

Luzie U Wingen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4637296/publications.pdf>

Version: 2024-02-01

38
papers

1,973
citations

279798

23
h-index

330143

37
g-index

45
all docs

45
docs citations

45
times ranked

2787
citing authors

#	ARTICLE	IF	CITATIONS
1	An Integrated Linkage Map of Three Recombinant Inbred Populations of Pea (<i>Pisum sativum</i> L.). <i>Genes</i> , 2022, 13, 196.	2.4	3
2	Opinion Exploiting genomics to improve the benefits of wheat: Prospects and limitations. <i>Journal of Cereal Science</i> , 2022, 105, 103444.	3.7	4
3	Trend, population structure, and trait mapping from 15 years of national varietal trials of UK winter wheat. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
4	Interactions between two QTLs for time to anthesis on spike development and fertility in wheat. <i>Scientific Reports</i> , 2021, 11, 2451.	3.3	10
5	The role of gene flow and chromosomal instability in shaping the bread wheat genome. <i>Nature Plants</i> , 2021, 7, 172-183.	9.3	36
6	Resolving a QTL complex for height, heading, and grain yield on chromosome 3A in bread wheat. <i>Journal of Experimental Botany</i> , 2021, 72, 2965-2978.	4.8	8
7	Diversity of Pod Shape in <i>Pisum</i> . <i>Diversity</i> , 2021, 13, 203.	1.7	7
8	CerealsDBâ€”new tools for the analysis of the wheat genome: update 2020. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	16
9	A haplotype-led approach to increase the precision of wheat breeding. <i>Communications Biology</i> , 2020, 3, 712.	4.4	68
10	Genetic variation in wheat grain quality is associated with differences in the galactolipid content of flour and the gas bubble properties of dough liquor. <i>Food Chemistry: X</i> , 2020, 6, 100093.	4.3	12
11	Functional QTL mapping and genomic prediction of canopy height in wheat measured using a robotic field phenotyping platform. <i>Journal of Experimental Botany</i> , 2020, 71, 1885-1898.	4.8	30
12	Identification of a major QTL and associated molecular marker for high arabinoxylan fibre in white wheat flour. <i>PLoS ONE</i> , 2020, 15, e0227826.	2.5	20
13	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. <i>ELife</i> , 2020, 9, .	6.0	78
14	Analysis of the recombination landscape of hexaploid bread wheat reveals genes controlling recombination and gene conversion frequency. <i>Genome Biology</i> , 2019, 20, 69.	8.8	79
15	Natural Selection Towards Wild-Type in Composite Cross Populations of Winter Wheat. <i>Frontiers in Plant Science</i> , 2019, 10, 1757.	3.6	15
16	Highâ€”density genotyping of the A.E. Watkins Collection of hexaploid landraces identifies a large molecular diversity compared to elite bread wheat. <i>Plant Biotechnology Journal</i> , 2018, 16, 165-175.	8.3	67
17	Wheat Landrace Genome Diversity. <i>Genetics</i> , 2017, 205, 1657-1676.	2.9	76
18	The identification of new candidate genes <i>Triticum aestivum</i> <i>FLOWERING LOCUS T3</i> (<i>TaFT3</i>) and <i>TARGET OF EAT1</i> (<i>TaTOE1</i>) controlling the shortâ€”day photoperiod response in bread wheat. <i>Plant, Cell and Environment</i> , 2017, 40, 2678-2690.	5.7	45

#	ARTICLE	IF	CITATIONS
19	Application of a library of near isogenic lines to understand context dependent expression of QTL for grain yield and adaptive traits in bread wheat. <i>BMC Plant Biology</i> , 2016, 16, 161.	3.6	35
20	Delimitation of the <i>Earliness per se D1</i> (<i>Eps-D1</i>) flowering gene to a subtelomeric chromosomal deletion in bread wheat (<i>Triticum aestivum</i>). <i>Journal of Experimental Botany</i> , 2016, 67, 287-299.	4.8	100
21	Phenotyping pipeline reveals major seedling root growth QTL in hexaploid wheat. <i>Journal of Experimental Botany</i> , 2015, 66, 2283-2292.	4.8	196
22	Using the UK reference population Avalon—Cadenza as a platform to compare breeding strategies in elite Western European bread wheat. <i>Molecular Breeding</i> , 2015, 35, 70.	2.1	24
23	Genetic Dissection of Grain Size and Grain Number Trade-Offs in CIMMYT Wheat Germplasm. <i>PLoS ONE</i> , 2015, 10, e0118847.	2.5	88
24	Validation of a 1DL earliness per se (<i>eps</i>) flowering QTL in bread wheat (<i>Triticum aestivum</i>). <i>Molecular Breeding</i> , 2014, 34, 1023-1033.	2.1	76
25	Establishing the A. E. Watkins landrace cultivar collection as a resource for systematic gene discovery in bread wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1831-1842.	3.6	89
26	Long-distance dispersal and its influence on adaptation to host resistance in a heterogeneous landscape. <i>Plant Pathology</i> , 2013, 62, 9-20.	2.4	27
27	Molecular genetic basis of pod corn (<i>Tunicate</i> maize). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7115-7120.	7.1	48
28	Meta-QTL analysis of the genetic control of crop height in elite European winter wheat germplasm. <i>Molecular Breeding</i> , 2012, 29, 159-171.	2.1	127
29	Analysis of Array-CGH Data Using the R and Bioconductor Software Suite. <i>Comparative and Functional Genomics</i> , 2009, 2009, 1-8.	2.0	8
30	Meta-QTL analysis of the genetic control of ear emergence in elite European winter wheat germplasm. <i>Theoretical and Applied Genetics</i> , 2009, 119, 383-395.	3.6	225
31	Epigenetic defects of hepatocellular carcinoma are already found in non-neoplastic liver cells from patients with hereditary haemochromatosis. <i>Human Molecular Genetics</i> , 2007, 16, 1335-1342.	2.9	45
32	The Population Genetic Structure of Clonal Organisms Generated by Exponentially Bounded and Fat-Tailed Dispersal. <i>Genetics</i> , 2007, 177, 435-448.	2.9	27
33	Quantitative High-Resolution CpG Island Mapping with Pyrosequencing Reveals Disease-Specific Methylation Patterns of the <i>CDKN2B</i> Gene in Myelodysplastic Syndrome and Myeloid Leukemia. <i>Clinical Chemistry</i> , 2007, 53, 17-23.	3.2	69
34	Assessment of Differentiation and Progression of Hepatic Tumors Using Array-Based Comparative Genomic Hybridization. <i>Clinical Gastroenterology and Hepatology</i> , 2006, 4, 1283-1291.	4.4	42
35	Communicating BRCA1 and BRCA2 Genetic Test Results. <i>Journal of Clinical Oncology</i> , 2006, 24, 2969-2970.	1.6	12
36	Distinct Methylation Patterns of Benign and Malignant Liver Tumors Revealed by Quantitative Methylation Profiling. <i>Clinical Cancer Research</i> , 2005, 11, 3654-3660.	7.0	60

#	ARTICLE	IF	CITATIONS
37	Induction of aneuploidy by increasing chromosomal instability during dedifferentiation of hepatocellular carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1309-1314.	7.1	91
38	Drug-Response Signature Predicts Outcome in Adult Acute Myeloid Leukemia and Associates Poor Response with Molecular Characteristics of Hematopoietic Stem Cells.. Blood, 2004, 104, 2024-2024.	1.4	0