

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	Breeding for Economically and Environmentally Sustainable Wheat Varieties: An Integrated Approach from Genomics to Selection. <i>Biology</i> , 2022, 11, 149.	2.8	5
2	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
3	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	2.8	16
4	Insights on decoding wheat and barley genomes. <i>Functional and Integrative Genomics</i> , 2021, 21, 157-159.	3.5	4
5	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
6	Dissecting Bread Wheat Heterosis through the Integration of Agronomic and Physiological Traits. <i>Biology</i> , 2021, 10, 907.	2.8	6
7	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
8	Structural Variations Affecting Genes and Transposable Elements of Chromosome 3B in Wheats. <i>Frontiers in Genetics</i> , 2020, 11, 891.	2.3	16
9	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
10	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
11	Wheat chromatin architecture is organized in genome territories and transcription factories. <i>Genome Biology</i> , 2020, 21, 104.	8.8	99
12	Cost-Effective Markers and Candidate Genes Analysis at Wheat MQTL Loci. , 2020, 4, .		0
13	Worldwide phylogeography and history of wheat genetic diversity. <i>Science Advances</i> , 2019, 5, eaav0536.	10.3	118
14	Development of 1AS.1AL-1DL durum wheat chromosome carrying Glu-D1a locus encoding high molecular weight glutenin subunits 2â€™+â€™12. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	1
15	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
16	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
17	Structural features of two major nucleolar organizer regions (NORs), <i>Norâ€™1</i> and <i>Norâ€™2</i> , and chromosomeâ€™specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.	5.7	17
18	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

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19	Annotation, classification, genomic organization and expression of the <i>Vitis vinifera</i> CYPome. PLoS ONE, 2018, 13, e0199902.	2.5	11
20	The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. Plant Journal, 2018, 95, 1039-1054.	5.7	97
21	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
22	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
23	Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biology, 2018, 19, 103.	8.8	226
24	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. Genome Biology, 2018, 19, 111.	8.8	232
25	High throughput SNP discovery and genotyping in hexaploid wheat. PLoS ONE, 2018, 13, e0186329.	2.5	200
26	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. Field Crops Research, 2017, 202, 108-121.	5.1	27
27	High-Resolution Mapping of Crossover Events in the Hexaploid Wheat Genome Suggests a Universal Recombination Mechanism. Genetics, 2017, 206, 1373-1388.	2.9	72
28	Physical Map of the Short Arm of Bread Wheat Chromosome 3D. Plant Genome, 2017, 10, plantgenome2017.03.0021.	2.8	11
29	Exploiting the Repetitive Fraction of the Wheat Genome for High-Throughput Single-Nucleotide Polymorphism Discovery and Genotyping. Plant Genome, 2016, 9, plantgenome2015.09.0078.	2.8	13
30	A whole-genome, radiation hybrid mapping resource of hexaploid wheat. Plant Journal, 2016, 86, 195-207.	5.7	23
31	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. Genome Biology, 2015, 16, 29.	8.8	101
32	Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. Genome Biology, 2015, 16, 188.	8.8	76
33	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. European Journal of Agronomy, 2015, 68, 57-68.	4.1	10
34	Evolutionary history of Methyltransferase 1 genes in hexaploid wheat. BMC Genomics, 2014, 15, 922.	2.8	12
35	Predictions of heading date in bread wheat (<i>Triticum aestivum</i> L.) using QTL-based parameters of an ecophysiological model. Journal of Experimental Botany, 2014, 65, 5849-5865.	4.8	74
36	Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biology, 2014, 15, 546.	8.8	88

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37	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
38	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
39	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
40	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
41	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
42	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
43	Radiation hybrid QTL mapping of <i>Tdes2</i> involved in the first meiotic division of wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1977-1990.	3.6	12
44	Wheat centromeric retrotransposons: the new ones take a major role in centromeric structure. <i>Plant Journal</i> , 2013, 73, 952-965.	5.7	78
45	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
46	A Physical Map of the Short Arm of Wheat Chromosome 1A. <i>PLoS ONE</i> , 2013, 8, e80272.	2.5	30
47	Sequence-based marker development in wheat: Advances and applications to breeding. <i>Biotechnology Advances</i> , 2012, 30, 1071-1088.	11.7	108
48	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
49	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
50	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
51	The Application of LTR Retrotransposons as Molecular Markers in Plants. <i>Methods in Molecular Biology</i> , 2012, 859, 115-153.	0.9	58
52	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
53	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
54	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

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55	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
56	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
57	Fat element—a new marker for chromosome and genome analysis in the Triticeae. <i>Chromosome Research</i> , 2010, 18, 697-709.	2.2	20
58	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
59	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
60	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
61	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
62	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
63	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
64	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
65	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
66	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
67	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
68	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. <i>Science</i> , 2008, 322, 101-104.	12.6	356
69	A universal classification of eukaryotic transposable elements implemented in Repbase. <i>Nature Reviews Genetics</i> , 2008, 9, 414-414.	16.3	5
70	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
71	Mating system and recombination affect molecular evolution in four Triticeae species. <i>Genetical Research</i> , 2008, 90, 97-109.	0.9	66
72	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007, 8, 973-982.	16.3	2,396

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73	Chromosome-based genomics in the cereals. <i>Chromosome Research</i> , 2007, 15, 51-66.	2.2	146
74	Transcript profiling of a xylem vs phloem cDNA subtractive library identifies new genes expressed during xylogenesis in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2006, 170, 739-752.	7.3	72
75	Characterizing the composition and evolution of homoeologous genomes in hexaploid wheat through BAC sequencing on chromosome 3B. <i>Plant Journal</i> , 2006, 48, 463-474.	5.7	189
76	Transcript profiling of <i>Eucalyptus</i> xylem genes during tension wood formation. <i>New Phytologist</i> , 2005, 167, 89-100.	7.3	131
77	Identification of genes preferentially expressed during wood formation in <i>Eucalyptus</i> . <i>Plant Molecular Biology</i> , 2004, 55, 263-280.	3.9	99
78	Capturing Wheat Phenotypes at the Genome Level. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	8