

# Fabrice Legeai

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

7,932  
citations

126901

33  
h-index

91872

69  
g-index

78  
all docs

78  
docs citations

78  
times ranked

11257  
citing authors

#	ARTICLE	IF	CITATIONS
1	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	27.8	3,384
2	Predotar: A tool for rapidly screening proteomes for N-terminal targeting sequences. <i>Proteomics</i> , 2004, 4, 1581-1590.	2.2	817
3	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017, 18, 27.	8.8	624
4	FEELnc: a tool for long non-coding RNA annotation and its application to the dog transcriptome. <i>Nucleic Acids Research</i> , 2017, 45, gkw1306.	14.5	281
5	Two genomes of highly polyphagous lepidopteran pests ( <i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. <i>Scientific Reports</i> , 2017, 7, 11816.	3.3	242
6	An Expressed Sequence Tag collection from the male antennae of the Noctuid moth <i>Spodoptera littoralis</i> : a resource for olfactory and pheromone detection research. <i>BMC Genomics</i> , 2011, 12, 86.	2.8	145
7	Analysis of Virion Structural Components Reveals Vestiges of the Ancestral Ichnovirus Genome. <i>PLoS Pathogens</i> , 2010, 6, e1000923.	4.7	126
8	Large-scale gene discovery in the pea aphid <i>Acyrtosiphon pisum</i> (Hemiptera). <i>Genome Biology</i> , 2006, 7, R21.	9.6	123
9	<i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) host-plant variants: two host strains or two distinct species?. <i>Genetica</i> , 2015, 143, 305-316.	1.1	117
10	A Comparison of the Olfactory Gene Repertoires of Adults and Larvae in the Noctuid Moth <i>Spodoptera littoralis</i> . <i>PLoS ONE</i> , 2013, 8, e60263.	2.5	109
11	Bioinformatic prediction, deep sequencing of microRNAs and expression analysis during phenotypic plasticity in the pea aphid, <i>Acyrtosiphon pisum</i> . <i>BMC Genomics</i> , 2010, 11, 281.	2.8	95
12	Whole genome sequence of the soybean aphid, <i>Aphis glycines</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 123, 102917.	2.7	91
13	Candidate chemosensory Genes in Female Antennae of the Noctuid Moth <i>Spodoptera littoralis</i> . <i>International Journal of Biological Sciences</i> , 2012, 8, 1036-1050.	6.4	83
14	Large Gene Family Expansion and Variable Selective Pressures for Cathepsin B in Aphids. <i>Molecular Biology and Evolution</i> , 2007, 25, 5-17.	8.9	75
15	MiR-202 controls female fecundity by regulating medaka oogenesis. <i>PLoS Genetics</i> , 2018, 14, e1007593.	3.5	75
16	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012, 3, 5.	3.6	73
17	Genetic Control of Contagious Asexuality in the Pea Aphid. <i>PLoS Genetics</i> , 2014, 10, e1004838.	3.5	67
18	Fast Evolution and Lineage-Specific Gene Family Expansions of Aphid Salivary Effectors Driven by Interactions with Host-Plants. <i>Genome Biology and Evolution</i> , 2018, 10, 1554-1572.	2.5	67

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19	Differential gene expression according to race and host plant in the pea aphid. <i>Molecular Ecology</i> , 2016, 25, 4197-4215.	3.9	59
20	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , 2017, 49, 6.	3.0	59
21	Masculinization of the X Chromosome in the Pea Aphid. <i>PLoS Genetics</i> , 2013, 9, e1003690.	3.5	56
22	Accelerated Evolution of Sex Chromosomes in Aphids, an XO System. <i>Molecular Biology and Evolution</i> , 2012, 29, 837-847.	8.9	55
23	Global patterns in genomic diversity underpinning the evolution of insecticide resistance in the aphid crop pest <i>Myzus persicae</i> . <i>Communications Biology</i> , 2021, 4, 847.	4.4	55
24	Candidate Chemosensory Genes in the Stemborer <i>Sesamia nonagrioides</i> . <i>International Journal of Biological Sciences</i> , 2013, 9, 481-495.	6.4	47
25	Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. <i>Microbiome</i> , 2018, 6, 181.	11.1	47
26	Anchoring of a large set of markers onto a BAC library for the development of a draft physical map of the grapevine genome. <i>Theoretical and Applied Genetics</i> , 2006, 113, 344-356.	3.6	46
27	Genomic Approach to Study Floral Development Genes in <i>Rosa</i> sp.. <i>PLoS ONE</i> , 2011, 6, e28455.	2.5	44
28	Transcriptomic profiling of the reproductive mode switch in the pea aphid in response to natural autumnal photoperiod. <i>Journal of Insect Physiology</i> , 2012, 58, 1517-1524.	2.0	43
29	Disentangling the Causes for Faster-X Evolution in Aphids. <i>Genome Biology and Evolution</i> , 2018, 10, 507-520.	2.5	42
30	Adaptation by copy number variation increases insecticide resistance in the fall armyworm. <i>Communications Biology</i> , 2020, 3, 664.	4.4	41
31	Large-scale identification of genes in the fungus <i>Hebeloma cylindrosporium</i> paves the way to molecular analyses of ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2004, 164, 505-513.	7.3	40
32	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90.	3.8	40
33	Identification of long non-coding RNAs in insects genomes. <i>Current Opinion in Insect Science</i> , 2015, 7, 37-44.	4.4	39
34	New resources for studying the rose flowering process. <i>Genome</i> , 2008, 51, 827-837.	2.0	37
35	Dosage compensation and sex-specific epigenetic landscape of the X chromosome in the pea aphid. <i>Epigenetics and Chromatin</i> , 2017, 10, 30.	3.9	34
36	Identifying genomic hotspots of differentiation and candidate genes involved in the adaptive divergence of pea aphid host races. <i>Molecular Ecology</i> , 2018, 27, 3287-3300.	3.9	34

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37	AphidBase: a database for aphid genomic resources. <i>Bioinformatics</i> , 2007, 23, 783-784.	4.1	32
38	Cytoneuclear interactions remain stable during allopolyploid evolution despite repeated whole-genome duplications in <i>Brassica</i> . <i>Plant Journal</i> , 2019, 98, 434-447.	5.7	32
39	Cabomba as a model for studies of early angiosperm evolution. <i>Annals of Botany</i> , 2011, 108, 589-598.	2.9	30
40	GenoPlante-Info (GPI): a collection of databases and bioinformatics resources for plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 179-182.	14.5	29
41	Establishment and analysis of a reference transcriptome for <i>Spodoptera frugiperda</i> . <i>BMC Genomics</i> , 2014, 15, 704.	2.8	27
42	Differential Expression of Candidate Salivary Effector Genes in Pea Aphid Biotypes With Distinct Host Plant Specificity. <i>Frontiers in Plant Science</i> , 2019, 10, 1301.	3.6	27
43	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. <i>Communications Biology</i> , 2021, 4, 104.	4.4	27
44	Genome sequence of the wheat stem sawfly, <i>Cephus cinctus</i> , representing an early-branching lineage of the Hymenoptera, illuminates evolution of hymenopteran chemoreceptors. <i>Genome Biology and Evolution</i> , 2018, 10, 2997-3011.	2.5	24
45	Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. <i>BMC Biology</i> , 2020, 18, 89.	3.8	24
46	Characterization and expression profiling of microRNAs in response to plant feeding in two host-plant strains of the lepidopteran pest <i>Spodoptera frugiperda</i> . <i>BMC Genomics</i> , 2018, 19, 804.	2.8	23
47	Expressed sequence tags from the phytopathogenic fungus <i>Botrytis cinerea</i> . <i>European Journal of Plant Pathology</i> , 2005, 111, 139-146.	1.7	20
48	De novo transcriptome assembly of the grapevine phylloxera allows identification of genes differentially expressed between leaf- and root-feeding forms. <i>BMC Genomics</i> , 2016, 17, 219.	2.8	19
49	Functional insights from the GC-poor genomes of two aphid parasitoids, <i>Aphidius ervi</i> and <i>Lysiphlebus fabarum</i> . <i>BMC Genomics</i> , 2020, 21, 376.	2.8	19
50	Physical mapping in large genomes: accelerating anchoring of BAC contigs to genetic maps through in silico analysis. <i>Functional and Integrative Genomics</i> , 2008, 8, 29-32.	3.5	17
51	Differential expression of the chemosensory transcriptome in two populations of the stemborer <i>Sesamia nonagrioides</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2015, 65, 28-34.	2.7	16
52	First extensive characterization of the venom gland from an egg parasitoid: structure, transcriptome and functional role. <i>Journal of Insect Physiology</i> , 2018, 107, 68-80.	2.0	15
53	Soybean aphid biotype 1 genome: Insights into the invasive biology and adaptive evolution of a major agricultural pest. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 120, 103334.	2.7	15
54	Selection following Gene Duplication Shapes Recent Genome Evolution in the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2601-2615.	8.9	12

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55	Strong Heterogeneity in Nucleotidic Composition and Codon Bias in the Pea Aphid ( <i>Acyrtosiphon</i> ) Tj ETQq1 1 0.784314 rgBT /Overlaid 413-424.	1.8	11
56	Expression differences in <i>Aphidius ervi</i> (Hymenoptera: Braconidae) females reared on different aphid host species. PeerJ, 2017, 5, e3640.	2.0	11
57	RNA interference identifies domesticated viral genes involved in assembly and trafficking of virus-derived particles in ichneumonid wasps. PLoS Pathogens, 2019, 15, e1008210.	4.7	9
58	Contrasting genomic and phenotypic outcomes of hybridization between pairs of mimetic butterfly taxa across a suture zone. Molecular Ecology, 2020, 29, 1328-1343.	3.9	9
59	Evidence for an ichnovirus machinery in parasitoids of coleopteran larvae. Virus Research, 2019, 263, 189-206.	2.2	8
60	Big Genes, Small Effectors: Pea Aphid Cassette Effector Families Composed From Miniature Exons. Frontiers in Plant Science, 2020, 11, 1230.	3.6	8
61	Plant phenotypic changes induced by parasitoid ichnoviruses enhance the performance of both unparasitized and parasitized caterpillars. Molecular Ecology, 2021, 30, 4567-4583.	3.9	7
62	Transcriptome Profiling of Starvation in the Peripheral Chemosensory Organs of the Crop Pest <i>Spodoptera littoralis</i> Caterpillars. Insects, 2021, 12, 573.	2.2	6
63	MinYS: mine your symbiont by targeted genome assembly in symbiotic communities. NAR Genomics and Bioinformatics, 2020, 2, lqaa047.	3.2	5
64	Proteo-Transcriptomic Analyses Reveal a Large Expansion of Metalloprotease-Like Proteins in Atypical Venom Vesicles of the Wasp <i>Meteorus pulchricornis</i> (Braconidae). Toxins, 2021, 13, 502.	3.4	5
65	LRez: a C++ API and toolkit for analyzing and managing Linked-Reads data. Bioinformatics Advances, 2021, 1, .	2.4	4
66	Genomics of Phenotypic Plasticity in Aphids. , 2016, , 65-96.		3
67	BioMAJ2Galaxy: automatic update of reference data in Galaxy using BioMAJ. GigaScience, 2015, 4, 22.	6.4	2
68	Comparative transcriptome analysis at the onset of speciation in a mimetic butterflyâ€”The <i>Ithomiini</i> <i>Melinaea marsaeus</i> . Journal of Evolutionary Biology, 2021, 34, 1704-1721.	1.7	2
69	RNA sequencing data for responses to drought stress and/or clubroot infection in developing seeds of <i>Brassica napus</i> . Data in Brief, 2021, 38, 107392.	1.0	1
70	AskOR, A R Package for Easy RNASeq Data Analysis. , 0, , .		1