Zachary B Lippman

List of Publications by Year
in descending order

46	11,798	94433 37	233421 45
papers	citations	h-index	g-index

52	52	52	11780
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Dynamic evolution of small signalling peptide compensation in plant stem cell control. Nature Plants, 2022, 8, 346-355.	9.3	27
2	Identification of Genetic Factors Controlling the Formation of Multiple Flowers Per Node in Pepper (Capsicum spp.). Frontiers in Plant Science, 2022, 13, .	3.6	0
3	Newly Discovered Alleles of the Tomato Antiflorigen Gene SELF PRUNING Provide a Range of Plant Compactness and Yield. International Journal of Molecular Sciences, 2022, 23, 7149.	4.1	2
4	Optimized sample selection for cost-efficient long-read population sequencing. Genome Research, 2021, 31, 910-918.	5.5	4
5	Conserved pleiotropy of an ancient plant homeobox gene uncovered by cis-regulatory dissection. Cell, 2021, 184, 1724-1739.e16.	28.9	103
6	Dissecting cis-regulatory control of quantitative trait variation in a plant stem cell circuit. Nature Plants, 2021, 7, 419-427.	9.3	72
7	Rapid customization of Solanaceae fruit crops for urban agriculture. Nature Biotechnology, 2020, 38, 182-188.	17.5	133
8	New Horizons for Dissecting Epistasis in Crop Quantitative Trait Variation. Annual Review of Genetics, 2020, 54, 287-307.	7.6	23
9	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. Cell, 2020, 182, 145-161.e23.	28.9	464
10	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. Genome Biology, 2019, 20, 224.	8.8	469
11	Revolutions in agriculture chart a course for targeted breeding of old and new crops. Science, 2019, 366, .	12.6	197
12	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. Nature Plants, 2019, 5, 471-479.	9.3	66
13	Evolution of buffering in a genetic circuit controlling plant stem cell proliferation. Nature Genetics, 2019, 51, 786-792.	21.4	129
14	Rapid improvement of domestication traits in an orphan crop by genome editing. Nature Plants, 2018, 4, 766-770.	9.3	361
15	Control of flowering and inflorescence architecture in tomato by synergistic interactions between ALOG transcription factors. Journal of Genetics and Genomics, 2018, 45, 557-560.	3.9	13
16	Variation in the flowering gene SELF PRUNING 5G promotes day-neutrality and early yield in tomato. Nature Genetics, 2017, 49, 162-168.	21.4	344
17	Bypassing Negative Epistasis on Yield in Tomato Imposed by a Domestication Gene. Cell, 2017, 169, 1142-1155.e12.	28.9	286
18	Engineering Quantitative Trait Variation for Crop Improvement by Genome Editing. Cell, 2017, 171, 470-480.e8.	28.9	797

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19	Hydroxyproline Oâ€arabinosyltransferase mutants oppositely alter tip growth in Arabidopsis thaliana and Physcomitrella patens. Plant Journal, 2016, 85, 193-208.	5.7	40
20	Control of inflorescence architecture in tomato by BTB/POZ transcriptional regulators. Genes and Development, 2016, 30, 2048-2061.	5.9	128
21	The evolution of inflorescence diversity in the nightshades and heterochrony during meristem maturation. Genome Research, 2016, 26, 1676-1686.	5.5	51
22	A cascade of arabinosyltransferases controls shoot meristem size in tomato. Nature Genetics, 2015, 47, 784-792.	21.4	348
23	Efficient Gene Editing in Tomato in the First Generation Using the Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR-Associated9 System. Plant Physiology, 2014, 166, 1292-1297.	4.8	675
24	Optimization of crop productivity in tomato using induced mutations in the florigen pathway. Nature Genetics, 2014, 46, 1337-1342.	21.4	169
25	Meristem maturation and inflorescence architectureâ€"lessons from the Solanaceae. Current Opinion in Plant Biology, 2014, 17, 70-77.	7.1	67
26	Tomato Yield Heterosis Is Triggered by a Dosage Sensitivity of the Florigen Pathway That Fine-Tunes Shoot Architecture. PLoS Genetics, 2013, 9, e1004043.	3.5	85
27	Rate of meristem maturation determines inflorescence architecture in tomato. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 639-644.	7.1	171
28	Synchronization of the flowering transition by the tomato TERMINATING FLOWER gene. Nature Genetics, 2012, 44, 1393-1398.	21.4	122
29	The flowering gene SINGLE FLOWER TRUSS drives heterosis for yield in tomato. Nature Genetics, 2010, 42, 459-463.	21.4	438
30	Winning a plant campaign. Nature, 2008, 453, 954-954.	27.8	0
31	The Making of a Compound Inflorescence in Tomato and Related Nightshades. PLoS Biology, 2008, 6, e288.	5.6	207
32	An integrated view of quantitative trait variation using tomato interspecific introgression lines. Current Opinion in Genetics and Development, 2007, 17, 545-552.	3.3	178
33	Heterosis: revisiting the magic. Trends in Genetics, 2007, 23, 60-66.	6.7	517
34	Epigenetic Natural Variation in Arabidopsis thaliana. PLoS Biology, 2007, 5, e174.	5.6	400
35	Overdominant quantitative trait loci for yield and fitness in tomato. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12981-12986.	7.1	266
36	Profiling histone modification patterns in plants using genomic tiling microarrays. Nature Methods, 2005, 2, 213-218.	19.0	521

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37	Profiling DNA methylation patterns using genomic tiling microarrays. Nature Methods, 2005, 2, 219-224.	19.0	119
38	Differential Regulation of Strand-Specific Transcripts from Arabidopsis Centromeric Satellite Repeats. PLoS Genetics, 2005, 1, e79.	3.5	162
39	Vernalization requires epigenetic silencing of FLC by histone methylation. Nature, 2004, 427, 164-167.	27.8	866
40	Role of transposable elements in heterochromatin and epigenetic control. Nature, 2004, 430, 471-476.	27.8	1,103
41	The role of RNA interference in heterochromatic silencing. Nature, 2004, 431, 364-370.	27.8	514
42	Transposons, Tandem Repeats, and the Silencing of Imprinted Genes. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 371-380.	1.1	27
43	Distinct Mechanisms Determine Transposon Inheritance and Methylation via Small Interfering RNA and Histone Modification. PLoS Biology, 2003, 1, e67.	5.6	369
44	Extremely elongated tomato fruit controlled by four quantitative trait loci with epistatic interactions. Theoretical and Applied Genetics, 2002, 104, 241-247.	3.6	61
45	Dependence of Heterochromatic Histone H3 Methylation Patterns on the Arabidopsis Gene DDM1. Science, 2002, 297, 1871-1873.	12.6	417
46	Dissecting the Genetic Pathway to Extreme Fruit Size in Tomato Using a Cross Between the Small-Fruited Wild SpeciesLycopersicon pimpinellifoliumandL. esculentumvar. Giant Heirloom. Genetics, 2001, 158, 413-422.	2.9	191