

# Stephen Byrne

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

1,705  
citations

257101

24  
h-index

301761

39  
g-index

48  
all docs

48  
docs citations

48  
times ranked

1781  
citing authors

#	ARTICLE	IF	CITATIONS
1	A synteny-based draft genome sequence of the forage grass <i>Lolium perenne</i> . <i>Plant Journal</i> , 2015, 84, 816-826.	2.8	166
2	Genomic prediction of starch content and chipping quality in tetraploid potato using genotyping-by-sequencing. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2091-2108.	1.8	99
3	Genome Wide Allele Frequency Fingerprints (GWAFs) of Populations via Genotyping by Sequencing. <i>PLoS ONE</i> , 2013, 8, e57438.	1.1	91
4	Transcriptional and metabolic profiles of <i>Lolium perenne</i> L. genotypes in response to a PEG-induced water stress. <i>Plant Biotechnology Journal</i> , 2009, 7, 719-732.	4.1	79
5	A Gene Encoding a DUF247 Domain Protein Cosegregates with the <i>S</i> Self-Incompatibility Locus in Perennial Ryegrass. <i>Molecular Biology and Evolution</i> , 2016, 33, 870-884.	3.5	78
6	Genomic dissection and prediction of heading date in perennial ryegrass. <i>BMC Genomics</i> , 2015, 16, 921.	1.2	77
7	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics. <i>Plant Physiology</i> , 2013, 161, 571-582.	2.3	75
8	Early response mechanisms of perennial ryegrass ( <i>Lolium perenne</i> ) to phosphorus deficiency. <i>Annals of Botany</i> , 2011, 107, 243-254.	1.4	60
9	A transcriptome map of perennial ryegrass ( <i>Lolium perenne</i> L.). <i>BMC Genomics</i> , 2012, 13, 140.	1.2	60
10	Segregation distortion in <i>Lolium</i> : evidence for genetic effects. <i>Theoretical and Applied Genetics</i> , 2008, 117, 297-306.	1.8	54
11	Accuracy of Genomic Prediction in a Commercial Perennial Ryegrass Breeding Program. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0110.	1.6	51
12	Estimating genomic heritabilities at the level of family-pool samples of perennial ryegrass using genotyping-by-sequencing. <i>Theoretical and Applied Genetics</i> , 2016, 129, 45-52.	1.8	51
13	Characterization of Potato Virus Y Isolates and Assessment of Nanopore Sequencing to Detect and Genotype Potato Viruses. <i>Viruses</i> , 2020, 12, 478.	1.5	48
14	De Novo Assembly of the Perennial Ryegrass Transcriptome Using an RNA-Seq Strategy. <i>PLoS ONE</i> , 2014, 9, e103567.	1.1	44
15	Short-term response in leaf metabolism of perennial ryegrass ( <i>Lolium perenne</i> ) to alterations in nitrogen supply. <i>Metabolomics</i> , 2013, 9, 145-156.	1.4	42
16	Optimized Use of Low-Depth Genotyping-by-Sequencing for Genomic Prediction Among Multi-Parental Family Pools and Single Plants in Perennial Ryegrass ( <i>Lolium perenne</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 369.	1.7	42
17	Fructan metabolism and changes in fructan composition during cold acclimation in perennial ryegrass. <i>Frontiers in Plant Science</i> , 2015, 6, 329.	1.7	41
18	Candidate gene association mapping for winter survival and spring regrowth in perennial ryegrass. <i>Plant Science</i> , 2015, 235, 37-45.	1.7	37

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19	Identification of coincident QTL for days to heading, spike length and spikelets per spike in <i>Lolium perenne</i> L.. <i>Euphytica</i> , 2009, 166, 61-70.	0.6	33
20	The genome sequence of <i>Barbarea vulgaris</i> facilitates the study of ecological biochemistry. <i>Scientific Reports</i> , 2017, 7, 40728.	1.6	33
21	Genome-Wide Association and Genomic Prediction for Fry Color in Potato. <i>Agronomy</i> , 2020, 10, 90.	1.3	33
22	Quantitative trait loci mapping for biomass yield traits in a <i>Lolium</i> inbred line derived F2 population. <i>Euphytica</i> , 2009, 170, 99-107.	0.6	30
23	Identification of ABC transporters from <i>Lolium perenne</i> L. that are regulated by toxic levels of selenium. <i>Planta</i> , 2010, 231, 901-911.	1.6	29
24	The genome and transcriptome of perennial ryegrass mitochondria. <i>BMC Genomics</i> , 2013, 14, 202.	1.2	29
25	Changes in <i>Lolium perenne</i> transcriptome during cold acclimation in two genotypes adapted to different climatic conditions. <i>BMC Plant Biology</i> , 2015, 15, 250.	1.6	29
26	Genomic prediction of crown rust resistance in <i>Lolium perenne</i> . <i>BMC Genetics</i> , 2018, 19, 35.	2.7	28
27	Pooled DNA sequencing to identify SNPs associated with a major QTL for bacterial wilt resistance in Italian ryegrass ( <i>Lolium multiflorum</i> Lam.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 947-958.	1.8	26
28	Comparative sequence analysis of VRN1 alleles of <i>Lolium perenne</i> with the co-linear regions in barley, wheat, and rice. <i>Molecular Genetics and Genomics</i> , 2011, 286, 433-447.	1.0	25
29	Comparative transcriptome analysis within the <i>Lolium/Festuca</i> species complex reveals high sequence conservation. <i>BMC Genomics</i> , 2015, 16, 249.	1.2	24
30	First assembly of the genome of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. <i>Grassland Science</i> , 2019, 65, 125-134.	0.6	20
31	Genetic Analysis Using a Multi-Parent Wheat Population Identifies Novel Sources of Septoria Tritici Blotch Resistance. <i>Genes</i> , 2020, 11, 887.	1.0	19
32	Genetic linkage mapping in an F2 perennial ryegrass population using DArT markers. <i>Plant Breeding</i> , 2012, 131, 345-349.	1.0	17
33	Vernalization Mediated Changes in the <i>Lolium perenne</i> Transcriptome. <i>PLoS ONE</i> , 2014, 9, e107365.	1.1	17
34	Using variable importance measures to identify a small set of SNPs to predict heading date in perennial ryegrass. <i>Scientific Reports</i> , 2017, 7, 3566.	1.6	17
35	Markers associated with heading and aftermath heading in perennial ryegrass full-sib families. <i>BMC Plant Biology</i> , 2016, 16, 160.	1.6	16
36	Rapid Development of KASP Markers for Disease Resistance Genes Using Pooled Whole-Genome Resequencing. <i>Potato Research</i> , 2020, 63, 57-73.	1.2	16

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37	Overcoming challenges in variant calling: exploring sequence diversity in candidate genes for plant development in perennial ryegrass ( <i>Lolium perenne</i> ). DNA Research, 2019, 26, 1-12.	1.5	14
38	Quantitative trait loci analysis to study the genetic regulation of non-polar metabolites in perennial ryegrass. Metabolomics, 2015, 11, 412-424.	1.4	11
39	Using a Candidate Gene-Based Genetic Linkage Map to Identify QTL for Winter Survival in Perennial Ryegrass. PLoS ONE, 2016, 11, e0152004.	1.1	10
40	Genome sequence of the English grain aphid, <i>Sitobion avenae</i> and its endosymbiont <i>Buchnera aphidicola</i> . G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	4
41	Predicting anthesis date of perennial ryegrass ( <i>Lolium perenne</i> L.) with growing degree-days at heading. Grass and Forage Science, 2018, 73, 233-238.	1.2	3
42	Genomic Prediction of Complex Traits in Forage Plants Species: Perennial Grasses Case. Methods in Molecular Biology, 2022, 2467, 521-541.	0.4	3
43	Identification of genes involved in the floral transition at the shoot apical meristem of <i>Lolium perenne</i> L. by use of suppression subtractive hybridisation. Plant Growth Regulation, 2009, 59, 215-225.	1.8	2
44	Propensity for seed-mediated gene flow from potato crops and potential consequences for the coexistence of GM and non-GM potato systems. European Journal of Agronomy, 2015, 67, 52-60.	1.9	2
45	Genetic characterization of buckwheat accessions through genome-wide allele frequency fingerprints / Genetska karakterizacija vzorcev ajde z odtisi frekvence alelov v genomu. , 2020, 61, 17-23.	0.3	2
46	Quantitative trait loci associated with different polar metabolites in perennial ryegrass - providing scope for breeding towards increasing certain polar metabolites. BMC Genetics, 2017, 18, 84.	2.7	1
47	Allele Re-sequencing Technologies. , 2013, , 91-118.		0