

# John M Hickey

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

2,377  
citations

304368

22  
h-index

344852

36  
g-index

57  
all docs

57  
docs citations

57  
times ranked

2364  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery. <i>Nature Genetics</i> , 2017, 49, 1297-1303.	9.4	263
2	The importance of information on relatives for the prediction of genomic breeding values and the implications for the makeup of reference data sets in livestock breeding schemes. <i>Genetics Selection Evolution</i> , 2012, 44, 4.	1.2	249
3	Evaluation of Genomic Selection Training Population Designs and Genotyping Strategies in Plant Breeding Programs Using Simulation. <i>Crop Science</i> , 2014, 54, 1476-1488.	0.8	164
4	A Two-Part Strategy for Using Genomic Selection to Develop Inbred Lines. <i>Crop Science</i> , 2017, 57, 2372-2386.	0.8	140
5	A combined long-range phasing and long haplotype imputation method to impute phase for SNP genotypes. <i>Genetics Selection Evolution</i> , 2011, 43, 12.	1.2	133
6	Potential of promotion of alleles by genome editing to improve quantitative traits in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2015, 47, 55.	1.2	125
7	Optimal cross selection for long-term genetic gain in two-part programs with rapid recurrent genomic selection. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1953-1966.	1.8	120
8	AlphaSimR: an R package for breeding program simulations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	109
9	Potential of genotyping-by-sequencing for genomic selection in livestock populations. <i>Genetics Selection Evolution</i> , 2015, 47, 12.	1.2	107
10	AlphaSim: Software for Breeding Program Simulation. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0013.	1.6	105
11	Potential of Low-Coverage Genotyping-by-Sequencing and Imputation for Cost-Effective Genomic Selection in Biparental Segregating Populations. <i>Crop Science</i> , 2017, 57, 1404-1420.	0.8	64
12	Simulated Data for Genomic Selection and Genome-Wide Association Studies Using a Combination of Coalescent and Gene Drop Methods. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 425-427.	0.8	61
13	Reliability of pedigree-based and genomic evaluations in selected populations. <i>Genetics Selection Evolution</i> , 2015, 47, 65.	1.2	54
14	Prospects for Cost-Effective Genomic Selection via Accurate Within-Family Imputation. <i>Crop Science</i> , 2017, 57, 216-228.	0.8	48
15	Hybrid peeling for fast and accurate calling, phasing, and imputation with sequence data of any coverage in pedigrees. <i>Genetics Selection Evolution</i> , 2018, 50, 67.	1.2	46
16	Removal of alleles by genome editing (RAGE) against deleterious load. <i>Genetics Selection Evolution</i> , 2019, 51, 14.	1.2	44
17	Impact of index hopping and bias towards the reference allele on accuracy of genotype calls from low-coverage sequencing. <i>Genetics Selection Evolution</i> , 2018, 50, 64.	1.2	38
18	Imputation of Single Nucleotide Polymorphism Genotypes in Biparental, Backcross, and Topcross Populations with a Hidden Markov Model. <i>Crop Science</i> , 2015, 55, 1934-1946.	0.8	37

#	ARTICLE	IF	CITATIONS
19	AlphaMate: a program for optimizing selection, maintenance of diversity and mate allocation in breeding programs. <i>Bioinformatics</i> , 2018, 34, 3408-3411.	1.8	36
20	A hybrid method for the imputation of genomic data in livestock populations. <i>Genetics Selection Evolution</i> , 2017, 49, 30.	1.2	34
21	A method for allocating low-coverage sequencing resources by targeting haplotypes rather than individuals. <i>Genetics Selection Evolution</i> , 2017, 49, 78.	1.2	34
22	Accuracy of whole-genome sequence imputation using hybrid peeling in large pedigreed livestock populations. <i>Genetics Selection Evolution</i> , 2020, 52, 17.	1.2	30
23	Surrogate broodstock to enhance biotechnology research and applications in aquaculture. <i>Biotechnology Advances</i> , 2021, 49, 107756.	6.0	28
24	A method for the allocation of sequencing resources in genotyped livestock populations. <i>Genetics Selection Evolution</i> , 2017, 49, 47.	1.2	27
25	A Strategy To Exploit Surrogate Sire Technology in Livestock Breeding Programs. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 203-215.	0.8	26
26	Analysis of a large dataset reveals haplotypes carrying putatively recessive lethal and semi-lethal alleles with pleiotropic effects on economically important traits in beef cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 9.	1.2	24
27	Extending long-range phasing and haplotype library imputation methods to impute genotypes on sex chromosomes. <i>Genetics Selection Evolution</i> , 2013, 45, 10.	1.2	23
28	GplusE: beyond genomic selection. <i>Food and Energy Security</i> , 2015, 4, 25-35.	2.0	20
29	A heuristic method for fast and accurate phasing and imputation of single-nucleotide polymorphism data in bi-parental plant populations. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2345-2357.	1.8	20
30	Evaluation of sequencing strategies for whole-genome imputation with hybrid peeling. <i>Genetics Selection Evolution</i> , 2020, 52, 18.	1.2	17
31	Genetic variation in recombination rate in the pig. <i>Genetics Selection Evolution</i> , 2021, 53, 54.	1.2	17
32	Sequence variation, evolutionary constraint, and selection at the CD163 gene in pigs. <i>Genetics Selection Evolution</i> , 2018, 50, 69.	1.2	11
33	Long-term comparison between index selection and optimal independent culling in plant breeding programs with genomic prediction. <i>PLoS ONE</i> , 2021, 16, e0235554.	1.1	11
34	AlphaPartâ€™R implementation of the method for partitioning genetic trends. <i>Genetics Selection Evolution</i> , 2021, 53, 30.	1.2	9
35	Rare and population-specific functional variation across pig lines. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	9
36	Phasing and imputation of single nucleotide polymorphism data of missing parents of biparental plant populations. <i>Crop Science</i> , 2021, 61, 2243-2253.	0.8	5