## Levi Yant

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8828569/publications.pdf

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57	5,916	117625	149698
papers	citations	h-index	g-index
73 all docs	73 docs citations	73 times ranked	7269 citing authors

#	Article	IF	CITATIONS
1	The selenoprotein GPX4 is essential for mouse development and protects from radiation and oxidative damage insults. Free Radical Biology and Medicine, 2003, 34, 496-502.	2.9	615
2	Orchestration of the Floral Transition and Floral Development in <i>Arabidopsis</i> Bifunctional Transcription Factor APETALA2 Â. Plant Cell, 2010, 22, 2156-2170.	6.6	427
3	Temperature-dependent regulation of flowering by antagonistic FLM variants. Nature, 2013, 503, 414-417.	27.8	409
4	Repression of Flowering by the miR172 Target SMZ. PLoS Biology, 2009, 7, e1000148.	5.6	382
5	Reversion of CTL escape–variant immunodeficiency viruses in vivo. Nature Medicine, 2004, 10, 275-281.	30.7	349
6	The High-Frequency Major Histocompatibility Complex Class I Allele Mamu-B * 17 Is Associated with Control of Simian Immunodeficiency Virus SIVmac239 Replication. Journal of Virology, 2006, 80, 5074-5077.	3.4	266
7	Vaccine-Induced Cellular Immune Responses Reduce Plasma Viral Concentrations after Repeated Low-Dose Challenge with Pathogenic Simian Immunodeficiency Virus SIVmac239. Journal of Virology, 2006, 80, 5875-5885.	3.4	237
8	Meiotic Adaptation to Genome Duplication in Arabidopsis arenosa. Current Biology, 2013, 23, 2151-2156.	3.9	217
9	Subdominant CD8 + T-Cell Responses Are Involved in Durable Control of AIDS Virus Replication. Journal of Virology, 2007, 81, 3465-3476.	3.4	199
10	Local-Scale Patterns of Genetic Variability, Outcrossing, and Spatial Structure in Natural Stands of Arabidopsis thaliana. PLoS Genetics, 2010, 6, e1000890.	3.5	172
11	Genetic Architecture of Flowering-Time Variation in <i>Arabidopsis thaliana</i> . Genetics, 2011, 188, 421-433.	2.9	160
12	The recombination landscape in Arabidopsis thaliana F2 populations. Heredity, 2012, 108, 447-455.	2.6	155
13	Prediction of Regulatory Interactions from Genome Sequences Using a Biophysical Model for the <i>Arabidopsis &lt; /i&gt;LEAFY Transcription Factor Â. Plant Cell, 2011, 23, 1293-1306.</i>	6.6	148
14	Meiosis evolves: adaptation to external and internal environments. New Phytologist, 2015, 208, 306-323.	7.3	148
15	Borrowed alleles and convergence in serpentine adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8320-8325.	7.1	147
16	The "Polyploid Hop― Shifting Challenges and Opportunities Over the Evolutionary Lifespan of Genome Duplications. Frontiers in Ecology and Evolution, 2018, 6, .	2.2	136
17	FT Modulates Genome-Wide DNA-Binding of the bZIP Transcription Factor FD. Plant Physiology, 2019, 180, 367-380.	4.8	115
18	Pervasive population genomic consequences of genome duplication in Arabidopsis arenosa. Nature Ecology and Evolution, 2019, 3, 457-468.	7.8	102

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19	Extraepitopic Compensatory Substitutions Partially Restore Fitness to Simian Immunodeficiency Virus Variants That Escape from an Immunodominant Cytotoxic-T-Lymphocyte Response. Journal of Virology, 2004, 78, 2581-2585.	3.4	99
20	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. Journal of Virology, 2004, 78, 3140-3144.	3.4	95
21	The end of innocence: flowering networks explode in complexity. Current Opinion in Plant Biology, 2012, 15, 45-50.	7.1	93
22	A Dominant Role for CD8 + -T-Lymphocyte Selection in Simian Immunodeficiency Virus Sequence Variation. Journal of Virology, 2004, 78, 14012-14022.	3.4	89
23	The floral homeotic protein APETALA2 recognizes and acts through an AT-rich sequence element. Development (Cambridge), 2012, 139, 1978-1986.	2.5	87
24	Just say no: floral repressors help Arabidopsis bide the time. Current Opinion in Plant Biology, 2009, 12, 580-586.	7.1	68
25	Interspecific introgression mediates adaptation to whole genome duplication. Nature Communications, 2019, 10, 5218.	12.8	59
26	Comprehensive Immunological Evaluation Reveals Surprisingly Few Differences between Elite Controller and Progressor <i>Mamu-B*17</i> Positive Simian Immunodeficiency Virus-Infected Rhesus Macaques. Journal of Virology, 2008, 82, 5245-5254.	3.4	56
27	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. Journal of Virology, 2005, 79, 14986-14991.	3.4	53
28	Molecular basis for three-dimensional elaboration of the <i>Aquilegia </i> petal spur. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142778.	2.6	51
29	Formation and diversification of a paradigm biosynthetic gene cluster in plants. Nature Communications, 2020, 11, 5354.	12.8	50
30	Fluctuating selection on migrant adaptive sodium transporter alleles in coastal <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12443-E12452.	7.1	44
31	Convergent evolution in <i>Arabidopsis halleri</i> i>and <i>Arabidopsis arenosa</i> on calamine metalliferous soils. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180243.	4.0	43
32	Control of Simian Immunodeficiency Virus SIVmac239 Is Not Predicted by Inheritance of Mamu-B * 17 -Containing Haplotypes. Journal of Virology, 2007, 81, 406-410.	3.4	40
33	The genome-wide impact of cadmium on microRNA and mRNA expression in contrasting Cd responsive wheat genotypes. BMC Genomics, 2019, 20, 615.	2.8	40
34	Polyploidy breaks speciation barriers in Australian burrowing frogs Neobatrachus. PLoS Genetics, 2020, 16, e1008769.	3.5	40
35	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
36	Consequences of Cytotoxic T-Lymphocyte Escape: Common Escape Mutations in Simian Immunodeficiency Virus Are Poorly Recognized in Nail´ve Hosts. Journal of Virology, 2004, 78, 10064-10073.	3.4	35

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37	Genome management and mismanagement—cell-level opportunities and challenges of whole-genome duplication. Genes and Development, 2015, 29, 2405-2419.	5.9	33
38	Genome-wide identification, phylogenetic and expression analysis of the heat shock transcription factor family in bread wheat (Triticum aestivum L.). BMC Genomics, 2019, 20, 505.	2.8	33
39	Adaptive introgression: how polyploidy reshapes gene flow landscapes. New Phytologist, 2021, 230, 457-461.	7.3	31
40	Understanding the development and evolution of novel floral form in Aquilegia. Current Opinion in Plant Biology, 2014, 17, 22-27.	7.1	30
41	A novel allele of ASY3 is associated with greater meiotic stability in autotetraploid Arabidopsis lyrata. PLoS Genetics, 2020, 16, e1008900.	3.5	26
42	Genomic studies of adaptive evolution in outcrossing Arabidopsis species. Current Opinion in Plant Biology, 2017, 36, 9-14.	7.1	25
43	Hybrids and horizontal transfer: introgression allows adaptive allele discovery. Journal of Experimental Botany, 2017, 68, 5453-5470.	4.8	24
44	Population genomic and historical analysis suggests a global invasion by bridgehead processes in Mimulus guttatus. Communications Biology, 2021, 4, 327.	4.4	24
45	Maintenance of Adaptive Dynamics and No Detectable Load in a Range-Edge Outcrossing Plant Population. Molecular Biology and Evolution, 2021, 38, 1820-1836.	8.9	24
46	Novelty and Convergence in Adaptation to Whole Genome Duplication. Molecular Biology and Evolution, 2021, 38, 3910-3924.	8.9	22
47	Parallel adaptation in autopolyploid Arabidopsis arenosa is dominated by repeated recruitment of shared alleles. Nature Communications, 2021, 12, 4979.	12.8	22
48	Circular <scp>RNA</scp> in disease: Basic properties and biomedical relevance. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1723.	6.4	21
49	De Novo Mutation and Rapid Protein (Co-)evolution during Meiotic Adaptation in <i>Arabidopsis arenosa</i> . Molecular Biology and Evolution, 2021, 38, 1980-1994.	8.9	18
50	The Evolutionary Genomics of Serpentine Adaptation. Frontiers in Plant Science, 2020, 11, 574616.	3.6	17
51	Genomeâ€wide mapping of transcription factor binding reveals developmental process integration and a fresh look at evolutionary dynamics. American Journal of Botany, 2012, 99, 277-290.	1.7	12
52	Transposable element annotation in nonâ€model species: The benefits of speciesâ€specific repeat libraries using semiâ€automated EDTA and DeepTE de novo pipelines. Molecular Ecology Resources, 2022, 22, 823-833.	4.8	10
53	Adaptation to coastal soils through pleiotropic boosting of ion and stress hormone concentrations in wild <i>Arabidopsis thaliana</i> New Phytologist, 2021, 232, 208-220.	7.3	9
54	Evolutionary footprints of a cold relic in a rapidly warming world. ELife, 2021, 10, .	6.0	5

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55	DNA-Binding Factor Target Identification by Chromatin Immunoprecipitation (ChIP) in Plants. Methods in Molecular Biology, 2016, 1363, 25-35.	0.9	3
56	When two is a crowd: mitochondrial genome merger and its aftermath. New Phytologist, 2015, 206, 8-9.	7.3	0
57	Help or hindrance? The evolutionary impact of wholeâ€genome duplication on immunogenetic diversity and parasite load. Ecology and Evolution, 2020, 10, 13949-13956.	1.9	0