling Epistasis With Triple Testcross Progenies of Near-Isogenic Lines. <i>Genetics</i> , 2009, 181, 247-257.	2.9	28
62	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1897-1908.	3.6	28
63	Sensitivity to prior specification in Bayesian genome-based prediction models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 375-91.	0.6	27
64	Carbon isotope composition, water use efficiency, and drought sensitivity are controlled by a common genomic segment in maize. <i>Theoretical and Applied Genetics</i> , 2019, 132, 53-63.	3.6	26
65	Is there an optimum level of diversity in utilization of genetic resources?. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2283-2295.	3.6	25
66	Prospects for hybrid breeding in winter triticale: II. Relationship between parental genetic distance and specific combining ability. <i>Plant Breeding</i> , 2006, 125, 331-336.	1.9	24
67	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. <i>Genetics</i> , 2017, 206, 1611-1619.	2.9	24
68	Diversity analysis and genomic prediction of Sclerotinia resistance in sunflower using a new 25K SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2016, 129, 317-329.	3.6	22
69	Exploring new alleles for frost tolerance in winter rye. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2151-2164.	3.6	20
70	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. <i>Genetics</i> , 2018, 210, 1185-1196.	2.9	18
71	Exploiting genetic diversity in two European maize landraces for improving Gibberella ear rot resistance using genomic tools. <i>Theoretical and Applied Genetics</i> , 2021, 134, 793-805.	3.6	18
72	Geography and end use drive the diversification of worldwide winter rye populations. <i>Molecular Ecology</i> , 2016, 25, 500-514.	3.9	17

#	ARTICLE	IF	CITATIONS
73	Bayesian Networks Illustrate Genomic and Residual Trait Connections in Maize (<i>Zea mays</i> L.). G3: Genes, Genomes, Genetics, 2017, 7, 2779-2789.	1.8	16
74	Hybrid performance and AFLP- based genetic similarity in faba bean. Euphytica, 2004, 139, 207-216.	1.2	14
75	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
76	Transcriptomic diversity in seedling roots of European flint maize in response to cold. BMC Genomics, 2020, 21, 300.	2.8	14
77	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
78	Resemblance between two relatives – animal and plant breeding. Journal of Animal Breeding and Genetics, 2015, 132, 1-2.	2.0	9
79	Inferring trait-specific similarity among individuals from molecular markers and phenotypes with Bayesian regression. Theoretical Population Biology, 2020, 132, 47-59.	1.1	9
80	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
81	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
82	Oligogenic control of resistance to soil-borne viruses <i>SBCMV</i> and <i>WSSMV</i> in rye (<i>Secale cereale</i> L.). Plant Breeding, 2016, 135, 552-559.	1.9	6
83	Assay for abscisic acid 8-hydroxylase activity of cloned plant cytochrome P450 oxidases in <i>Saccharomyces cerevisiae</i> . Analytical Biochemistry, 2018, 553, 24-27.	2.4	6
84	QTL mapping under truncation selection in homozygous lines derived from biparental crosses. Theoretical and Applied Genetics, 2012, 124, 543-553.	3.6	5
85	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
86	High-resolution association mapping with libraries of immortalized lines from ancestral landraces. Theoretical and Applied Genetics, 2022, 135, 243-256.	3.6	5
87	Increasing calling accuracy, coverage, and read-depth in sequence data by the use of haplotype blocks. PLoS Genetics, 2021, 17, e1009944.	3.5	5
88	Natural alleles of the abscisic acid catabolism gene <i>ZmAbh4</i> modulate water use efficiency and carbon isotope discrimination in maize. Plant Cell, 2022, 34, 3860-3872.	6.6	5
89	The genetics of environmental variation of dry matter grain yield in maize. Genetical Research, 2012, 94, 113-119.	0.9	4
90	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	2.6	4

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	Statistical Models for the Prediction of Genetic Values. , 2014, , 183-205.		0