

Etienne Paux

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

12,829
citations

81900

39
h-index

76900

74
g-index

85
all docs

85
docs citations

85
times ranked

11408
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
2	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007, 8, 973-982.	16.3	2,396
3	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	12.6	1,479
4	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
5	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
6	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
7	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. <i>Science</i> , 2008, 322, 101-104.	12.6	356
8	Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. <i>Plant Cell</i> , 2010, 22, 1686-1701.	6.6	258
9	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. <i>Genome Biology</i> , 2018, 19, 111.	8.8	232
10	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	8.8	226
11	High throughput SNP discovery and genotyping in hexaploid wheat. <i>PLoS ONE</i> , 2018, 13, e0186329.	2.5	200
12	Characterizing the composition and evolution of homoeologous genomes in hexaploid wheat through BAC-end sequencing on chromosome 3B. <i>Plant Journal</i> , 2006, 48, 463-474.	5.7	189
13	Cross-genome map based dissection of a nitrogen use efficiency ortho-metaQTL in bread wheat unravels concerted cereal genome evolution. <i>Plant Journal</i> , 2011, 65, 745-756.	5.7	177
14	Detailed Recombination Studies Along Chromosome 3B Provide New Insights on Crossover Distribution in Wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2009, 181, 393-403.	2.9	157
15	Chromosome-based genomics in the cereals. <i>Chromosome Research</i> , 2007, 15, 51-66.	2.2	146
16	Transcript profiling of Eucalyptus xylem genes during tension wood formation. <i>New Phytologist</i> , 2005, 167, 89-100.	7.3	131
17	A multiple resistance locus on chromosome arm 3BS in wheat confers resistance to stem rust (Sr2), leaf rust (Lr27) and powdery mildew. <i>Theoretical and Applied Genetics</i> , 2011, 123, 615-623.	3.6	118
18	Worldwide phylogeography and history of wheat genetic diversity. <i>Science Advances</i> , 2019, 5, eaav0536.	10.3	118

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19	Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3961-3972.	1.8	114
20	Insertion site-based polymorphism markers open new perspectives for genome saturation and marker-assisted selection in wheat. <i>Plant Biotechnology Journal</i> , 2010, 8, 196-210.	8.3	111
21	Sequence-based marker development in wheat: Advances and applications to breeding. <i>Biotechnology Advances</i> , 2012, 30, 1071-1088.	11.7	108
22	A first survey of the rye (<i>Secale cereale</i>) genome composition through BAC end sequencing of the short arm of chromosome 1R. <i>BMC Plant Biology</i> , 2008, 8, 95.	3.6	106
23	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. <i>Genome Biology</i> , 2015, 16, 29.	8.8	101
24	Identification of genes preferentially expressed during wood formation in Eucalyptus. <i>Plant Molecular Biology</i> , 2004, 55, 263-280.	3.9	99
25	Wheat chromatin architecture is organized in genome territories and transcription factories. <i>Genome Biology</i> , 2020, 21, 104.	8.8	99
26	The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. <i>Plant Journal</i> , 2018, 95, 1039-1054.	5.7	97
27	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014, 15, 546.	8.8	88
28	Wheat centromeric retrotransposons: the new ones take a major role in centromeric structure. <i>Plant Journal</i> , 2013, 73, 952-965.	5.7	78
29	Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. <i>Genome Biology</i> , 2015, 16, 188.	8.8	76
30	Predictions of heading date in bread wheat (<i>Triticum aestivum</i> L.) using QTL-based parameters of an ecophysiological model. <i>Journal of Experimental Botany</i> , 2014, 65, 5849-5865.	4.8	74
31	Transcript profiling of a xylem vs phloem cDNA subtractive library identifies new genes expressed during xylogenesis in Eucalyptus. <i>New Phytologist</i> , 2006, 170, 739-752.	7.3	72
32	High-Resolution Mapping of Crossover Events in the Hexaploid Wheat Genome Suggests a Universal Recombination Mechanism. <i>Genetics</i> , 2017, 206, 1373-1388.	2.9	72
33	Mating system and recombination affect molecular evolution in four <i>Triticeae</i> species. <i>Genetical Research</i> , 2008, 90, 97-109.	0.9	66
34	Whole-genome prediction of reaction norms to environmental stress in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14	9.1	62
35	The Application of LTR Retrotransposons as Molecular Markers in Plants. <i>Methods in Molecular Biology</i> , 2012, 859, 115-153.	0.9	58
36	Variation in crossover rates across a 3-Mb contig of bread wheat (<i>Triticum aestivum</i>) reveals the presence of a meiotic recombination hotspot. <i>Chromosoma</i> , 2011, 120, 185-198.	2.2	55

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37	A 3,000-Loci Transcription Map of Chromosome 3B Unravels the Structural and Functional Features of Gene Islands in Hexaploid Wheat. <i>Plant Physiology</i> , 2011, 157, 1596-1608.	4.8	49
38	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <i>Genome Biology</i> , 2013, 14, R64.	8.8	45
39	Reply: A unified classification system for eukaryotic transposable elements should reflect their phylogeny. <i>Nature Reviews Genetics</i> , 2009, 10, 276-276.	16.3	41
40	The physical map of wheat chromosome 1BS provides insights into its gene space organization and evolution. <i>Genome Biology</i> , 2013, 14, R138.	9.6	40
41	LTC: a novel algorithm to improve the efficiency of contig assembly for physical mapping in complex genomes. <i>BMC Bioinformatics</i> , 2010, 11, 584.	2.6	37
42	BAC-derived markers for assaying the stem rust resistance gene, Sr2, in wheat breeding programs. <i>Molecular Breeding</i> , 2008, 22, 15-24.	2.1	36
43	A Physical Map of the Short Arm of Wheat Chromosome 1A. <i>PLoS ONE</i> , 2013, 8, e80272.	2.5	30
44	Whole Genome Profiling provides a robust framework for physical mapping and sequencing in the highly complex and repetitive wheat genome. <i>BMC Genomics</i> , 2012, 13, 47.	2.8	29
45	Transcriptional profile analysis of E3 ligase and hormone-related genes expressed during wheat grain development. <i>BMC Plant Biology</i> , 2012, 12, 35.	3.6	29
46	Bridging the gap between ideotype and genotype: Challenges and prospects for modelling as exemplified by the case of adapting wheat (<i>Triticum aestivum</i> L.) phenology to climate change in France. <i>Field Crops Research</i> , 2017, 202, 108-121.	5.1	27
47	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. <i>GigaScience</i> , 2022, 11, .	6.4	26
48	High Resolution Melting and Insertion Site-Based Polymorphism Markers for Wheat Variability Analysis and Candidate Genes Selection at Drought and Heat MQTL Loci. <i>Agronomy</i> , 2020, 10, 1294.	3.0	25
49	A whole-genome, radiation hybrid mapping resource of hexaploid wheat. <i>Plant Journal</i> , 2016, 86, 195-207.	5.7	23
50	Specific patterns of gene space organisation revealed in wheat by using the combination of barley and wheat genomic resources. <i>BMC Genomics</i> , 2010, 11, 714.	2.8	21
51	Fat element—a new marker for chromosome and genome analysis in the Triticeae. <i>Chromosome Research</i> , 2010, 18, 697-709.	2.2	20
52	DNA repair and crossing over favor similar chromosome regions as discovered in radiation hybrid of <i>Triticum</i> . <i>BMC Genomics</i> , 2012, 13, 339.	2.8	20
53	Physical mapping in large genomes: accelerating anchoring of BAC contigs to genetic maps through in silico analysis. <i>Functional and Integrative Genomics</i> , 2008, 8, 29-32.	3.5	17
54	Structural features of two major nucleolar organizer regions (NORs), NOR1 and NOR2, and chromosome-specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.	5.7	17

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55	A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. <i>BMC Plant Biology</i> , 2010, 10, 98.	3.6	16
56	Structural Variations Affecting Genes and Transposable Elements of Chromosome 3B in Wheats. <i>Frontiers in Genetics</i> , 2020, 11, 891.	2.3	16
57	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	2.8	16
58	Fine mapping of LrSV2, a race-specific adult plant leaf rust resistance gene on wheat chromosome 3BS. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1133-1141.	3.6	15
59	Exploiting the Repetitive Fraction of the Wheat Genome for High-Throughput Single-Nucleotide Polymorphism Discovery and Genotyping. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0078.	2.8	13
60	Radiation hybrid QTL mapping of Tdes2 involved in the first meiotic division of wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1977-1990.	3.6	12
61	Evolutionary history of Methyltransferase 1 genes in hexaploid wheat. <i>BMC Genomics</i> , 2014, 15, 922.	2.8	12
62	Genetic diversity and linkage disequilibrium studies on a 3.1-Mb genomic region of chromosome 3B in European and Asian bread wheat (<i>Triticum aestivum</i> L.) populations. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1209-1225.	3.6	11
63	High-resolution analysis of a QTL for resistance to <i>Stagonospora nodorum</i> glume blotch in wheat reveals presence of two distinct resistance loci in the target interval. <i>Theoretical and Applied Genetics</i> , 2014, 127, 573-586.	3.6	11
64	Physical Map of the Short Arm of Bread Wheat Chromosome 3D. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0021.	2.8	11
65	Annotation, classification, genomic organization and expression of the <i>Vitis vinifera</i> CYPome. <i>PLoS ONE</i> , 2018, 13, e0199902.	2.5	11
66	A simple approach to predict growth stages in winter wheat (<i>Triticum aestivum</i> L.) combining prediction of a crop model and marker based prediction of the deviation to a reference cultivar: A case study in France. <i>European Journal of Agronomy</i> , 2015, 68, 57-68.	4.1	10
67	Genome wide association mapping for resistance to multiple fungal pathogens in a panel issued from a broad composite cross-population of tetraploid wheat <i>Triticum turgidum</i> . <i>Euphytica</i> , 2020, 216, 1.	1.2	10
68	Integrated physical map of bread wheat chromosome arm 7DS to facilitate gene cloning and comparative studies. <i>New Biotechnology</i> , 2019, 48, 12-19.	4.4	9
69	Capturing Wheat Phenotypes at the Genome Level. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	8
70	Dissecting Bread Wheat Heterosis through the Integration of Agronomic and Physiological Traits. <i>Biology</i> , 2021, 10, 907.	2.8	6
71	A universal classification of eukaryotic transposable elements implemented in Repbase. <i>Nature Reviews Genetics</i> , 2008, 9, 414-414.	16.3	5
72	Breeding for Economically and Environmentally Sustainable Wheat Varieties: An Integrated Approach from Genomics to Selection. <i>Biology</i> , 2022, 11, 149.	2.8	5

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73	Insights on decoding wheat and barley genomes. <i>Functional and Integrative Genomics</i> , 2021, 21, 157-159.	3.5	4
74	Association between SNP Markers and 11 Vitamin Contents in Grains of a Worldwide Bread Wheat Core Collection. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 4307-4318.	5.2	2
75	Development of 1AS.1AL-1DL durum wheat chromosome carrying Glu-D1a locus encoding high molecular weight glutenin subunits 2. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	1
76	CNVmap: A Method and Software To Detect and Map Copy Number Variants from Segregation Data. <i>Genetics</i> , 2020, 214, 561-576.	2.9	1
77	Evaluation of the genetic variability of homoeologous group 3 SSRS in bread wheat. <i>Cytology and Genetics</i> , 2009, 43, 99-111.	0.5	0
78	Cost-Effective Markers and Candidate Genes Analysis at Wheat MQTL Loci. , 2020, 4, .		0