

Huw Jones

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,466
citations

430874

18
h-index

580821

25
g-index

27
all docs

27
docs citations

27
times ranked

2001
citing authors

#	ARTICLE	IF	CITATIONS
1	Barley heads east: Genetic analyses reveal routes of spread through diverse Eurasian landscapes. PLoS ONE, 2018, 13, e0196652.	2.5	54
2	The trans-Eurasian crop exchange in prehistory: Discerning pathways from barley phylogeography. Quaternary International, 2016, 426, 26-32.	1.5	19
3	Flanking SNP markers for vicineâ€“convicine concentration in faba bean (<i>Vicia faba</i> L.). Molecular Breeding, 2015, 35, 1.	2.1	36
4	Implications of using genomic prediction within a high-density SNP dataset to predict DUS traits in barley. Theoretical and Applied Genetics, 2015, 128, 2461-2470.	3.6	14
5	Strategy for exploiting exotic germplasm using genetic, morphological, and environmental diversity: the <i>Aegilops tauschii</i> Coss. example. Theoretical and Applied Genetics, 2013, 126, 1793-1808.	3.6	62
6	Remnant genetic diversity detected in an ancient crop: <i>Triticum dicocon</i> Schrank landraces from Asturias, Spain. Genetic Resources and Crop Evolution, 2013, 60, 355-365.	1.6	3
7	Evaluation of the use of high-density SNP genotyping to implement UPOV Model 2 for DUS testing in barley. Theoretical and Applied Genetics, 2013, 126, 901-911.	3.6	30
8	Variety Protection and Plant Breedersâ€™ Rights in the â€“DNA Eraâ€™. , 2013, , 369-402.		5
9	Using diversity of the chloroplast genome to examine evolutionary history of wheat species. Genetic Resources and Crop Evolution, 2013, 60, 1831-1842.	1.6	12
10	Analysis of DNA polymorphism in ancient barley herbarium material: Validation of the KASP SNP genotyping platform. Taxon, 2013, 62, 779-789.	0.7	21
11	Waxy Phenotype Evolution in the Allotetraploid Cereal Broomcorn Millet: Mutations at the GBSSI Locus in Their Functional and Phylogenetic Context. Molecular Biology and Evolution, 2013, 30, 109-122.	8.9	31
12	A baseline study of vicineâ€“convicine levels in faba bean (<i>Vicia faba</i> L.) germplasm. Plant Genetic Resources: Characterisation and Utilisation, 2013, 11, 250-257.	0.8	35
13	Evaluation of diagnostic molecular markers for DUS phenotypic assessment in the cereal crop, barley (<i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). Theoretical and Applied Genetics, 2012, 125, 1735-1749.	3.6	42
14	Phylogeographic analysis of barley DNA as evidence for the spread of Neolithic agriculture through Europe. Journal of Archaeological Science, 2012, 39, 3230-3238.	2.4	43
15	Tetraploid Wheat Landraces in the Mediterranean Basin: Taxonomy, Evolution and Genetic Diversity. PLoS ONE, 2012, 7, e37063.	2.5	75
16	<i>CorrSieve</i> : software for summarizing and evaluating Structure output. Molecular Ecology Resources, 2011, 11, 349-352.	4.8	66
17	Phylogeography of einkorn landraces in the Mediterranean basin and Central Europe: population structure and cultivation history. Archaeological and Anthropological Sciences, 2011, 3, 327-341.	1.8	16
18	Evolutionary history of barley cultivation in Europe revealed by genetic analysis of extant landraces. BMC Evolutionary Biology, 2011, 11, 320.	3.2	50

#	ARTICLE	IF	CITATIONS
19	The cosmopolitan maternal heritage of the Thoroughbred racehorse breed shows a significant contribution from British and Irish native mares. <i>Biology Letters</i> , 2011, 7, 316-320.	2.3	47
20	Latitudinal variation in a photoperiod response gene in European barley: insight into the dynamics of agricultural spread from "historic" specimens. <i>Journal of Archaeological Science</i> , 2009, 36, 1092-1098.	2.4	57
21	Minimising inter-laboratory variation when constructing a unified molecular database of plant varieties in an allogamous crop. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1335-1344.	3.6	9
22	Approaches and constraints of using existing landrace and extant plant material to understand agricultural spread in prehistory. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 98-112.	0.8	45
23	Population-Based Resequencing Reveals That the Flowering Time Adaptation of Cultivated Barley Originated East of the Fertile Crescent. <i>Molecular Biology and Evolution</i> , 2008, 25, 2211-2219.	8.9	219
24	Control of flowering time in temperate cereals: genes, domestication, and sustainable productivity. <i>Journal of Experimental Botany</i> , 2007, 58, 1231-1244.	4.8	422
25	Toxic Secondary Metabolite Production in Genetically Modified Potatoes in Response to Stress. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 7766-7776.	5.2	37
26	Title is missing!. <i>Euphytica</i> , 2003, 132, 175-184.	1.2	15