

Vincent Colot

List of Publications by Year in descending order

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82
papers

14,064
citations

31976

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53230

85
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docs citations

95
times ranked

13234
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast evolution of anti-silencing systems shapes the invasiveness of <i>Mu</i> -like DNA transposons in eudicots. <i>EMBO Journal</i> , 2022, 41, e110070.	7.8	7
2	Efficient Detection of Transposable Element Insertion Polymorphisms Between Genomes Using Short-Read Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2250, 157-169.	0.9	10
3	Detection of Transposable Element Insertions in Arabidopsis Using Sequence Capture. <i>Methods in Molecular Biology</i> , 2021, 2250, 141-155.	0.9	3
4	How does epigenetics influence the course of evolution?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200111.	4.0	73
5	The epiallelic potential of transposable elements and its evolutionary significance in plants. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200123.	4.0	37
6	Genetic and environmental modulation of transposition shapes the evolutionary potential of <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2021, 22, 138.	8.8	76
7	Male fertility in <i>Arabidopsis</i> requires active DNA demethylation of genes that control pollen tube function. <i>Nature Communications</i> , 2021, 12, 410.	12.8	41
8	Polycomb mutant partially suppresses DNA hypomethylation-associated phenotypes in <i>Arabidopsis</i> . <i>Life Science Alliance</i> , 2021, 4, e202000848.	2.8	23
9	The impact of transposable elements on tomato diversity. <i>Nature Communications</i> , 2020, 11, 4058.	12.8	92
10	Mild drought in the vegetative stage induces phenotypic, gene expression, and DNA methylation plasticity in <i>Arabidopsis</i> but no transgenerational effects. <i>Journal of Experimental Botany</i> , 2020, 71, 3588-3602.	4.8	48
11	Differential retention of transposable element-derived sequences in outcrossing <i>Arabidopsis</i> genomes. <i>Mobile DNA</i> , 2019, 10, 30.	3.6	26
12	Transposition favors the generation of large effect mutations that may facilitate rapid adaptation. <i>Nature Communications</i> , 2019, 10, 3421.	12.8	134
13	Relaxed purifying selection in autopolyploids drives transposable element over-accumulation which provides variants for local adaptation. <i>Nature Communications</i> , 2019, 10, 5818.	12.8	70
14	Quantitative resistance to clubroot infection mediated by transgenerational epigenetic variation in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2019, 222, 468-479.	7.3	42
15	Identification and characterisation of hypomethylated DNA loci controlling quantitative resistance in <i>Arabidopsis</i> . <i>ELife</i> , 2019, 8, .	6.0	73
16	DNA methylation dynamics during early plant life. <i>Genome Biology</i> , 2017, 18, 179.	8.8	182
17	Comparative epigenomics in the Brassicaceae reveals two evolutionarily conserved modes of PRC2-mediated gene regulation. <i>Genome Biology</i> , 2017, 18, 207.	8.8	8
18	The <i>Arabidopsis thaliana</i> mobilome and its impact at the species level. <i>ELife</i> , 2016, 5, .	6.0	271

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19	A versatile Multisite Gateway-compatible promoter and transgenic line collection for cell type-specific functional genomics in Arabidopsis. <i>Plant Journal</i> , 2016, 85, 320-333.	5.7	116
20	50 years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016, 209, 921-944.	7.3	186
21	Plant Transgenerational Epigenetics. <i>Annual Review of Genetics</i> , 2016, 50, 467-491.	7.6	236
22	DNA DAMAGE BINDING PROTEIN2 Shapes the DNA Methylation Landscape. <i>Plant Cell</i> , 2016, 28, 2043-2059.	6.6	16
23	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 159-178.	5.7	81
24	Genome expansion of <i>Arabis alpina</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
25	Epigenetic Basis of Morphological Variation and Phenotypic Plasticity in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 337-348.	6.6	178
26	Genome-Wide Negative Feedback Drives Transgenerational DNA Methylation Dynamics in Arabidopsis. <i>PLoS Genetics</i> , 2015, 11, e1005154.	3.5	56
27	The Arabidopsis miR472-RDR6 Silencing Pathway Modulates PAMP- and Effector-Triggered Immunity through the Post-transcriptional Control of Disease Resistance Genes. <i>PLoS Pathogens</i> , 2014, 10, e1003883.	4.7	233
28	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. <i>BMC Bioinformatics</i> , 2014, 15, 377.	2.6	27
29	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	12.6	403
30	Natural occurring epialleles determine vitamin E accumulation in tomato fruits. <i>Nature Communications</i> , 2014, 5, 3027.	12.8	179
31	Genome-Wide Analysis of DNA Methylation in Arabidopsis Using MeDIP-Chip. <i>Methods in Molecular Biology</i> , 2014, 1112, 125-149.	0.9	15
32	Hyperosmotic priming of Arabidopsis seedlings establishes a long-term somatic memory accompanied by specific changes of the epigenome. <i>Genome Biology</i> , 2013, 14, R59.	8.8	264
33	Reconstructing de novo silencing of an active plant retrotransposon. <i>Nature Genetics</i> , 2013, 45, 1029-1039.	21.4	248
34	Mobilization of a plant transposon by expression of the transposon-encoded anti-silencing factor. <i>EMBO Journal</i> , 2013, 32, 2407-2417.	7.8	60
35	Epigenetic diversity increases the productivity and stability of plant populations. <i>Nature Communications</i> , 2013, 4, 2875.	12.8	163
36	Epigenetic variation creates potential for evolution of plant phenotypic plasticity. <i>New Phytologist</i> , 2013, 197, 314-322.	7.3	330

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37	Profiling spatial enrichment of chromatin marks suggests an additional epigenomic dimension in gene regulation. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2013, 7, 80-87.	1.1	9
38	Extensive Natural Epigenetic Variation at a De Novo Originated Gene. <i>PLoS Genetics</i> , 2013, 9, e1003437.	3.5	114
39	Evaluation of MeDIP-Chip in the Context of Whole-Genome Bisulfite Sequencing (WGBS-Seq) in Arabidopsis. <i>Methods in Molecular Biology</i> , 2013, 1067, 203-224.	0.9	11
40	Histone H2B Monoubiquitination Facilitates the Rapid Modulation of Gene Expression during Arabidopsis Photomorphogenesis. <i>PLoS Genetics</i> , 2012, 8, e1002825.	3.5	115
41	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16240-16245.	7.1	145
42	Epialleles in plant evolution. <i>Genome Biology</i> , 2012, 13, 249.	9.6	142
43	NERD, a Plant-Specific GW Protein, Defines an Additional RNAi-Dependent Chromatin-Based Pathway in Arabidopsis. <i>Molecular Cell</i> , 2012, 48, 121-132.	9.7	134
44	Polycomb Repressive Complex 2 Controls the Embryo-to-Seedling Phase Transition. <i>PLoS Genetics</i> , 2011, 7, e1002014.	3.5	318
45	Additive inheritance of histone modifications in <i>Arabidopsis thaliana</i> intra-specific hybrids. <i>Plant Journal</i> , 2011, 67, 691-700.	5.7	48
46	Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. <i>EMBO Journal</i> , 2011, 30, 1928-1938.	7.8	600
47	Genome-wide evidence for local DNA methylation spreading from small RNA-targeted sequences in Arabidopsis. <i>Nucleic Acids Research</i> , 2011, 39, 6919-6931.	14.5	142
48	Genome-Wide Epigenetic Perturbation Jump-Starts Patterns of Heritable Variation Found in Nature. <i>Genetics</i> , 2011, 188, 1015-1017.	2.9	109
49	Misregulation of AUXIN RESPONSE FACTOR 8 Underlies the Developmental Abnormalities Caused by Three Distinct Viral Silencing Suppressors in Arabidopsis. <i>PLoS Pathogens</i> , 2011, 7, e1002035.	4.7	85
50	Highly Dynamic and Sex-Specific Expression of microRNAs During Early ES Cell Differentiation. <i>PLoS Genetics</i> , 2009, 5, e1000620.	3.5	73
51	Assessing the Impact of Transgenerational Epigenetic Variation on Complex Traits. <i>PLoS Genetics</i> , 2009, 5, e1000530.	3.5	669
52	Chromatin indexing in Arabidopsis: an epigenomic tale of tails and more. <i>Trends in Genetics</i> , 2009, 25, 511-517.	6.7	98
53	Gene body DNA methylation in plants: a means to an end or an end to a means?. <i>EMBO Journal</i> , 2009, 28, 997-998.	7.8	58
54	A Role for RNAi in the Selective Correction of DNA Methylation Defects. <i>Science</i> , 2009, 323, 1600-1604.	12.6	338

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55	Epigenome dynamics: a quantitative genetics perspective. <i>Nature Reviews Genetics</i> , 2008, 9, 883-890.	16.3	183
56	Improved detection and annotation of transposable elements in sequenced genomes using multiple reference sequence sets. <i>Genomics</i> , 2008, 91, 467-475.	2.9	67
57	Chromosome Structural Proteins and RNA-Mediated Epigenetic Silencing. <i>Developmental Cell</i> , 2008, 14, 813-814.	7.0	5
58	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. <i>PLoS ONE</i> , 2008, 3, e3306.	2.5	99
59	Arabidopsis TFL2/LHP1 Specifically Associates with Genes Marked by Trimethylation of Histone H3 Lysine 27. <i>PLoS Genetics</i> , 2007, 3, e86.	3.5	537
60	Epigenetic Natural Variation in Arabidopsis thaliana. <i>PLoS Biology</i> , 2007, 5, e174.	5.6	400
61	Variation in crossing-over rates across chromosome 4 of <i>Arabidopsis thaliana</i> reveals the presence of meiotic recombination "hot spots". <i>Genome Research</i> , 2006, 16, 106-114.	5.5	162
62	Profiling histone modification patterns in plants using genomic tiling microarrays. <i>Nature Methods</i> , 2005, 2, 213-218.	19.0	521
63	Profiling DNA methylation patterns using genomic tiling microarrays. <i>Nature Methods</i> , 2005, 2, 219-224.	19.0	119
64	Arabidopsis epigenetics: when RNA meets chromatin. <i>Current Opinion in Plant Biology</i> , 2005, 8, 142-147.	7.1	55
65	Epigenomic mapping in Arabidopsis using tiling microarrays. <i>Chromosome Research</i> , 2005, 13, 299-308.	2.2	46
66	Reinforcement of silencing at transposons and highly repeated sequences requires the concerted action of two distinct RNA polymerases IV in Arabidopsis. <i>Genes and Development</i> , 2005, 19, 2030-2040.	5.9	347
67	Versatile Gene-Specific Sequence Tags for Arabidopsis Functional Genomics: Transcript Profiling and Reverse Genetics Applications. <i>Genome Research</i> , 2004, 14, 2176-2189.	5.5	282
68	The development of an Arabidopsis model system for genome-wide analysis of polyploidy effects. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 689-700.	1.6	69
69	Role of transposable elements in heterochromatin and epigenetic control. <i>Nature</i> , 2004, 430, 471-476.	27.8	1,103
70	Understanding mechanisms of novel gene expression in polyploids. <i>Trends in Genetics</i> , 2003, 19, 141-147.	6.7	812
71	Changes in 5S rDNA Chromatin Organization and Transcription during Heterochromatin Establishment in Arabidopsis. <i>Plant Cell</i> , 2003, 15, 2929-2939.	6.6	120
72	Dependence of Heterochromatic Histone H3 Methylation Patterns on the <i>Arabidopsis</i> Gene <i>DDM1</i> . <i>Science</i> , 2002, 297, 1871-1873.	12.6	417

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73	DNA Methylation and Epigenetic Inheritance in Plants and Filamentous Fungi. <i>Science</i> , 2001, 293, 1070-1074.	12.6	456
74	Translational misreading: a tRNA modification counteracts a +2 ribosomal frameshift. <i>Genes and Development</i> , 2001, 15, 2295-2306.	5.9	142
75	Eukaryotic DNA methylation as an evolutionary device. <i>BioEssays</i> , 1999, 21, 402-411.	2.5	287
76	Extensive, Nonrandom Diversity of Excision Footprints Generated by <i>Ds</i> -Like Transposon <i>Ascot-1</i> Suggests New Parallels with V(D)J Recombination. <i>Molecular and Cellular Biology</i> , 1998, 18, 4337-4346.	2.3	56
77	The Wheat Transcriptional Activator SPA: A Seed-Specific bZIP Protein That Recognizes the GCN4-Like Motif in the Bifactorial Endosperm Box of Prolamin Genes. <i>Plant Cell</i> , 1997, 9, 171.	6.6	47
78	Interchromosomal Transfer of Epigenetic States in <i>Ascobolus</i> : Transfer of DNA Methylation Is Mechanistically Related to Homologous Recombination. <i>Cell</i> , 1996, 86, 855-864.	28.9	135
79	The maize transcription factor Opaque-2 activates a wheat glutenin promoter in plant and yeast cells. <i>Plant Molecular Biology</i> , 1995, 29, 711-720.	3.9	36
80	Methylation of repeated DNA sequences and genome stability in <i>Ascobolus immersus</i> . <i>Canadian Journal of Botany</i> , 1995, 73, 221-225.	1.1	19
81	Molecular characterization of an active wheat LMW glutenin gene and its relation to other wheat and barley prolamin genes. <i>Molecular Genetics and Genomics</i> , 1989, 216, 81-90.	2.4	121
82	Interaction of a tryptophan-containing peptide with chromatin core particles. <i>FEBS Letters</i> , 1984, 169, 205-209.	2.8	3