

Uwe Scholz

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

13,310
citations

38660

50
h-index

24915

109
g-index

126
all docs

126
docs citations

126
times ranked

12389
citing authors

#	ARTICLE	IF	CITATIONS
1	From Genotypes to Phenotypes: A Plant Perspective on Current Developments in Data Management and Data Publication. , 2022, , 11-43.		2
2	From data to knowledge â€“ big data needs stewardship, a plant phenomics perspective. Plant Journal, 2022, 111, 335-347.	2.8	11
3	Editorial: Advances in Applied Bioinformatics in Crops. Frontiers in Plant Science, 2021, 12, 640394.	1.7	3
4	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. Briefings in Bioinformatics, 2021, 22, .	3.2	18
5	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	9.4	138
6	Long-read sequence assembly: a technical evaluation in barley. Plant Cell, 2021, 33, 1888-1906.	3.1	180
7	Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat. Science Advances, 2021, 7, .	4.7	22
8	Quantitative monitoring of nucleotide sequence data from genetic resources in context of their citation in the scientific literature. GigaScience, 2021, 10, .	3.3	3
9	Kmasker plants â€“ a tool for assessing complex sequence space in plant species. Plant Journal, 2020, 102, 631-642.	2.8	8
10	The barley pan-genome reveals the hidden legacy of mutation breeding. Nature, 2020, 588, 284-289.	13.7	314
11	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	13.7	513
12	Mobilizing Crop Biodiversity. Molecular Plant, 2020, 13, 1341-1344.	3.9	50
13	Chromosome-scale genome assembly for the duckweed Spirodela intermedia, integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. Scientific Reports, 2020, 10, 19230.	1.6	23
14	Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. Science Advances, 2020, 6, eaay4897.	4.7	40
15	BRIDGE â€“ A Visual Analytics Web Tool for Barley Genebank Genomics. Frontiers in Plant Science, 2020, 11, 701.	1.7	31
16	Supernumerary B chromosomes of Aegilops speltoides undergo precise elimination in roots early in embryo development. Nature Communications, 2020, 11, 2764.	5.8	30
17	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	3.5	84
18	isa4j: a scalable Java library for creating ISA-Tab metadata. F1000Research, 2020, 9, 1388.	0.8	4

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19	The on-premise data sharing infrastructure e!DAL: Foster FAIR data for faster data acquisition. <i>GigaScience</i> , 2020, 9, .	3.3	11
20	BrAPI – an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	1.8	82
21	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019, 51, 1076-1081.	9.4	176
22	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	1.7	22
23	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
24	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322
25	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	2.8	50
26	A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. <i>Briefings in Bioinformatics</i> , 2019, 20, 1215-1221.	3.2	1
27	Programmatic Access to FAIRified Digital Plant Genetic Resources. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	9
28	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019, 8, 1877.	0.8	1
29	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019, 8, 1877.	0.8	3
30	Databases and Tools for the Analysis of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 377-394.	0.3	1
31	LAILAPS-QSM: A RESTful API and JAVA library for semantic query suggestions. <i>PLoS Computational Biology</i> , 2018, 14, e1006058.	1.5	4
32	MISA-web: a web server for microsatellite prediction. <i>Bioinformatics</i> , 2017, 33, 2583-2585.	1.8	1,248
33	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
34	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
35	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017, 261, 46-52.	1.9	29
36	Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives. <i>Journal of Biotechnology</i> , 2017, 261, 37-45.	1.9	12

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37	Rye B chromosomes encode a functional Argonaute-like protein with <i>in vitro</i> slicer activities similar to its A chromosome paralog. <i>New Phytologist</i> , 2017, 213, 916-928.	3.5	51
38	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
39	How Next-Generation Sequencing Has Aided Our Understanding of the Sequence Composition and Origin of B Chromosomes. <i>Genes</i> , 2017, 8, 294.	1.0	36
40	Agdc1p – a Gallic Acid Decarboxylase Involved in the Degradation of Tannic Acid in the Yeast <i>Blastobotrys (Arxula) adenivorans</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1777.	1.5	30
41	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	1.6	8
42	Aadh2p: an <i>Arxula adenivorans</i> alcohol dehydrogenase involved in the first step of the 1-butanol degradation pathway. <i>Microbial Cell Factories</i> , 2016, 15, 175.	1.9	6
43	A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.	2.3	41
44	PGP repository: a plant phenomics and genomics data publication infrastructure. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw033.	1.4	90
45	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016, 12, 44.	1.9	109
46	Phosphoproteomics Profiling of Tobacco Mature Pollen and Pollen Activated <i>in vitro</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1338-1350.	2.5	24
47	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
48	Quantitative monitoring of <i>Arabidopsis thaliana</i> growth and development using high-throughput plant phenotyping. <i>Scientific Data</i> , 2016, 3, 160055.	2.4	30
49	The distribution of \pm -kleisin during meiosis in the holocentromeric plant <i>Luzula elegans</i> . <i>Chromosome Research</i> , 2016, 24, 393-405.	1.0	16
50	Species-wide genome sequence and nucleotide polymorphisms from the model allopolyploid plant <i>Brassica napus</i> . <i>Scientific Data</i> , 2015, 2, 150072.	2.4	79
51	Cytogenetic mapping with centromeric bacterial artificial chromosomes contigs shows that this recombination-poor region comprises more than half of barley chromosome 3H. <i>Plant Journal</i> , 2015, 84, 385-394.	2.8	32
52	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	1.6	45
53	Metatranscriptome analysis reveals host-microbiome interactions in traps of carnivorous <i>Genlisea</i> species. <i>Frontiers in Microbiology</i> , 2015, 6, 526.	1.5	23
54	Targeted Sequencing Reveals Large-Scale Sequence Polymorphism in Maize Candidate Genes for Biomass Production and Composition. <i>PLoS ONE</i> , 2015, 10, e0132120.	1.1	28

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55	Towards recommendations for metadata and data handling in plant phenotyping. <i>Journal of Experimental Botany</i> , 2015, 66, 5417-5427.	2.4	116
56	An integrated functional approach to dissect systemic responses in maize to arbuscular mycorrhizal symbiosis. <i>Plant, Cell and Environment</i> , 2015, 38, 1591-1612.	2.8	53
57	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256
58	LAILAPS: The Plant Science Search Engine. <i>Plant and Cell Physiology</i> , 2015, 56, e8-e8.	1.5	7
59	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	3.9	114
60	Comprehensive Transcriptome Analysis Unravels the Existence of Crucial Genes Regulating Primary Metabolism during Adventitious Root Formation in <i>Petunia hybrida</i> . <i>PLoS ONE</i> , 2014, 9, e100997.	1.1	38
61	Sequence and Iomic Analysis of Divergent Strains of Maize Inbred Line B73 with an Altered Growth Phenotype. <i>PLoS ONE</i> , 2014, 9, e96782.	1.1	13
62	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	4.1	111
63	<i>PROTEIN DISULFIDE ISOMERASE LIKE 5-1</i> is a susceptibility factor to plant viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2104-2109.	3.3	85
64	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	164
65	High-resolution mapping of the barley <i>Ryd3</i> locus controlling tolerance to BYDV. <i>Molecular Breeding</i> , 2014, 33, 477-488.	1.0	13
66	e!DAL - a framework to store, share and publish research data. <i>BMC Bioinformatics</i> , 2014, 15, 214.	1.2	84
67	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
68	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57
69	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	2.3	77
70	Data Management Experiences and Best Practices from the Perspective of a Plant Research Institute. <i>Lecture Notes in Computer Science</i> , 2014, , 41-49.	1.0	2
71	A Query Suggestion Workflow for Life Science IR-Systems. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 15-26.	1.0	4
72	A query suggestion workflow for life science IR-systems. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 237.	1.0	3

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73	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
74	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. <i>Plant Journal</i> , 2013, 76, 494-505.	2.8	260
75	Adaptation of maize source leaf metabolism to stress related disturbances in carbon, nitrogen and phosphorus balance. <i>BMC Genomics</i> , 2013, 14, 442.	1.2	100
76	Asexual genome evolution in the apomictic <i>Ranunculus auricomus</i> complex: examining the effects of hybridization and mutation accumulation. <i>Molecular Ecology</i> , 2013, 22, 5908-5921.	2.0	118
77	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	1.4	10
78	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
79	Patterns of nucleotide asymmetries in plant and animal genomes. <i>BioSystems</i> , 2013, 111, 181-189.	0.9	17
80	Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene <i>rym11</i> in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1201-1212.	1.8	28
81	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	194
82	Extraction and Prediction of Biomedical Database Identifier Using Neural Networks towards Data Network Construction. , 2013, , 58-83.		0
83	MetaCrop 2.0: managing and exploring information about crop plant metabolism. <i>Nucleic Acids Research</i> , 2012, 40, D1173-D1177.	6.5	56
84	The e!DAL JAVA-API: Store, share and cite primary data in life sciences. , 2012, , .		0
85	Maize Source Leaf Adaptation to Nitrogen Deficiency Affects Not Only Nitrogen and Carbon Metabolism But Also Control of Phosphate Homeostasis. <i>Plant Physiology</i> , 2012, 160, 1384-1406.	2.3	170
86	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	3.3	173
87	The Garlic and Shallot Core Collection image database of IPK presenting two vegetatively maintained crops in the Federal ex situ genebank for agricultural and horticultural crops at Gatersleben, Germany. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1407-1415.	0.8	8
88	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
89	A putative role for amino acid permeases in sink-source communication of barley tissues uncovered by RNA-seq. <i>BMC Plant Biology</i> , 2012, 12, 154.	1.6	46
90	OPTIMAS-DW: A comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. <i>BMC Plant Biology</i> , 2012, 12, 245.	1.6	47

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91	Fine mapping and comparative genomics integration of two quantitative trait loci controlling resistance to powdery mildew in a Spanish barley landrace. <i>Theoretical and Applied Genetics</i> , 2012, 124, 49-62.	1.8	25
92	454 Transcriptome Sequencing Suggests a Role for Two-Component Signalling in Cellularization and Differentiation of Barley Endosperm Transfer Cells. <i>PLoS ONE</i> , 2012, 7, e41867.	1.1	29
93	IDPredictor: predict database links in biomedical database. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 190.	1.0	1
94	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. <i>Plant Cell</i> , 2011, 23, 1706-1718.	3.1	190
95	A case study for efficient management of high throughput primary lab data. <i>BMC Research Notes</i> , 2011, 4, 413.	0.6	2
96	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	3.1	448
97	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	1.6	109
98	Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011, 4, 411.	0.6	13
99	Systems Analysis of a Maize Leaf Developmental Gradient Redefines the Current C4 Model and Provides Candidates for Regulation. <i>Plant Cell</i> , 2011, 23, 4208-4220.	3.1	165
100	ABA biosynthesis and degradation contributing to ABA homeostasis during barley seed development under control and terminal drought-stress conditions. <i>Journal of Experimental Botany</i> , 2011, 62, 2615-2632.	2.4	251
101	Phosphate systemically inhibits development of arbuscular mycorrhiza in <i>Petunia hybrida</i> and represses genes involved in mycorrhizal functioning. <i>Plant Journal</i> , 2010, 64, 1002-1017.	2.8	354
102	The LAILAPS search engine: relevance ranking in life science databases. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 110.	1.0	8
103	The LAILAPS search engine: a feature model for relevance ranking in life science databases. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	0
104	Novel developments of the MetaCrop information system for facilitating systems biological approaches. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	2
105	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
106	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. <i>BMC Genomics</i> , 2009, 10, 547.	1.2	69
107	Manipulation of plant innate immunity and gibberellin as factor of compatibility in the mutualistic association of barley roots with <i>Piriformospora indica</i> . <i>Plant Journal</i> , 2009, 59, 461-474.	2.8	183
108	An Integration and Analysis Pipeline for Systems Biology in Crop Plant Metabolism. <i>Lecture Notes in Computer Science</i> , 2009, , 196-203.	1.0	0

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109	Genes driving potato tuber initiation and growth: identification based on transcriptional changes using the POCl array. <i>Functional and Integrative Genomics</i> , 2008, 8, 329-340.	1.4	114
110	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools. <i>Plant Physiology</i> , 2008, 146, 1738-1758.	2.3	250
111	MetaCrop: a detailed database of crop plant metabolism. <i>Nucleic Acids Research</i> , 2007, 36, D954-D958.	6.5	44
112	Using Data Warehouse Technology in Crop Plant Bioinformatics. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 145-159.	1.0	4
113	A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. <i>Theoretical and Applied Genetics</i> , 2007, 114, 823-839.	1.8	239
114	Macroarray expression analysis of barley susceptibility and nonhost resistance to <i>Blumeria graminis</i> . <i>Journal of Plant Physiology</i> , 2006, 163, 657-670.	1.6	24
115	Meta-All: a system for managing metabolic pathway information. <i>BMC Bioinformatics</i> , 2006, 7, 465.	1.2	17
116	Transcriptome analysis of mlo-mediated resistance in the epidermis of barley. <i>Molecular Plant Pathology</i> , 2005, 6, 139-151.	2.0	72
117	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
118	PhenoApp: A mobile tool for plant phenotyping to record field and greenhouse observations. <i>F1000Research</i> , 0, 11, 12.	0.8	3
119	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. <i>F1000Research</i> , 0, 11, 231.	0.8	2
120	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. <i>F1000Research</i> , 0, 11, 231.	0.8	4