

# Bevan E Huang

## List of Publications by Year in descending order

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29  
papers

4,804  
citations

331670

21  
h-index

477307

29  
g-index

29  
all docs

29  
docs citations

29  
times ranked

4934  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014, 12, 787-796.	8.3	1,828
2	Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8057-8062.	7.1	1,065
3	A multiparent advanced generation inter-cross population for genetic analysis in wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 826-839.	8.3	290
4	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015, 128, 999-1017.	3.6	230
5	ELF3 Controls Thermo-responsive Growth in Arabidopsis. <i>Current Biology</i> , 2015, 25, 194-199.	3.9	225
6	Potential of a tomato MAGIC population to decipher the genetic control of quantitative traits and detect causal variants in the resequencing era. <i>Plant Biotechnology Journal</i> , 2015, 13, 565-577.	8.3	184
7	R/mpMap: a computational platform for the genetic analysis of multiparent recombinant inbred lines. <i>Bioinformatics</i> , 2011, 27, 727-729.	4.1	142
8	Multi-parent advanced generation inter-cross in barley: high-resolution quantitative trait locus mapping for flowering time as a proof of concept. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	134
9	Transcriptomic analysis of wheat near-isogenic lines identifies PM19-A1 and A2 as candidates for a major dormancy QTL. <i>Genome Biology</i> , 2015, 16, 93.	8.8	125
10	Simple and Efficient Analysis of Disease Association with Missing Genotype Data. <i>American Journal of Human Genetics</i> , 2008, 82, 444-452.	6.2	87
11	Efficient Association Mapping of Quantitative Trait Loci with Selective Genotyping. <i>American Journal of Human Genetics</i> , 2007, 80, 567-576.	6.2	61
12	Delay discounting, impulsiveness, and addiction severity in opioid-dependent patients. <i>Journal of Substance Abuse Treatment</i> , 2011, 41, 354-362.	2.8	49
13	A Linear Mixed Model Spline Framework for Analysing Time Course Omics Data. <i>PLoS ONE</i> , 2015, 10, e0134540.	2.5	46
14	The Use of Inferred Haplotypes in Downstream Analyses. <i>American Journal of Human Genetics</i> , 2007, 80, 577-579.	6.2	44
15	Interleukin-1 polymorphisms are associated with the inflammatory response in human muscle to acute resistance exercise. <i>Journal of Physiology</i> , 2004, 560, 617-626.	2.9	43
16	QTLs for Tolerance of Drought and Breeding for Tolerance of Abiotic and Biotic Stress: An Integrated Approach. <i>PLoS ONE</i> , 2014, 9, e109574.	2.5	43
17	Detecting haplotype effects in genomewide association studies. <i>Genetic Epidemiology</i> , 2007, 31, 803-812.	1.3	39
18	Efficient Imputation of Missing Markers in Low-Coverage Genotyping-by-Sequencing Data from Multiparental Crosses. <i>Genetics</i> , 2014, 197, 401-404.	2.9	32

#	ARTICLE	IF	CITATIONS
19	The effect of microbial colonization on the host proteome varies by gastrointestinal location. <i>ISME Journal</i> , 2016, 10, 1170-1181.	9.8	29
20	Postprandial total and HMW adiponectin following a high-fat meal in lean, obese and diabetic men. <i>European Journal of Clinical Nutrition</i> , 2013, 67, 377-384.	2.9	25
21	The Effect of a High-Fat Meal on Postprandial Arterial Stiffness in Men with Obesity and Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2010, 95, 4455-4459.	3.6	21
22	Selecting subsets of genotyped experimental populations for phenotyping to maximize genetic diversity. <i>Theoretical and Applied Genetics</i> , 2013, 126, 379-388.	3.6	16
23	Computationally efficient map construction in the presence of segregation distortion. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2585-2597.	3.6	10
24	Characterizing Uncertainty in High-Density Maps from Multiparental Populations. <i>Genetics</i> , 2014, 198, 117-128.	2.9	10
25	Reply to Peter Kraft and Daniel O. Stram. <i>American Journal of Human Genetics</i> , 2007, 81, 865-866.	6.2	6
26	AlphaMPSim: flexible simulation of multi-parent crosses. <i>Bioinformatics</i> , 2014, 30, 2686-2688.	4.1	6
27	Look before you leap: a new approach to mapping QTL. <i>Theoretical and Applied Genetics</i> , 2009, 119, 899-911.	3.6	5
28	iDArTs: increasing the value of genomic resources at no cost. <i>Molecular Breeding</i> , 2012, 30, 927-938.	2.1	5
29	Sibling Family Practices: Guidelines for Healthy Boundaries. <i>Journal of Child Sexual Abuse</i> , 2009, 18, 339-354.	1.3	4