

# Levi Yant

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

5,916  
citations

117453

34  
h-index

149479

56  
g-index

73  
all docs

73  
docs citations

73  
times ranked

7269  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposable element annotation in non-model species: The benefits of species-specific repeat libraries using semi-automated EDTA and DeepTE de novo pipelines. <i>Molecular Ecology Resources</i> , 2022, 22, 823-833.	2.2	10
2	Circular <i>scnRNA</i> in disease: Basic properties and biomedical relevance. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022, 13, e1723.	3.2	21
3	De Novo Mutation and Rapid Protein (Co-)evolution during Meiotic Adaptation in <i>Arabidopsis arenosa</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 1980-1994.	3.5	18
4	Adaptive introgression: how polyploidy reshapes gene flow landscapes. <i>New Phytologist</i> , 2021, 230, 457-461.	3.5	31
5	Population genomic and historical analysis suggests a global invasion by bridgehead processes in <i>Mimulus guttatus</i> . <i>Communications Biology</i> , 2021, 4, 327.	2.0	24
6	Novelty and Convergence in Adaptation to Whole Genome Duplication. <i>Molecular Biology and Evolution</i> , 2021, 38, 3910-3924.	3.5	22
7	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
8	Adaptation to coastal soils through pleiotropic boosting of ion and stress hormone concentrations in wild <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2021, 232, 208-220.	3.5	9
9	Parallel adaptation in autopolyploid <i>Arabidopsis arenosa</i> is dominated by repeated recruitment of shared alleles. <i>Nature Communications</i> , 2021, 12, 4979.	5.8	22
10	Maintenance of Adaptive Dynamics and No Detectable Load in a Range-Edge Outcrossing Plant Population. <i>Molecular Biology and Evolution</i> , 2021, 38, 1820-1836.	3.5	24
11	Evolutionary footprints of a cold relic in a rapidly warming world. <i>ELife</i> , 2021, 10, .	2.8	5
12	A novel allele of <i>ASY3</i> is associated with greater meiotic stability in autotetraploid <i>Arabidopsis lyrata</i> . <i>PLoS Genetics</i> , 2020, 16, e1008900.	1.5	26
13	Formation and diversification of a paradigm biosynthetic gene cluster in plants. <i>Nature Communications</i> , 2020, 11, 5354.	5.8	50
14	The Evolutionary Genomics of Serpentine Adaptation. <i>Frontiers in Plant Science</i> , 2020, 11, 574616.	1.7	17
15	Help or hindrance? The evolutionary impact of whole-genome duplication on immunogenetic diversity and parasite load. <i>Ecology and Evolution</i> , 2020, 10, 13949-13956.	0.8	0
16	Polyploidy breaks speciation barriers in Australian burrowing frogs <i>Neobatrachus</i> . <i>PLoS Genetics</i> , 2020, 16, e1008769.	1.5	40
17	The genome-wide impact of cadmium on microRNA and mRNA expression in contrasting Cd responsive wheat genotypes. <i>BMC Genomics</i> , 2019, 20, 615.	1.2	40
18	Genome-wide identification, phylogenetic and expression analysis of the heat shock transcription factor family in bread wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2019, 20, 505.	1.2	33

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19	Convergent evolution in <i>Arabidopsis halleri</i> and <i>Arabidopsis arenosa</i> on calamine metalliferous soils. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180243.	1.8	43
20	Pervasive population genomic consequences of genome duplication in <i>Arabidopsis arenosa</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 457-468.	3.4	102
21	FT Modulates Genome-Wide DNA-Binding of the bZIP Transcription Factor FD. <i>Plant Physiology</i> , 2019, 180, 367-380.	2.3	115
22	Interspecific introgression mediates adaptation to whole genome duplication. <i>Nature Communications</i> , 2019, 10, 5218.	5.8	59
23	The “Polyploid Hop” Shifting Challenges and Opportunities Over the Evolutionary Lifespan of Genome Duplications. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	136
24	Fluctuating selection on migrant adaptive sodium transporter alleles in coastal <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E12443-E12452.	3.3	44
25	Genomic studies of adaptive evolution in outcrossing <i>Arabidopsis</i> species. <i>Current Opinion in Plant Biology</i> , 2017, 36, 9-14.	3.5	25
26	Hybrids and horizontal transfer: introgression allows adaptive allele discovery. <i>Journal of Experimental Botany</i> , 2017, 68, 5453-5470.	2.4	24
27	Borrowed alleles and convergence in serpentine adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8320-8325.	3.3	147
28	DNA-Binding Factor Target Identification by Chromatin Immunoprecipitation (ChIP) in Plants. <i>Methods in Molecular Biology</i> , 2016, 1363, 25-35.	0.4	3
29	Meiosis evolves: adaptation to external and internal environments. <i>New Phytologist</i> , 2015, 208, 306-323.	3.5	148
30	Genome management and mismanagement—cell-level opportunities and challenges of whole-genome duplication. <i>Genes and Development</i> , 2015, 29, 2405-2419.	2.7	33
31	Molecular basis for three-dimensional elaboration of the <i>Aquilegia</i> petal spur. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142778.	1.2	51
32	When two is a crowd: mitochondrial genome merger and its aftermath. <i>New Phytologist</i> , 2015, 206, 8-9.	3.5	0
33	Understanding the development and evolution of novel floral form in <i>Aquilegia</i> . <i>Current Opinion in Plant Biology</i> , 2014, 17, 22-27.	3.5	30
34	Meiotic Adaptation to Genome Duplication in <i>Arabidopsis arenosa</i> . <i>Current Biology</i> , 2013, 23, 2151-2156.	1.8	217
35	Temperature-dependent regulation of flowering by antagonistic FLM variants. <i>Nature</i> , 2013, 503, 414-417.	13.7	409
36	Genome-wide mapping of transcription factor binding reveals developmental process integration and a fresh look at evolutionary dynamics. <i>American Journal of Botany</i> , 2012, 99, 277-290.	0.8	12

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37	The floral homeotic protein APETALA2 recognizes and acts through an AT-rich sequence element. <i>Development (Cambridge)</i> , 2012, 139, 1978-1986.	1.2	87
38	The recombination landscape in <i>Arabidopsis thaliana</i> F2 populations. <i>Heredity</i> , 2012, 108, 447-455.	1.2	155
39	The end of innocence: flowering networks explode in complexity. <i>Current Opinion in Plant Biology</i> , 2012, 15, 45-50.	3.5	93
40	Genetic Architecture of Flowering-Time Variation in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2011, 188, 421-433.	1.2	160
41	Prediction of Regulatory Interactions from Genome Sequences Using a Biophysical Model for the <i>Arabidopsis</i> LEAFY Transcription Factor. <i>Plant Cell</i> , 2011, 23, 1293-1306.	3.1	148
42	Local-Scale Patterns of Genetic Variability, Outcrossing, and Spatial Structure in Natural Stands of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000890.	1.5	172
43	Orchestration of the Floral Transition and Floral Development in <i>Arabidopsis</i> by the Bifunctional Transcription Factor APETALA2. <i>Plant Cell</i> , 2010, 22, 2156-2170.	3.1	427
44	Repression of Flowering by the miR172 Target SMZ. <i>PLoS Biology</i> , 2009, 7, e1000148.	2.6	382
45	Just say no: floral repressors help <i>Arabidopsis</i> bide the time. <i>Current Opinion in Plant Biology</i> , 2009, 12, 580-586.	3.5	68
46	Comprehensive Immunological Evaluation Reveals Surprisingly Few Differences between Elite Controller and Progressor Mamu-B*17-Positive Simian Immunodeficiency Virus-Infected Rhesus Macaques. <i>Journal of Virology</i> , 2008, 82, 5245-5254.	1.5	56
47	Subdominant CD8 + T-Cell Responses Are Involved in Durable Control of AIDS Virus Replication. <i>Journal of Virology</i> , 2007, 81, 3465-3476.	1.5	199
48	Control of Simian Immunodeficiency Virus SIVmac239 Is Not Predicted by Inheritance of Mamu-B * 17 -Containing Haplotypes. <i>Journal of Virology</i> , 2007, 81, 406-410.	1.5	40
49	Vaccine-Induced Cellular Immune Responses Reduce Plasma Viral Concentrations after Repeated Low-Dose Challenge with Pathogenic Simian Immunodeficiency Virus SIVmac239. <i>Journal of Virology</i> , 2006, 80, 5875-5885.	1.5	237
50	The High-Frequency Major Histocompatibility Complex Class I Allele Mamu-B * 17 Is Associated with Control of Simian Immunodeficiency Virus SIVmac239 Replication. <i>Journal of Virology</i> , 2006, 80, 5074-5077.	1.5	266
51	Tat 28-35 SL8-Specific CD8 + T Lymphocytes Are More Effective than Gag 181-189 CM9-Specific CD8 + T Lymphocytes at Suppressing Simian Immunodeficiency Virus Replication in a Functional In Vitro Assay. <i>Journal of Virology</i> , 2005, 79, 14986-14991.	1.5	53
52	Extraepitopic Compensatory Substitutions Partially Restore Fitness to Simian Immunodeficiency Virus Variants That Escape from an Immunodominant Cytotoxic-T-Lymphocyte Response. <i>Journal of Virology</i> , 2004, 78, 2581-2585.	1.5	99
53	Repeated Low-Dose Mucosal Simian Immunodeficiency Virus SIVmac239 Challenge Results in the Same Viral and Immunological Kinetics as High-Dose Challenge: a Model for the Evaluation of Vaccine Efficacy in Nonhuman Primates. <i>Journal of Virology</i> , 2004, 78, 3140-3144.	1.5	95
54	A Dominant Role for CD8 + -T-Lymphocyte Selection in Simian Immunodeficiency Virus Sequence Variation. <i>Journal of Virology</i> , 2004, 78, 14012-14022.	1.5	89

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55	Consequences of Cytotoxic T-Lymphocyte Escape: Common Escape Mutations in Simian Immunodeficiency Virus Are Poorly Recognized in Naïve Hosts. <i>Journal of Virology</i> , 2004, 78, 10064-10073.	1.5	35
56	Reversion of CTL escapeâ€variant immunodeficiency viruses in vivo. <i>Nature Medicine</i> , 2004, 10, 275-281.	15.2	349
57	The selenoprotein GPX4 is essential for mouse development and protects from radiation and oxidative damage insults. <i>Free Radical Biology and Medicine</i> , 2003, 34, 496-502.	1.3	615