

# James Cockram

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

4,581  
citations

126907

33  
h-index

114465

63  
g-index

82  
all docs

82  
docs citations

82  
times ranked

4891  
citing authors

#	ARTICLE	IF	CITATIONS
1	Trends of genetic changes uncovered by Env- and Eigen-GWAS in wheat and barley. <i>Theoretical and Applied Genetics</i> , 2022, 135, 667-678.	3.6	8
2	Wheat genetic loci conferring resistance to stripe rust in the face of genetically diverse races of the fungus <i>Puccinia striiformis</i> f. sp. <i>tritici</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 301-319.	3.6	16
3	The evolving battle between yellow rust and wheat: implications for global food security. <i>Theoretical and Applied Genetics</i> , 2022, 135, 741-753.	3.6	22
4	Genome-wide association mapping of Hagberg falling number, protein content, test weight, and grain yield in U.K. wheat. <i>Crop Science</i> , 2022, 62, 965-981.	1.8	10
5	Stomata on the abaxial and adaxial leaf surfaces contribute differently to leaf gas exchange and photosynthesis in wheat. <i>New Phytologist</i> , 2022, 235, 1743-1756.	7.3	20
6	Septoria Nodorum Blotch of Wheat: Disease Management and Resistance Breeding in the Face of Shifting Disease Dynamics and a Changing Environment. <i>Phytopathology</i> , 2021, 111, 906-920.	2.2	24
7	Understanding the classics: the unifying concepts of transgressive segregation, inbreeding depression and heterosis and their central relevance for crop breeding. <i>Plant Biotechnology Journal</i> , 2021, 19, 26-34.	8.3	65
8	Identification and cross-validation of genetic loci conferring resistance to Septoria nodorum blotch using a German multi-founder winter wheat population. <i>Theoretical and Applied Genetics</i> , 2021, 134, 125-142.	3.6	11
9	Population genomic structure of Eurasian and African foxtail millet landrace accessions inferred from genotyping-by-sequencing. <i>Plant Genome</i> , 2021, 14, e20081.	2.8	14
10	Wheat genomics and breeding: bridging the gap.. , 2021, 2021, .		9
11	Identification of eight QTL controlling multiple yield components in a German multi-parental wheat population, including Rht24, WAPO-A1, WAPO-B1 and genetic loci on chromosomes 5A and 6A. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1435-1454.	3.6	20
12	Identification of Fusarium head blight resistance loci in two Brazilian wheat mapping populations. <i>PLoS ONE</i> , 2021, 16, e0248184.	2.5	7
13	Wheat root systems as a breeding target for climate resilience. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1645-1662.	3.6	74
14	Hidden in plain sight: a molecular field survey of three wheat leaf blotch fungal diseases in North-Western Europe shows co-infection is widespread. <i>European Journal of Plant Pathology</i> , 2021, 160, 949-962.	1.7	9
15	Limited haplotype diversity underlies polygenic trait architecture across 70% years of wheat breeding. <i>Genome Biology</i> , 2021, 22, 137.	8.8	39
16	Effects of breeding history and crop management on the root architecture of wheat. <i>Plant and Soil</i> , 2020, 452, 587-600.	3.7	42
17	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
18	Genetic Analysis Using a Multi-Parent Wheat Population Identifies Novel Sources of Septoria Tritici Blotch Resistance. <i>Genes</i> , 2020, 11, 887.	2.4	19

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19	Is plant variety registration keeping pace with speed breeding techniques?. <i>Euphytica</i> , 2020, 216, 1.	1.2	12
20	Dissecting the genetic basis of wheat blast resistance in the Brazilian wheat cultivar BR 18-Terena. <i>BMC Plant Biology</i> , 2020, 20, 398.	3.6	30
21	Genetic Characterization of a Wheat Association Mapping Panel Relevant to Brazilian Breeding Using a High-Density Single Nucleotide Polymorphism Array. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2229-2239.	1.8	12
22	CRISPR/Cas9 Gene Editing of Gluten in Wheat to Reduce Gluten Content and Exposure—Reviewing Methods to Screen for Coeliac Safety. <i>Frontiers in Nutrition</i> , 2020, 7, 51.	3.7	59
23	Genetic Structure of the Norwegian <i>Parastagonospora nodorum</i> Population. <i>Frontiers in Microbiology</i> , 2020, 11, 1280.	3.5	11
24	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.	2.6	124
25	Genetic mapping using a wheat multi-founder population reveals a locus on chromosome 2A controlling resistance to both leaf and glume blotch caused by the necrotrophic fungal pathogen <i>Parastagonospora nodorum</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 785-808.	3.6	48
26	Genetic analysis of wheat sensitivity to the ToxB fungal effector from <i>Pyrenophora tritici-repentis</i> , the causal agent of tan spot. <i>Theoretical and Applied Genetics</i> , 2020, 133, 935-950.	3.6	31
27	Use of genetic markers for the detection of off-types for DUS phenotypic traits in the inbreeding crop, barley. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	16
28	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. <i>ELife</i> , 2020, 9, .	6.0	78
29	Outlook for coeliac disease patients: towards bread wheat with hypoimmunogenic gluten by gene editing of $\text{I}\alpha$ - and $\text{I}\beta$ -gliadin gene families. <i>BMC Plant Biology</i> , 2019, 19, 333.	3.6	75
30	Genotypic, Developmental and Environmental Effects on the Rapidity of gs in Wheat: Impacts on Carbon Gain and Water-Use Efficiency. <i>Frontiers in Plant Science</i> , 2019, 10, 492.	3.6	29
31	Development of the GlutEnSeq capture system for sequencing gluten gene families in hexaploid bread wheat with deletions or mutations induced by $\text{I}^3$ -irradiation or CRISPR/Cas9. <i>Journal of Cereal Science</i> , 2019, 88, 157-166.	3.7	28
32	Insights into deployment of DNA markers in plant variety protection and registration. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1911-1929.	3.6	56
33	A large-scale pedigree resource of wheat reveals evidence for adaptation and selection by breeders. <i>PLoS Biology</i> , 2019, 17, e3000071.	5.6	71
34	$\frac{1}{4}$ CT trait analysis reveals morphometric differences between domesticated temperate small grain cereals and their wild relatives. <i>Plant Journal</i> , 2019, 99, 98-111.	5.7	19
35	Genetic Dissection of Resistance to the Three Fungal Plant Pathogens <i>Blumeria graminis</i> , <i>Zymoseptoria tritici</i> , and <i>Pyrenophora tritici-repentis</i> Using a Multiparental Winter Wheat Population. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1745-1757.	1.8	26
36	Genetic Mapping Populations for Conducting High-Resolution Trait Mapping in Plants. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 109-138.	1.1	64

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37	<i>TEOSINTE BRANCHED1</i> Regulates Inflorescence Architecture and Development in Bread Wheat (<i>Triticum aestivum</i>). <i>Plant Cell</i> , 2018, 30, 563-581.	6.6	215
38	Food processing and breeding strategies for coeliac-safe and healthy wheat products. <i>Food Research International</i> , 2018, 110, 11-21.	6.2	35
39	Assessing European Wheat Sensitivities to <i>Parastagonospora nodorum</i> Necrotrophic Effectors and Fine-Mapping the Snn3-B1 Locus Conferring Sensitivity to the Effector SnTox3. <i>Frontiers in Plant Science</i> , 2018, 9, 881.	3.6	48
40	Barley heads east: Genetic analyses reveal routes of spread through diverse Eurasian landscapes. <i>PLoS ONE</i> , 2018, 13, e0196652.	2.5	54
41	Systematic Investigation of FLOWERING LOCUS T-Like Poaceae Gene Families Identifies the Short-Day Expressed Flowering Pathway Gene, TaFT3 in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 857.	3.6	37
42	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	8.3	221
43	The trans-Eurasian crop exchange in prehistory: Discerning pathways from barley phylogeography. <i>Quaternary International</i> , 2016, 426, 26-32.	1.5	19
44	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	3.6	243
45	Molecular and phenotypic characterization of the alternative seasonal growth habit and flowering time in barley ( <i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	16
46	Fine-Mapping the Wheat <i>Snn1</i> Locus Conferring Sensitivity to the <i>Parastagonospora nodorum</i> Necrotrophic Effector SnTox1 Using an Eight Founder Multiparent Advanced Generation Inter-Cross Population. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2257-2266.	1.8	38
47	Discovery, evaluation and distribution of haplotypes and new alleles of the Photoperiod-A1 gene in wheat. <i>Plant Molecular Biology</i> , 2015, 88, 149-164.	3.9	17
48	The New Wheat Vernalization Response Allele Vrn-D1s is Caused by DNA Transposon Insertion in the First Intron. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 294-303.	1.8	28
49	Genetic diversity in <i>Vicia faba</i> L. populations cultivated in Tunisia revealed by simple sequence repeat analysis. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, 278-285.	0.8	7
50	An Eight-Parent Multiparent Advanced Generation Inter-Cross Population for Winter-Sown Wheat: Creation, Properties, and Validation. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1603-1610.	1.8	215
51	Applying association mapping and genomic selection to the dissection of key traits in elite European wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2619-2633.	3.6	100
52	Molecular genetic analysis of cereal Î <sup>2</sup> -amylase genes using exon-primed intron-crossing (EPIC) PCR. <i>Ratarstvo i Povrtarstvo</i> , 2014, 51, 175-189.	0.5	1
53	Evaluation of the use of high-density SNP genotyping to implement UPOV Model 2 for DUS testing in barley. <i>Theoretical and Applied Genetics</i> , 2013, 126, 901-911.	3.6	30
54	Variety Protection and Plant Breedersâ€™ Rights in the â€œDNA Eraâ€™. , 2013, , 369-402.		5

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55	Analysis of DNA polymorphism in ancient barley herbarium material: Validation of the KASP SNP genotyping platform. <i>Taxon</i> , 2013, 62, 779-789.	0.7	21
56	Flowering Time. , 2013, , 1-66.		26
57	Screening a diverse collection of <i>Artemisia annua</i> germplasm accessions for the antimalarial compound, artemisinin. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2012, 10, 152-154.	0.8	17
58	Evaluation of diagnostic molecular markers for DUS phenotypic assessment in the cereal crop, barley ( <i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 1735-1749.	3.6	42
59	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. <i>PLoS ONE</i> , 2012, 7, e45307.	2.5	93
60	Molecular, phylogenetic and comparative genomic analysis of the cytokinin oxidase/dehydrogenase gene family in the Poaceae. <i>Plant Biotechnology Journal</i> , 2012, 10, 67-82.	8.3	47
61	Genome-wide association mapping of agronomic and morphologic traits in highly structured populations of barley cultivars. <i>Theoretical and Applied Genetics</i> , 2012, 124, 233-246.	3.6	122
62	Evolutionary history of barley cultivation in Europe revealed by genetic analysis of extant landraces. <i>BMC Evolutionary Biology</i> , 2011, 11, 320.	3.2	50
63	Genetic variation at flowering time loci in wild and cultivated barley. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 264-267.	0.8	26
64	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21611-21616.	7.1	259
65	Segmental chromosomal duplications harbouring group IV CONSTANS-like genes in cereals. <i>Genome</i> , 2010, 53, 231-240.	2.0	17
66	Whole-genome association mapping in elite inbred crop varieties This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 967-972.	2.0	22
67	PCR-Based Markers Diagnostic for Spring and Winter Seasonal Growth Habit in Barley. <i>Crop Science</i> , 2009, 49, 403-410.	1.8	45
68	Association mapping of partitioning loci in barley. <i>BMC Genetics</i> , 2008, 9, 16.	2.7	75
69	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
70	The Role of Double-Stranded Break Repair in the Creation of Phenotypic Diversity at Cereal <i>VRN1</i> Loci. <i>Genetics</i> , 2007, 177, 2535-2539.	2.9	37
71	Haplotype analysis of vernalization loci in European barley germplasm reveals novel VRN-H1 alleles and a predominant winter VRN-H1/VRN-H2 multi-locus haplotype. <i>Theoretical and Applied Genetics</i> , 2007, 115, 993-1001.	3.6	139
72	Comparative genetic approaches to the identification of flowering time genes in temperate cereals. <i>Field Crops Research</i> , 2004, 90, 87-99.	5.1	59

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73	Capturing Wheat Phenotypes at the Genome Level. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	8