

# 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	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
2	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
3	MISA-web: a web server for microsatellite prediction. <i>Bioinformatics</i> , 2017, 33, 2583-2585.	1.8	1,248
4	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
5	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	3.1	448
6	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
7	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322
8	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
9	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
10	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
11	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256
12	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
13	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
14	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
15	Towards a whole-genome sequence for rye ( <i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
16	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	194
17	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
18	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

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19	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
20	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
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	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
23	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
24	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
25	Plant genome sequencing applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	164
26	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
27	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
28	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
29	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
30	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
31	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
32	Asexual genome evolution in the apomictic <i>anunculus auricomus</i> complex: examining the effects of hybridization and mutation accumulation. <i>Molecular Ecology</i> , 2013, 22, 5908-5921.	2.0	118
33	Towards recommendations for metadata and data handling in plant phenotyping. <i>Journal of Experimental Botany</i> , 2015, 66, 5417-5427.	2.4	116
34	Genes driving potato tuber initiation and growth: identification based on transcriptional changes using the POCI array. <i>Functional and Integrative Genomics</i> , 2008, 8, 329-340.	1.4	114
35	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	3.9	114
36	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	4.1	111

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37	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
38	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016, 12, 44.	1.9	109
39	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
40	PGP repository: a plant phenomics and genomics data publication infrastructure. Database: the <i>Journal of Biological Databases and Curation</i> , 2016, 2016, baw033.	1.4	90
41	<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
42	e!DAL - a framework to store, share and publish research data. <i>BMC Bioinformatics</i> , 2014, 15, 214.	1.2	84
43	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	3.5	84
44	BrAPI – an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	1.8	82
45	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
46	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
47	Transcriptome analysis of mlo-mediated resistance in the epidermis of barley. <i>Molecular Plant Pathology</i> , 2005, 6, 139-151.	2.0	72
48	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
49	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
50	MetaCrop 2.0: managing and exploring information about crop plant metabolism. <i>Nucleic Acids Research</i> , 2012, 40, D1173-D1177.	6.5	56
51	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
52	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
53	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	2.8	50
54	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	50

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55	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
56	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
57	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
58	MetaCrop: a detailed database of crop plant metabolism. <i>Nucleic Acids Research</i> , 2007, 36, D954-D958.	6.5	44
59	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
60	Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. <i>Science Advances</i> , 2020, 6, eaay4897.	4.7	40
61	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
62	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
63	Cytogenetic mapping with centromeric bacterial artificial chromosomes contigs shows that this recombination-poor region comprises more than half of barley chromosome 3. <i>Plant Journal</i> , 2015, 84, 385-394.	2.8	32
64	BRIDGE – A Visual Analytics Web Tool for Barley Genebank Genomics. <i>Frontiers in Plant Science</i> , 2020, 11, 701.	1.7	31
65	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
66	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
67	Supernumerary B chromosomes of <i>Aegilops speltoides</i> undergo precise elimination in roots early in embryo development. <i>Nature Communications</i> , 2020, 11, 2764.	5.8	30
68	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017, 261, 46-52.	1.9	29
69	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
70	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
71	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
72	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

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73	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
74	Phosphoproteomics Profiling of Tobacco Mature Pollen and Pollen Activated in vitro. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1338-1350.	2.5	24
75	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
76	Chromosome-scale genome assembly for the duckweed <i>Spirodela intermedia</i> , integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. <i>Scientific Reports</i> , 2020, 10, 19230.	1.6	23
77	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	1.7	22
78	Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat. <i>Science Advances</i> , 2021, 7, .	4.7	22
79	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
80	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
81	Meta-All: a system for managing metabolic pathway information. <i>BMC Bioinformatics</i> , 2006, 7, 465.	1.2	17
82	Patterns of nucleotide asymmetries in plant and animal genomes. <i>BioSystems</i> , 2013, 111, 181-189.	0.9	17
83	The distribution of $\hat{\mu}$ -kleisin during meiosis in the holocentromeric plant <i>Luzula elegans</i> . <i>Chromosome Research</i> , 2016, 24, 393-405.	1.0	16
84	Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011, 4, 411.	0.6	13
85	Sequence and Ionomic Analysis of Divergent Strains of Maize Inbred Line B73 with an Altered Growth Phenotype. <i>PLoS ONE</i> , 2014, 9, e96782.	1.1	13
86	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
87	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
88	The on-premise data sharing infrastructure e!DAL: Foster FAIR data for faster data acquisition. <i>GigaScience</i> , 2020, 9, .	3.3	11
89	From data to knowledge – big data needs stewardship, a plant phenomics perspective. <i>Plant Journal</i> , 2022, 111, 335-347.	2.8	11
90	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	1.4	10

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91	Programmatic Access to FAIRified Digital Plant Genetic Resources. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	9
92	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
93	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	1.6	8
94	Kmasker plants – a tool for assessing complex sequence space in plant species. <i>Plant Journal</i> , 2020, 102, 631-642.	2.8	8
95	The LAILAPS search engine: relevance ranking in life science databases. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 110.	1.0	8
96	LAILAPS: The Plant Science Search Engine. <i>Plant and Cell Physiology</i> , 2015, 56, e8-e8.	1.5	7
97	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
98	Using Data Warehouse Technology in Crop Plant Bioinformatics. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 145-159.	1.0	4
99	isa4j: a scalable Java library for creating ISA-Tab metadata. <i>F1000Research</i> , 2020, 9, 1388.	0.8	4
100	LAILAPS-QSM: A RESTful API and JAVA library for semantic query suggestions. <i>PLoS Computational Biology</i> , 2018, 14, e1006058.	1.5	4
101	A Query Suggestion Workflow for Life Science IR-Systems. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 15-26.	1.0	4
102	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
103	Editorial: Advances in Applied Bioinformatics in Crops. <i>Frontiers in Plant Science</i> , 2021, 12, 640394.	1.7	3
104	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
105	PhenoApp: A mobile tool for plant phenotyping to record field and greenhouse observations. <i>F1000Research</i> , 0, 11, 12.	0.8	3
106	Quantitative monitoring of nucleotide sequence data from genetic resources in context of their citation in the scientific literature. <i>GigaScience</i> , 2021, 10, .	3.3	3
107	A query suggestion workflow for life science IR-systems. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 237.	1.0	3
108	A case study for efficient management of high throughput primary lab data. <i>BMC Research Notes</i> , 2011, 4, 413.	0.6	2

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109	Data Management Experiences and Best Practices from the Perspective of a Plant Research Institute. Lecture Notes in Computer Science, 2014, , 41-49.	1.0	2
110	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. F1000Research, 0, 11, 231.	0.8	2
111	From Genotypes to Phenotypes: A Plant Perspective on Current Developments in Data Management and Data Publication. , 2022, , 11-43.		2
112	Novel developments of the MetaCrop information system for facilitating systems biological approaches. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
113	Databases and Tools for the Analysis of the Barley Genome. Compendium of Plant Genomes, 2018, , 377-394.	0.3	1
114	A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. Briefings in Bioinformatics, 2019, 20, 1215-1221.	3.2	1
115	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. F1000Research, 2019, 8, 1877.	0.8	1
116	IDPredictor: predict database links in biomedical database. Journal of Integrative Bioinformatics, 2012, 9, 190.	1.0	1
117	The e!DAL JAVA-API: Store, share and cite primary data in life sciences. , 2012, , .		0
118	An Integration and Analysis Pipeline for Systems Biology in Crop Plant Metabolism. Lecture Notes in Computer Science, 2009, , 196-203.	1.0	0
119	Extraction and Prediction of Biomedical Database Identifier Using Neural Networks towards Data Network Construction. , 2013, , 58-83.		0
120	The LAILAPS search engine: a feature model for relevance ranking in life science databases. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	0