

# M Eric Schranz

## List of Publications by Year in descending order

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115  
papers

8,149  
citations

57631

44  
h-index

58464

82  
g-index

144  
all docs

144  
docs citations

144  
times ranked

8701  
citing authors

#	ARTICLE	IF	CITATIONS
1	A PARTHENOGENESIS allele from apomictic dandelion can induce egg cell division without fertilization in lettuce. <i>Nature Genetics</i> , 2022, 54, 84-93.	9.4	56
2	Genetic analysis reveals three novel QTLs underpinning a butterfly egg-induced hypersensitive response-like cell death in <i>Brassica rapa</i> . <i>BMC Plant Biology</i> , 2022, 22, 140.	1.6	7
3	Expanding the Menu: Are Polyphagy and Gene Family Expansions Linked across Lepidoptera?. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	10
4	Genomic Architecture and Evolution of the Cellulose synthase Gene Superfamily as Revealed by Phylogenomic Analysis. <i>Frontiers in Plant Science</i> , 2022, 13, 870818.	1.7	6
5	The membrane associated NAC transcription factors ANAC060 and ANAC040 are functionally redundant in the inhibition of seed dormancy in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 5514-5528.	2.4	12
6	The tomato cytochrome <i>cyp712g1</i> catalyses the double oxidation of orobanchol en route to the rhizosphere signalling strigolactone, solanacol. <i>New Phytologist</i> , 2022, 235, 1884-1899.	3.5	19
7	Applying Synteny Networks (SynNet) to Study Genomic Arrangements of Protein-Coding Genes in Plants. <i>Methods in Molecular Biology</i> , 2022, , 199-215.	0.4	2
8	Insect egg-killing: a new front on the evolutionary arms-race between brassicaceous plants and pierid butterflies. <i>New Phytologist</i> , 2021, 230, 341-353.	3.5	27
9	<i>Aethionema arabicum</i> genome annotation using PacBio full-length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. <i>Plant Journal</i> , 2021, 106, 275-293.	2.8	20
10	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
11	Origin and Evolution of the Cannabinoid Oxidocyclase Gene Family. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	18
12	A new P450 involved in the furanocoumarin pathway underlies a recent case of convergent evolution. <i>New Phytologist</i> , 2021, 231, 1923-1939.	3.5	19
13	Whole-genome microsynteny-based phylogeny of angiosperms. <i>Nature Communications</i> , 2021, 12, 3498.	5.8	53
14	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	4.1	44
15	Genome and transcriptome analysis of the beet armyworm <i>Spodoptera exigua</i> reveals targets for pest control. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
16	New Insights Into the Evolution of C4 Photosynthesis Offered by the <i>Tarenaya</i> Cluster of Cleomaceae. <i>Frontiers in Plant Science</i> , 2021, 12, 756505.	1.7	5
17	Repeatome-Based Phylogenetics in <i>Pelargonium</i> Section <i>Ciconium</i> (Sweet) Harvey. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
18	Drivers of metabolic diversification: how dynamic genomic neighbourhoods generate new biosynthetic pathways in the Brassicaceae. <i>New Phytologist</i> , 2020, 227, 1109-1123.	3.5	49

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19	Fibrillar evolution through the Tree of Life: Comparative genomics and microsynteny network analyses provide new insights into the evolutionary history of Fibrillar. <i>PLoS Computational Biology</i> , 2020, 16, e1008318.	1.5	8
20	Natural variation in specialised metabolites production in the leafy vegetable spider plant ( <i>Gynandropsis gynandra</i> L. (Briq.)) in Africa and Asia. <i>Phytochemistry</i> , 2020, 178, 112468.	1.4	9
21	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	0.8	32
22	Interspecific Hybrids Between <i>Pelargonium hortorum</i> and Species From P. Section <i>Ciconium</i> Reveal Biparental Plastid Inheritance and Multi-Locus Cyto-Nuclear Incompatibility. <i>Frontiers in Plant Science</i> , 2020, 11, 614871.	1.7	4
23	Independent Recruitment of Duplicated $\beta$ -Subunit-Coding NAD-ME Genes Aided the Evolution of C4 Photosynthesis in Cleomaceae. <i>Frontiers in Plant Science</i> , 2020, 11, 572080.	1.7	12
24	Phylogenomic analysis of the APETALA2 transcription factor subfamily across angiosperms reveals both deep conservation and lineage-specific patterns. <i>Plant Journal</i> , 2020, 103, 1516-1524.	2.8	22
25	Genomic Blocks in <i>Aethionema arabicum</i> Support Arabideae as Next Diverging Clade in Brassicaceae. <i>Frontiers in Plant Science</i> , 2020, 11, 719.	1.7	12
26	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	1.7	10
27	The Genomics of <i>Cannabis</i> and Its Close Relatives. <i>Annual Review of Plant Biology</i> , 2020, 71, 713-739.	8.6	93
28	Capturing variation in floral shape: a virtual3D based morphospace for <i>Pelargonium</i> . <i>PeerJ</i> , 2020, 8, e8823.	0.9	4
29	The alternative reality of plant mitochondrial DNA: One ring does not rule them all. <i>PLoS Genetics</i> , 2019, 15, e1008373.	1.5	184
30	Network-based microsynteny analysis identifies major differences and genomic outliers in mammalian and angiosperm genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2165-2174.	3.3	89
31	Usability of reference-free transcriptome assemblies for detection of differential expression: a case study on <i>Aethionema arabicum</i> dimorphic seeds. <i>BMC Genomics</i> , 2019, 20, 95.	1.2	18
32	Recently duplicated sesterterpene (C25) gene clusters in <i>Arabidopsis thaliana</i> modulate root microbiota. <i>Science China Life Sciences</i> , 2019, 62, 947-958.	2.3	52
33	Association between vitamin content, plant morphology and geographical origin in a worldwide collection of the orphan crop <i>Gynandropsis gynandra</i> (Cleomaceae). <i>Planta</i> , 2019, 250, 933-947.	1.6	20
34	Origins and geographic diversification of African rice ( <i>Oryza glaberrima</i> ). <i>PLoS ONE</i> , 2019, 14, e0203508.	1.1	17
35	Plastome based phylogenetics and younger crown node age in <i>Pelargonium</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 33-43.	1.2	19
36	Genome Improvement and Genetic Map Construction for <i>Aethionema arabicum</i> , the First Divergent Branch in the Brassicaceae Family. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3521-3530.	0.8	17

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37	An influential meal: host plant dependent transcriptional variation in the beet armyworm, <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae). <i>BMC Genomics</i> , 2019, 20, 845.	1.2	5
38	Dissecting the Genomic Diversification of Late Embryogenesis Abundant (LEA) Protein Gene Families in Plants. <i>Genome Biology and Evolution</i> , 2019, 11, 459-471.	1.1	102
39	Comparative analysis of repetitive sequences among species from the potato and the tomato clades. <i>Annals of Botany</i> , 2019, 123, 521-532.	1.4	36
40	Identifying and Engineering Genes for Parthenogenesis in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 128.	1.7	32
41	Genome-wide nucleotide diversity and associations with geography, ploidy level and glucosinolate profiles in <i>Aethionema arabicum</i> (Brassicaceae). <i>Plant Systematics and Evolution</i> , 2018, 304, 619-630.	0.3	13
42	Natural Variation within a Species for Traits Underpinning C <sub>4</sub> Photosynthesis. <i>Plant Physiology</i> , 2018, 177, 504-512.	2.3	31
43	Brassicales phylogeny inferred from 72 plastid genes: A reanalysis of the phylogenetic localization of two paleopolyploid events and origin of novel chemical defenses. <i>American Journal of Botany</i> , 2018, 105, 463-469.	0.8	76
44	A roadmap for breeding orphan leafy vegetable species: a case study of <i>Gynandropsis gynandra</i> (Cleomaceae). <i>Horticulture Research</i> , 2018, 5, 2.	2.9	54
45	New insights into the phylogeny of the TMBIM superfamily across the tree of life: Comparative genomics and synteny networks reveal independent evolution of the BI and LFG families in plants. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 266-278.	1.2	15
46	Efficient inference of homologs in large eukaryotic pan-proteomes. <i>BMC Bioinformatics</i> , 2018, 19, 340.	1.2	10
47	Drivers of Management of Spider Plant ( <i>Gynandropsis gynandra</i> ) Across Different Socio-linguistic Groups in Benin and Togo. <i>Economic Botany</i> , 2018, 72, 411-435.	0.8	13
48	Andromonoecy in <i>Gynandropsis gynandra</i> (L.) Briq. (Cleomaceae) and effects on fruit and seed production. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 2231-2239.	0.8	8
49	Lessons from Cleomaceae, the Sister of Crucifers. <i>Trends in Plant Science</i> , 2018, 23, 808-821.	4.3	35
50	Comparative genomics of the nonlegume <i>Parasponia</i> reveals insights into evolution of nitrogen-fixing rhizobium symbioses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4700-E4709.	3.3	253
51	The Functional Change and Deletion of FLC Homologs Contribute to the Evolution of Rapid Flowering in <i>Boechera stricta</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1078.	1.7	9
52	DIACYLGLYCEROL ACYLTRANSFERASE1 Contributes to Freezing Tolerance. <i>Plant Physiology</i> , 2018, 177, 1410-1424.	2.3	77
53	Cloning and Functional Analysis of three Cold Regulated CBF Genes in the Overwintering Crucifer <i>Boechera stricta</i> . <i>International Journal of Agriculture and Biology</i> , 2018, 20, 594-600.	0.2	3
54	Phylogenetic relationships within <i>Lactuca</i> L. (Asteraceae), including African species, based on chloroplast DNA sequence comparisons. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 55-71.	0.8	25

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55	Phylogenomic Synteny Network Analysis of MADS-Box Transcription Factor Genes Reveals Lineage-Specific Transpositions, Ancient Tandem Duplications, and Deep Positional Conservation. <i>Plant Cell</i> , 2017, 29, 1278-1292.	3.1	106
56	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	3.4	94
57	Network approaches for plant phylogenomic synteny analysis. <i>Current Opinion in Plant Biology</i> , 2017, 36, 129-134.	3.5	48
58	Polyploidy in deep and shallow evolutionary times: from ancient cotton, middle aged tobacco to recently formed monkey-flowers. <i>Plant Systematics and Evolution</i> , 2017, 303, 987-989.	0.3	3
59	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	1.6	24
60	Anatolian origins and diversification of <i>Aethionema</i> , the sister lineage of the core Brassicaceae. <i>American Journal of Botany</i> , 2017, 104, 1042-1054.	0.8	40
61	Identification of the Submergence Tolerance QTL Come Quick Drowning1 (CQD1) in <i>Arabidopsis thaliana</i> . <i>Journal of Heredity</i> , 2017, 108, 308-317.	1.0	9
62	Collinearity between potato ( <i>Solanum tuberosum</i> L.) and wild relatives assessed by comparative cytogenetic mapping. <i>Genome</i> , 2017, 60, 228-240.	0.9	11
63	Flowering Locus C (FLC) Is a Potential Major Regulator of Glucosinolate Content across Developmental Stages of <i>Aethionema arabicum</i> (Brassicaceae). <i>Frontiers in Plant Science</i> , 2017, 8, 876.	1.7	21
64	Functional network analysis of genes differentially expressed during xylogenesis in <i>soc1ful</i> woody <i>Arabidopsis</i> plants. <i>Plant Journal</i> , 2016, 86, 376-390.	2.8	27
65	Whole-genome duplications followed by tandem duplications drive diversification of the protein modifier <i>scp&gt;SUMO&lt;/scp&gt;</i> in Angiosperms. <i>New Phytologist</i> , 2016, 211, 172-185.	3.5	54
66	Comparative paleogenomics of crucifers: ancestral genomic blocks revisited. <i>Current Opinion in Plant Biology</i> , 2016, 30, 108-115.	3.5	84
67	Developmental Control and Plasticity of Fruit and Seed Dimorphism in <i>Aethionema arabicum</i> . <i>Plant Physiology</i> , 2016, 172, 1691-1707.	2.3	59
68	PanTools: representation, storage and exploration of pan-genomic data. <i>Bioinformatics</i> , 2016, 32, i487-i493.	1.8	46
69	Flower power and the mustard bomb: Comparative analysis of gene and genome duplications in glucosinolate biosynthetic pathway evolution in Cleomaceae and Brassicaceae. <i>American Journal of Botany</i> , 2016, 103, 1212-1222.	0.8	33
70	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 159-178.	2.8	81
71	Insight into the evolution of the Solanaceae from the parental genomes of <i>Petunia hybrida</i> . <i>Nature Plants</i> , 2016, 2, 16074.	4.7	311
72	Tracing ancestor rice of Suriname Maroons back to its African origin. <i>Nature Plants</i> , 2016, 2, 16149.	4.7	31

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73	Transcriptomes of eight <i>Arabidopsis thaliana</i> accessions reveal core conserved, genotype- and organ-specific responses to flooding stress. <i>Plant Physiology</i> , 2016, 172, pp.00472.2016.	2.3	92
74	Natural variation in rosette size under salt stress conditions corresponds to developmental differences between <i>Arabidopsis</i> accessions and allelic variation in the <i>LRR-KISS</i> gene. <i>Journal of Experimental Botany</i> , 2016, 67, 2127-2138.	2.4	66
75	Positionally-conserved but sequence-diverged: identification of long non-coding RNAs in the Brassicaceae and Cleomaceae. <i>BMC Plant Biology</i> , 2015, 15, 217.	1.6	64
76	Large-Scale Evolutionary Analysis of Genes and Supergene Clusters from Terpenoid Modular Pathways Provides Insights into Metabolic Diversification in Flowering Plants. <i>PLoS ONE</i> , 2015, 10, e0128808.	1.1	19
77	A Complex Interplay of Tandem- and Whole-Genome Duplication Drives Expansion of the L-Type Lectin Receptor Kinase Gene Family in the Brassicaceae. <i>Genome Biology and Evolution</i> , 2015, 7, 720-734.	1.1	46
78	Nicotinate O-Glucosylation Is an Evolutionarily Metabolic Trait Important for Seed Germination under Stress Conditions in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 1907-1924.	3.1	42
79	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8362-8366.	3.3	458
80	Karyotype evolution in apomictic <i>Boechera</i> and the origin of the aberrant chromosomes. <i>Plant Journal</i> , 2015, 82, 785-793.	2.8	42
81	Introggression browser: high-throughput whole-genome <i>scn</i> visualization. <i>Plant Journal</i> , 2015, 82, 174-182.	2.8	17
82	Gene and genome duplications and the origin of C4 photosynthesis: Birth of a trait in the Cleomaceae. <i>Current Plant Biology</i> , 2014, 1, 2-9.	2.3	46
83	A novel approach for multi-domain and multi-gene family identification provides insights into evolutionary dynamics of disease resistance genes in core eudicot plants. <i>BMC Genomics</i> , 2014, 15, 966.	1.2	29
84	Abiotic stress QTL in lettuce crop-wild hybrids: comparing greenhouse and field experiments. <i>Ecology and Evolution</i> , 2014, 4, 2395-2409.	0.8	28
85	Exploring genetic variation in the tomato ( <i>Solanum</i> section <i>Lycopersicon</i> ) clade by whole-genome sequencing. <i>Plant Journal</i> , 2014, 80, 136-148.	2.8	397
86	Group VII Ethylene Response Factor diversification and regulation in four species from flood-prone environments. <i>Plant, Cell and Environment</i> , 2014, 37, 2421-2432.	2.8	58
87	Identification of quantitative trait loci and a candidate locus for freezing tolerance in controlled and outdoor environments in the overwintering crucifer <i>B. oleracea</i> ssp. <i>capitata</i> . <i>Plant, Cell and Environment</i> , 2014, 37, 2459-2469.	2.8	10
88	A mixed-model QTL analysis for salt tolerance in seedlings of crop-wild hybrids of lettuce. <i>Molecular Breeding</i> , 2014, 34, 1389-1400.	1.0	10
89	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	9.4	350
90	On the origin and evolution of apomixis in <i>Boechera</i> . <i>Plant Reproduction</i> , 2013, 26, 309-315.	1.3	56

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91	QTL analysis reveals the genetic architecture of domestication traits in Crisphead lettuce. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1487-1500.	0.8	28
92	Root Transcript Profiling of Two <i>Rorippa</i> Species Reveals Gene Clusters Associated with Extreme Submergence Tolerance. <i>Plant Physiology</i> , 2013, 163, 1277-1292.	2.3	62
93	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers. <i>Plant Cell</i> , 2013, 25, 2813-2830.	3.1	95
94	Genomic and environmental selection patterns in two distinct lettuce crop-wild hybrid crosses. <i>Evolutionary Applications</i> , 2013, 6, 569-584.	1.5	23
95	Whole Genome and Tandem Duplicate Retention Facilitated Glucosinolate Pathway Diversification in the Mustard Family. <i>Genome Biology and Evolution</i> , 2013, 5, 2155-2173.	1.1	85
96	Wait or escape? Contrasting submergence tolerance strategies of <i>Rorippa amphibia</i> , <i>Rorippa sylvestris</i> and their hybrid. <i>Annals of Botany</i> , 2012, 109, 1263-1276.	1.4	66
97	A Gain-of-Function Polymorphism Controlling Complex Traits and Fitness in Nature. <i>Science</i> , 2012, 337, 1081-1084.	6.0	158
98	Ancient whole genome duplications, novelty and diversification: the WGD Radiation Lag-Time Model. <i>Current Opinion in Plant Biology</i> , 2012, 15, 147-153.	3.5	267
99	Quantitative variation for apomictic reproduction in the genus <i>Boechera</i> (Brassicaceae). <i>American Journal of Botany</i> , 2010, 97, 1719-1731.	0.8	136
100	Paleopolyploidy in the Brassicales: Analyses of the Cleome Transcriptome Elucidate the History of Genome Duplications in Arabidopsis and Other Brassicales. <i>Genome Biology and Evolution</i> , 2009, 1, 391-399.	1.1	226
101	Multilocus Patterns of Nucleotide Diversity, Population Structure and Linkage Disequilibrium in <i>Boechera stricta</i> , a Wild Relative of Arabidopsis. <i>Genetics</i> , 2009, 181, 1021-1033.	1.2	54
102	Ecological genomics of <i>Boechera stricta</i> : identification of a QTL controlling the allocation of methionine- vs branched-chain amino acid-derived glucosinolates and levels of insect herbivory. <i>Heredity</i> , 2009, 102, 465-474.	1.2	59
103	Diploid apomicts of the <i>Boechera holboellii</i> complex display large-scale chromosome substitutions and aberrant chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14026-14031.	3.3	136
104	Comparative Genetic Mapping in <i>Boechera stricta</i> , a Close Relative of Arabidopsis. <i>Plant Physiology</i> , 2007, 144, 286-298.	2.3	67
105	Comparative genomics in the Brassicaceae: a family-wide perspective. <i>Current Opinion in Plant Biology</i> , 2007, 10, 168-175.	3.5	84
106	Independent Ancient Polyploidy Events in the Sister Families Brassicaceae and Cleomaceae. <i>Plant Cell</i> , 2006, 18, 1152-1165.	3.1	171
107	The ABC's of comparative genomics in the Brassicaceae: building blocks of crucifer genomes. <i>Trends in Plant Science</i> , 2006, 11, 535-542.	4.3	535
108	Asexual reproduction in a close relative of Arabidopsis : a genetic investigation of apomixis in <i>Boechera</i> (Brassicaceae). <i>New Phytologist</i> , 2006, 171, 425-438.	3.5	50

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109	Partial Shotgun Sequencing of the <i>Boechera stricta</i> Genome Reveals Extensive Microsynteny and Promoter Conservation with <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2006, 140, 1169-1182.	2.3	33
110	Sexual reproduction, hybridization, apomixis, and polyploidization in the genus <i>Boechera</i> (Brassicaceae). <i>American Journal of Botany</i> , 2005, 92, 1797-1810.	0.8	131
111	De novo variation in life-history traits and responses to growth conditions of resynthesized polyploid <i>Brassica napus</i> (Brassicaceae). <i>American Journal of Botany</i> , 2004, 91, 174-183.	0.8	95
112	Flowering time divergence and genomic rearrangements in resynthesized Brassica polyploids (Brassicaceae). <i>Biological Journal of the Linnean Society</i> , 2004, 82, 675-688.	0.7	313
113	Genome redundancy and plasticity within ancient and recent Brassica crop species. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 665-674.	0.7	106
114	Characterization and Effects of the Replicated Flowering Time Gene <i>FLC</i> in <i>Brassica rapa</i> . <i>Genetics</i> , 2002, 162, 1457-1468.	1.2	240
115	Novel flowering time variation in the resynthesized polyploid <i>Brassica napus</i> . , 2000, 91, 242-246.		129