

Korbinian Schneeberger

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5034695/publications.pdf>

Version: 2024-02-01

95
papers

12,062
citations

38742

50
h-index

39675

94
g-index

112
all docs

112
docs citations

112
times ranked

14670
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-scale and haplotype-resolved genome assembly of a tetraploid potato cultivar. <i>Nature Genetics</i> , 2022, 54, 342-348.	21.4	87
2	plots: visualizing structural similarities and rearrangements between multiple genomes. <i>Bioinformatics</i> , 2022, 38, 2922-2926.	4.1	69
3	The megabase-scale crossover landscape is largely independent of sequence divergence. <i>Nature Communications</i> , 2022, 13, .	12.8	25
4	The Evolutionary Dynamics of Genetic Incompatibilities Introduced by Duplicated Genes in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 1225-1240.	8.9	11
5	A misregulated cyclic nucleotide-gated channel mediates cytosolic calcium elevation and activates immunity in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2021, 230, 1078-1094.	7.3	51
6	Natural variation identifies a <i>Pxy</i> gene controlling vascular organisation and formation of nodules and lateral roots in <i>Lotus japonicus</i> . <i>New Phytologist</i> , 2021, 230, 2459-2473.	7.3	7
7	Using the longest run subsequence problem within homology-based scaffolding. <i>Algorithms for Molecular Biology</i> , 2021, 16, 11.	1.2	1
8	Transposition and duplication of MADS-domain transcription factor genes in annual and perennial <i>Arabis</i> species modulates flowering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	6
9	Anno genominis XX: 20 years of <i>Arabidopsis</i> genomics. <i>Plant Cell</i> , 2021, 33, 832-845.	6.6	11
10	Genetic and Molecular Analysis of Root Hair Development in <i>Arabis alpina</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 767772.	3.6	2
11	The genetic and epigenetic landscape of the <i>Arabidopsis</i> centromeres. <i>Science</i> , 2021, 374, eabi7489.	12.6	188
12	Mutations in the miR396 binding site of the growth-regulating factor gene <i>VvGRF4</i> modulate inflorescence architecture in grapevine. <i>Plant Journal</i> , 2020, 101, 1234-1248.	5.7	19
13	Bacterial Infection Disrupts Clock Gene Expression to Attenuate Immune Responses. <i>Current Biology</i> , 2020, 30, 1740-1747.e6.	3.9	20
14	Mutagenesis of a Quintuple Mutant Impaired in Environmental Responses Reveals Roles for <i>CHROMATIN REMODELING4</i> in the <i>Arabidopsis</i> Floral Transition. <i>Plant Cell</i> , 2020, 32, 1479-1500.	6.6	17
15	Extreme genetic signatures of local adaptation during <i>Lotus japonicus</i> colonization of Japan. <i>Nature Communications</i> , 2020, 11, 253.	12.8	30
16	Chromosome-level assemblies of multiple <i>Arabidopsis</i> genomes reveal hotspots of rearrangements with altered evolutionary dynamics. <i>Nature Communications</i> , 2020, 11, 989.	12.8	162
17	Reciprocal cybrids reveal how organellar genomes affect plant phenotypes. <i>Nature Plants</i> , 2020, 6, 13-21.	9.3	40
18	Gamete binning: chromosome-level and haplotype-resolved genome assembly enabled by high-throughput single-cell sequencing of gamete genomes. <i>Genome Biology</i> , 2020, 21, 306.	8.8	44

#	ARTICLE	IF	CITATIONS
19	Interspecies association mapping links reduced CG to TG substitution rates to the loss of gene-body methylation. <i>Nature Plants</i> , 2019, 5, 846-855.	9.3	48
20	Strengths and potential pitfalls of hay transfer for ecological restoration revealed by RAD-seq analysis in floodplain <i>Arabidopsis</i> species. <i>Molecular Ecology</i> , 2019, 28, 3887-3901.	3.9	14
21	Linked-read sequencing of gametes allows efficient genome-wide analysis of meiotic recombination. <i>Nature Communications</i> , 2019, 10, 4310.	12.8	41
22	Genetic and molecular analysis of trichome development in <i>Arabidopsis alpina</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12078-12083.	7.1	28
23	SyRI: finding genomic rearrangements and local sequence differences from whole-genome assemblies. <i>Genome Biology</i> , 2019, 20, 277.	8.8	310
24	The Striking Flower-in-Flower Phenotype of <i>Arabidopsis thaliana</i> Nossen (No-0) is Caused by a Novel LEAFY Allele. <i>Plants</i> , 2019, 8, 599.	3.5	4
25	Brassinosteroids Dominate Hormonal Regulation of Plant Thermomorphogenesis via BZR1. <i>Current Biology</i> , 2018, 28, 303-310.e3.	3.9	158
26	findGSE: estimating genome size variation within human and <i>Arabidopsis</i> using k-mer frequencies. <i>Bioinformatics</i> , 2018, 34, 550-557.	4.1	167
27	Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants. <i>EFSA Journal</i> , 2018, 16, e05345.	1.8	23
28	The U1 snRNP Subunit LUC7 Modulates Plant Development and Stress Responses via Regulation of Alternative Splicing. <i>Plant Cell</i> , 2018, 30, 2838-2854.	6.6	48
29	The impact of third generation genomic technologies on plant genome assembly. <i>Current Opinion in Plant Biology</i> , 2017, 36, 64-70.	7.1	201
30	Improving and correcting the contiguity of long-read genome assemblies of three plant species using optical mapping and chromosome conformation capture data. <i>Genome Research</i> , 2017, 27, 778-786.	5.5	155
31	Ctf4-related protein recruits LHP1-PRC2 to maintain H3K27me3 levels in dividing cells in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4833-4838.	7.1	36
32	Editorial overview: Genome studies and molecular genetics. <i>Current Opinion in Plant Biology</i> , 2017, 36, iv-v.	7.1	0
33	Chlorosis caused by two recessively interacting genes reveals a role of RNA helicase in hybrid breakdown in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 91, 251-262.	5.7	24
34	Chromosome-level assembly of <i>Arabidopsis thaliana</i> Ler reveals the extent of translocation and inversion polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4052-60.	7.1	176
35	LVR2 ensures transgenerational genome stability under simulated natural UV-B in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2016, 7, 13522.	12.8	51
36	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9111-9116.	7.1	260

#	ARTICLE	IF	CITATIONS
37	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 159-178.	5.7	81
38	A multi-marker association method for genome-wide association studies without the need for population structure correction. <i>Nature Communications</i> , 2016, 7, 13299.	12.8	35
39	Plant genic methylation: Conserved for 400 million years. <i>Nature Plants</i> , 2016, 2, 16003.	9.3	0
40	Complementary Activities of TELOMERE REPEAT BINDING Proteins and Polycomb Group Complexes in Transcriptional Regulation of Target Genes. <i>Plant Cell</i> , 2016, 28, 87-101.	6.6	67
41	<i>Arabidopsis thaliana</i> DM2h (R8) within the Landsberg RPP1-like Resistance Locus Underlies Three Different Cases of EDS1-Conditioned Autoimmunity. <i>PLoS Genetics</i> , 2016, 12, e1005990.	3.5	38
42	cDNA Library Enrichment of Full Length Transcripts for SMRT Long Read Sequencing. <i>PLoS ONE</i> , 2016, 11, e0157779.	2.5	51
43	Genome expansion of <i>Arabis alpina</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
44	Improving the Annotation of <i>Arabidopsis lyrata</i> Using RNA-Seq Data. <i>PLoS ONE</i> , 2015, 10, e0137391.	2.5	82
45	Rice perception of symbiotic arbuscular mycorrhizal fungi requires the karrikin receptor complex. <i>Science</i> , 2015, 350, 1521-1524.	12.6	191
46	Mutations in the <i>EDR1</i> Gene Alter the Response of <i>Arabidopsis thaliana</i> to <i>Phytophthora infestans</i> and the Bacterial PAMPs flg22 and elf18. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 122-133.	2.6	12
47	Mutant Allele-Specific Uncoupling of PENETRATION3 Functions Reveals Engagement of the ATP-Binding Cassette Transporter in Distinct Tryptophan Metabolic Pathways. <i>Plant Physiology</i> , 2015, 168, 814-827.	4.8	71
48	Century-scale Methylome Stability in a Recently Diverged <i>Arabidopsis thaliana</i> Lineage. <i>PLoS Genetics</i> , 2015, 11, e1004920.	3.5	148
49	Combinatorial activities of SHORT VEGETATIVE PHASE and FLOWERING LOCUS C define distinct modes of flowering regulation in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2015, 16, 31.	8.8	150
50	Rapid and Inexpensive Whole-Genome Genotyping-by-Sequencing for Crossover Localization and Fine-Scale Genetic Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 385-398.	1.8	122
51	Floral induction in <i>Arabidopsis thaliana</i> by FLOWERING LOCUS T requires direct repression of BLADE-ON-PETIOLE genes by homeodomain protein PENNYWISE. <i>Plant Physiology</i> , 2015, 169, pp.00960.2015.	4.8	51
52	SHOREmap v3.0: Fast and Accurate Identification of Causal Mutations from Forward Genetic Screens. <i>Methods in Molecular Biology</i> , 2015, 1284, 381-395.	0.9	51
53	Kicking against the PRCs – A Domesticated Transposase Antagonises Silencing Mediated by Polycomb Group Proteins and Is an Accessory Component of Polycomb Repressive Complex 2. <i>PLoS Genetics</i> , 2015, 11, e1005660.	3.5	68
54	The DET1-COP1-HY5 Pathway Constitutes a Multipurpose Signaling Module Regulating Plant Photomorphogenesis and Thermomorphogenesis. <i>Cell Reports</i> , 2014, 9, 1983-1989.	6.4	166

#	ARTICLE	IF	CITATIONS
55	CHOLINE TRANSPORTER-LIKE1 is required for sieve plate development to mediate long-distance cell-to-cell communication. <i>Nature Communications</i> , 2014, 5, 4276.	12.8	69
56	A SHIFT FROM MAGNITUDE TO SIGN EPISTASIS DURING ADAPTIVE EVOLUTION OF A BACTERIAL SOCIAL TRAIT. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2701-2708.	2.3	14
57	Mapping-by-Sequencing Identifies <i>HvPHYTOCHROME C</i> as a Candidate Gene for the early maturity 5 Locus Modulating the Circadian Clock and Photoperiodic Flowering in Barley. <i>Genetics</i> , 2014, 198, 383-396.	2.9	102
58	Rapid Identification of a Natural Knockout Allele of ARMADILLO REPEAT-CONTAINING KINESIN1 That Causes Root Hair Branching by Mapping-By-Sequencing. <i>Plant Physiology</i> , 2014, 166, 1280-1287.	4.8	12
59	<i>Arabidopsis thaliana</i> RNase H2 Deficiency Counteracts the Needs for the WEE1 Checkpoint Kinase but Triggers Genome Instability. <i>Plant Cell</i> , 2014, 26, 3680-3692.	6.6	33
60	Towards the discovery of novel genetic component involved in stress resistance in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2014, 201, 810-824.	7.3	12
61	Using next-generation sequencing to isolate mutant genes from forward genetic screens. <i>Nature Reviews Genetics</i> , 2014, 15, 662-676.	16.3	219
62	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	21.4	391
63	Functional dissection of the <i>PROPEP2</i> and <i>PROPEP3</i> promoters reveals the importance of <i>WRKY</i> factors in mediating microbe-associated molecular pattern-induced expression. <i>New Phytologist</i> , 2013, 198, 1165-1177.	7.3	56
64	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2655-62.	7.1	325
65	Mechanisms of Age-Dependent Response to Winter Temperature in Perennial Flowering of <i>Arabis alpina</i> . <i>Science</i> , 2013, 340, 1094-1097.	12.6	207
66	Impaired sterol ester synthesis alters the response of <i>Arabidopsis thaliana</i> to <i>Phytophthora infestans</i> . <i>Plant Journal</i> , 2013, 73, 456-468.	5.7	62
67	Mutation identification by direct comparison of whole-genome sequencing data from mutant and wild-type individuals using k-mers. <i>Nature Biotechnology</i> , 2013, 31, 325-330.	17.5	149
68	<i>RACK1</i> scaffold proteins influence miRNA abundance in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2013, 76, 433-445.	5.7	85
69	User guide for mapping-by-sequencing in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2013, 14, R61.	8.8	138
70	The genomic landscape of meiotic crossovers and gene conversions in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 2013, 2, e01426.	6.0	197
71	Fast Isogenic Mapping-by-Sequencing of Ethyl Methanesulfonate-Induced Mutant Bulks. <i>Plant Physiology</i> , 2012, 160, 591-600.	4.8	119
72	Natural Variation in Biogenesis Efficiency of Individual <i>Arabidopsis thaliana</i> MicroRNAs. <i>Current Biology</i> , 2012, 22, 166-170.	3.9	42

#	ARTICLE	IF	CITATIONS
73	FITNESS OF ARABIDOPSIS THALIANA MUTATION ACCUMULATION LINES WHOSE SPONTANEOUS MUTATIONS ARE KNOWN. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2335-2339.	2.3	46
74	Syntenya€based mappinga€bya€sequencing enabled by targeted enrichment. <i>Plant Journal</i> , 2012, 71, 517-526.	5.7	43
75	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	21.4	910
76	Fast-forward genetics enabled by new sequencing technologies. <i>Trends in Plant Science</i> , 2011, 16, 282-288.	8.8	216
77	LOCAS a€“ A Low Coverage Assembly Tool for Resequencing Projects. <i>PLoS ONE</i> , 2011, 6, e23455.	2.5	20
78	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	21.4	814
79	Reference-guided assembly of four diverse <i>Arabidopsis thaliana</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10249-10254.	7.1	237
80	Genome-Wide Comparison of Nucleotide-Binding Site-Leucine-Rich Repeat-Encoding Genes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 157, 757-769.	4.8	175
81	Structure Determinants for Accurate Processing of miR172a in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2010, 20, 42-48.	3.9	146
82	<i>Arabidopsis thaliana</i> Leaf Form Evolved via Loss of KNOX Expression in Leaves in Association with a Selective Sweep. <i>Current Biology</i> , 2010, 20, 2223-2228.	3.9	88
83	Identification of a Spontaneous Frame Shift Mutation in a Nonreference <i>Arabidopsis</i> Accession Using Whole Genome Sequencing. <i>Plant Physiology</i> , 2010, 153, 652-654.	4.8	39
84	The Rate and Molecular Spectrum of Spontaneous Mutations in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2010, 327, 92-94.	12.6	1,004
85	Deep sequencing to reveal new variants in pooled DNA samples. <i>Human Mutation</i> , 2009, 30, 1703-1712.	2.5	71
86	Selective epigenetic control of retrotransposition in <i>Arabidopsis</i> . <i>Nature</i> , 2009, 461, 427-430.	27.8	315
87	SHOREmap: simultaneous mapping and mutation identification by deep sequencing. <i>Nature Methods</i> , 2009, 6, 550-551.	19.0	558
88	A Genetic Defect Caused by a Triplet Repeat Expansion in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2009, 323, 1060-1063.	12.6	75
89	Simultaneous alignment of short reads against multiple genomes. <i>Genome Biology</i> , 2009, 10, R98.	9.6	215
90	Optimal spliced alignments of short sequence reads. <i>Bioinformatics</i> , 2008, 24, i174-i180.	4.1	86

#	ARTICLE	IF	CITATIONS
91	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. <i>Genome Research</i> , 2008, 18, 918-929.	5.5	50
92	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , 2008, 14, 2455-2459.	3.5	133
93	Sequencing of natural strains of <i>Arabidopsis thaliana</i> with short reads. <i>Genome Research</i> , 2008, 18, 2024-2033.	5.5	442
94	RBR: library-less repeat detection for ESTs. <i>Bioinformatics</i> , 2006, 22, 2232-2236.	4.1	19
95	Masking repeats while clustering ESTs. <i>Nucleic Acids Research</i> , 2005, 33, 2176-2180.	14.5	6