

Alain Vignal

List of Publications by Year in descending order

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129
papers

17,092
citations

66343

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123
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docs citations

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times ranked

12703
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#	ARTICLE	IF	CITATIONS
1	Two quantitative trait loci are associated with recapping of <i>Varroa destructor</i> -infested brood cells in <i>Apis mellifera mellifera</i> . <i>Animal Genetics</i> , 2022, 53, 156-160.	1.7	4
2	Genetic diversity and population genetic structure analysis of <i>Apis mellifera</i> subspecies in Algeria and Europe based on complementary sex determiner (CSD) gene. <i>Apidologie</i> , 2022, 53, 1.	2.0	4
3	Complex population structure and haplotype patterns in the Western European honey bee from sequencing a large panel of haploid drones. <i>Molecular Ecology Resources</i> , 2022, 22, 3068-3086.	4.8	9
4	Unraveling the history of the genus <i>Gallus</i> through whole genome sequencing. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107044.	2.7	9
5	Identification of quantitative trait loci associated with calmness and gentleness in honey bees using whole-genome sequences. <i>Animal Genetics</i> , 2021, 52, 472-481.	1.7	6
6	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
7	Descriptive Analysis of the <i>Varroa</i> Non-Reproduction Trait in Honey Bee Colonies and Association with Other Traits Related to <i>Varroa</i> Resistance. <i>Insects</i> , 2020, 11, 492.	2.2	15
8	The quail genome: insights into social behaviour, seasonal biology and infectious disease response. <i>BMC Biology</i> , 2020, 18, 14.	3.8	40
9	Bases de données en biologie. <i>INRA Productions Animales</i> , 2020, 13, 187-189.	0.5	0
10	Etat de la carte de la poule. <i>INRA Productions Animales</i> , 2020, 13, 113-114.	0.5	0
11	Génomique des canards. <i>INRA Productions Animales</i> , 2020, 26, 391-402.	0.5	1
12	Avian Genomics in Animal Breeding and the End of the Model Organism. , 2019, , 21-67.		3
13	Two new structural mutations in the 5' region of the ASIP gene cause diluted feather color phenotypes in Japanese quail. <i>Genetics Selection Evolution</i> , 2019, 51, 12.	3.0	14
14	A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. <i>Molecular Ecology Resources</i> , 2019, 19, 997-1014.	4.8	24
15	Structure of the intergenic spacers in chicken ribosomal DNA. <i>Genetics Selection Evolution</i> , 2019, 51, 59.	3.0	9
16	Developing reduced SNP assays from whole-genome sequence data to estimate introgression in an organism with complex genetic patterns, the Iberian honeybee (<i>Apis mellifera</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf		10
17	Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. <i>Genome Biology and Evolution</i> , 2018, 10, 220-238.	2.5	13
18	A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 109-117.	1.8	228

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19	Genome-wide scans between two honeybee populations reveal putative signatures of human-mediated selection. <i>Animal Genetics</i> , 2017, 48, 704-707.	1.7	9
20	Deciphering mechanisms underlying the genetic variation of general production and liver quality traits in the overfed mule duck by pQTL analyses. <i>Genetics Selection Evolution</i> , 2017, 49, 38.	3.0	3
21	Using Whole-Genome Sequence Information to Foster Conservation Efforts for the European Dark Honey Bee, <i>Apis mellifera mellifera</i> . <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	2.2	34
22	Whole-genome resequencing of honeybee drones to detect genomic selection in a population managed for royal jelly. <i>Scientific Reports</i> , 2016, 6, 27168.	3.3	35
23	Species difference in ANP32A underlies influenza A virus polymerase host restriction. <i>Nature</i> , 2016, 529, 101-104.	27.8	228
24	GWAS analyses reveal QTL in egg layers that differ in response to diet differences. <i>Genetics Selection Evolution</i> , 2015, 47, 83.	3.0	14
25	A medium density genetic map and QTL for behavioral and production traits in Japanese quail. <i>BMC Genomics</i> , 2015, 16, 10.	2.8	40
26	Transcriptome-wide investigation of genomic imprinting in chicken. <i>Nucleic Acids Research</i> , 2014, 42, 3768-3782.	14.5	59
27	Mapping and genotypic analysis of the NK-lysin gene in chicken. <i>Genetics Selection Evolution</i> , 2014, 46, 43.	3.0	3
28	Mule Duck "Foie Gras" Shows Different Metabolic States According to Its Quality Phenotype by Using a Proteomic Approach. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 7140-7150.	5.2	7
29	Detection of QTL controlling metabolism, meat quality, and liver quality traits of the overfed interspecific hybrid mule duck1. <i>Journal of Animal Science</i> , 2013, 91, 588-604.	0.5	11
30	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013, 45, 776-783.	21.4	327
31	Evidence of Phenotypic and Genetic Relationships between Sociality, Emotional Reactivity and Production Traits in Japanese Quail. <i>PLoS ONE</i> , 2013, 8, e82157.	2.5	18
32	A duck RH panel and its potential for assisting NGS genome assembly. <i>BMC Genomics</i> , 2012, 13, 513.	2.8	40
33	Fine mapping of complex traits in non-model species: using next generation sequencing and advanced intercross lines in Japanese quail. <i>BMC Genomics</i> , 2012, 13, 551.	2.8	20
34	Genome wide SNP discovery, analysis and evaluation in mallard (<i>Anas platyrhynchos</i>). <i>BMC Genomics</i> , 2011, 12, 150.	2.8	63
35	New QTL for resistance to <i>Salmonella</i> carrier-state identified on fowl microchromosomes. <i>Molecular Genetics and Genomics</i> , 2011, 285, 237-243.	2.1	23
36	Epilepsy Caused by an Abnormal Alternative Splicing with Dosage Effect of the SV2A Gene in a Chicken Model. <i>PLoS ONE</i> , 2011, 6, e26932.	2.5	37

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37	Evidence for introgressive hybridization of wild common quail (<i>Coturnix coturnix</i>) by domesticated Japanese quail (<i>Coturnix japonica</i>) in France. <i>Conservation Genetics</i> , 2010, 11, 1051-1062.	1.5	32
38	Mapping main, epistatic and sex-specific QTL for body composition in a chicken population divergently selected for low or high growth rate. <i>BMC Genomics</i> , 2010, 11, 107.	2.8	35
39	Integrative mapping analysis of chicken microchromosome 16 organization. <i>BMC Genomics</i> , 2010, 11, 616.	2.8	47
40	Non PCR-amplified Transcripts and AFLP® fragments as reduced representations of the quail genome for 454 Titanium sequencing. <i>BMC Research Notes</i> , 2010, 3, 214.	1.4	8
41	Genetic control of resistance to salmonellosis and to <i>Salmonella</i> carrier-state in fowl: a review. <i>Genetics Selection Evolution</i> , 2010, 42, 11.	3.0	87
42	Mapping QTL for growth and shank traits in chickens divergently selected for high or low body weight. <i>Animal Genetics</i> , 2010, 41, 400-405.	1.7	31
43	Contribution of Radiation Hybrids to Genome Mapping in Domestic Animals. <i>Cytogenetic and Genome Research</i> , 2009, 126, 21-33.	1.1	18
44	QTL for several metabolic traits map to loci controlling growth and body composition in an F ₂ intercross between high- and low-growth chicken lines. <i>Physiological Genomics</i> , 2009, 38, 241-249.	2.3	75
45	QTL for resistance to <i>Salmonella</i> carrier state confirmed in both experimental and commercial chicken lines. <i>Animal Genetics</i> , 2009, 40, 590-597.	1.7	37
46	Addition of the microchromosome GGA25 to the chicken genome sequence assembly through radiation hybrid and genetic mapping. <i>BMC Genomics</i> , 2008, 9, 129.	2.8	19
47	Whole genome comparative studies between chicken and turkey and their implications for avian genome evolution. <i>BMC Genomics</i> , 2008, 9, 168.	2.8	119
48	An Integrated Approach of Genetic Resistance to <i>Salmonella</i> Carrier State in Fowls: from Genetics to Genomics and Modelling. <i>Developments in Biologicals</i> , 2008, 132, 353-357.	0.5	0
49	Cloning of Ovocalyxin-36, a Novel Chicken Eggshell Protein Related to Lipopolysaccharide-binding Proteins, Bactericidal Permeability-increasing Proteins, and Plunc Family Proteins. <i>Journal of Biological Chemistry</i> , 2007, 282, 5273-5286.	3.4	101
50	Female-Specific DNA Sequences in the Chicken Genome. <i>Journal of Heredity</i> , 2007, 98, 238-242.	2.4	11
51	FISH mapping of 57 BAC clones reveals strong conservation of synteny between Galliformes and Anseriformes. <i>Animal Genetics</i> , 2007, 38, 303-307.	1.7	25
52	Identification of QTL controlling meat quality traits in an F ₂ cross between two chicken lines selected for either low or high growth rate. <i>BMC Genomics</i> , 2007, 8, 155.	2.8	43
53	The chicken RH map: current state of progress and microchromosome mapping. <i>Cytogenetic and Genome Research</i> , 2007, 117, 14-21.	1.1	22
54	Search for QTL affecting the shape of the egg laying curve of the Japanese quail. <i>BMC Genetics</i> , 2006, 7, 26.	2.7	17

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55	FISH on avian lampbrush chromosomes produces higher resolution gene mapping. <i>Genetica</i> , 2006, 128, 241-251.	1.1	50
56	Mapping quantitative trait loci affecting fatness and breast muscle weight in meat-type chicken lines divergently selected on abdominal fatness. <i>Genetics Selection Evolution</i> , 2006, 38, 85.	3.0	50
57	Fatness QTL on chicken chromosome 5 and interaction with sex. <i>Genetics Selection Evolution</i> , 2006, 38, 297-311.	3.0	29
58	Integrated maps in quail (<i>Coturnix japonica</i>) confirm the high degree of synteny conservation with chicken (<i>Gallus gallus</i>) despite 35 million years of divergence. <i>BMC Genomics</i> , 2006, 7, 101.	2.8	80
59	Mapping of plumage colour and blood protein loci on the microsatellite linkage map of the Japanese quail. <i>Animal Genetics</i> , 2005, 36, 396-400.	1.7	23
60	A genome scan with AFLPTM markers to detect fearfulness-related QTLs in Japanese quail. <i>Animal Genetics</i> , 2005, 36, 401-407.	1.7	41
61	A gene-based radiation hybrid map of chicken microchromosome 14: Comparison to human and alignment to the assembled chicken sequence. <i>Genetics Selection Evolution</i> , 2005, 37, 229-51.	3.0	13
62	A genome scan for quantitative trait loci affecting the Salmonella carrier-state in the chicken. <i>Genetics Selection Evolution</i> , 2005, 37, 539-61.	3.0	56
63	Construction of a radiation hybrid map of chicken chromosome 2 and alignment to the chicken draft sequence. <i>BMC Genomics</i> , 2005, 6, 12.	2.8	11
64	Microsatellite mapping of QTL affecting growth, feed consumption, egg production, tonic immobility and body temperature of Japanese quail. <i>BMC Genomics</i> , 2005, 6, 87.	2.8	63
65	Assignment of non-informative turkey genetic markers through comparative approaches. <i>Cytogenetic and Genome Research</i> , 2005, 109, 527-532.	1.1	8
66	Second report on chicken genes and chromosomes 2005. <i>Cytogenetic and Genome Research</i> , 2005, 109, 415-479.	1.1	136
67	Genomics and the Genetic Improvement of Broiler Chicken. <i>Outlook on Agriculture</i> , 2004, 33, 79-84.	3.4	1
68	A radiation hybrid map of chicken chromosome 15. <i>Animal Genetics</i> , 2004, 35, 63-65.	1.7	13
69	A first-generation microsatellite linkage map of the Japanese quail. <i>Animal Genetics</i> , 2004, 35, 195-200.	1.7	89
70	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	27.8	2,421
71	Assignment of CPS1, OTC, CRYD2, ARG2 and ASS genes to the chicken RH map. <i>Genetics Selection Evolution</i> , 2004, 36, 593-9.	3.0	4
72	A high-resolution radiation hybrid map of chicken chromosome 5 and comparison with human chromosomes. <i>BMC Genomics</i> , 2004, 5, 66.	2.8	21

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73	A radiation hybrid map of chicken Chromosome 4. <i>Mammalian Genome</i> , 2004, 15, 560-569.	2.2	12
74	Development of a gene-based radiation hybrid map of chicken Chromosome 7 and comparison to human and mouse. <i>Mammalian Genome</i> , 2004, 15, 732-739.	2.2	11
75	Molecular Cytogenetic Definition of the Chicken Genome: The First Complete Avian Karyotype. <i>Genetics</i> , 2004, 166, 1367-1373.	2.9	122
76	Genetic linkage and expression analysis of SREBP and lipogenic genes in fat and lean chicken. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2004, 137, 433-441.	1.6	27
77	Sex ratios in mule duck embryos at various stages of incubation. <i>Theriogenology</i> , 2004, 61, 573-580.	2.1	8
78	Biodiversity of 52 chicken populations assessed by microsatellite typing of DNA pools. <i>Genetics Selection Evolution</i> , 2003, 35, 533-57.	3.0	209
79	AFLP linkage map of the Japanese quail <i>Coturnix japonica</i> . <i>Genetics Selection Evolution</i> , 2003, 35, 559-72.	3.0	41
80	Cloning of cDNA encoding the nuclear form of chicken sterol response element binding protein-2 (SREBP-2), chromosomal localization, and tissue expression of chicken SREBP-1 and -2 genes. <i>Poultry Science</i> , 2003, 82, 54-61.	3.4	34
81	Effect of two candidate genes on the Salmonella carrier state in fowl. <i>Poultry Science</i> , 2003, 82, 721-726.	3.4	46
82	Integration of chicken genomic resources to enable whole-genome sequencing. <i>Cytogenetic and Genome Research</i> , 2003, 102, 297-303.	1.1	18
83	2003 Spring meeting of the WPSA French Branch. <i>British Poultry Science</i> , 2003, 44, 794-795.	1.7	3
84	2003 Spring meeting of the WPSA French Branch. <i>British Poultry Science</i> , 2003, 44, 795-797.	1.7	4
85	2003 Spring meeting of the WPSA French Branch. <i>British Poultry Science</i> , 2003, 44, 797-798.	1.7	5
86	A review on SNP and other types of molecular markers and their use in animal genetics. <i>Genetics Selection Evolution</i> , 2002, 34, 275-305.	3.0	676
87	ChickRH6: a chicken whole-genome radiation hybrid panel. <i>Genetics Selection Evolution</i> , 2002, 34, 521-33.	3.0	54
88	Development of 112 unique expressed sequence tags from chicken liver using an arbitrarily primed reverse transcriptase-polymerase chain reaction and single strand conformation gel purification method. <i>Animal Genetics</i> , 2001, 32, 289-297.	1.7	17
89	Assignment of <i>TERF1</i> to chicken chromosome 2q32 and <i>TERF2</i> to chicken microchromosome 11 by fluorescence in situ hybridization. <i>Cytogenetic and Genome Research</i> , 2001, 92, 175-176.	1.1	2
90	Empirical Evaluation of Genetic Clustering Methods Using Multilocus Genotypes From 20 Chicken Breeds. <i>Genetics</i> , 2001, 159, 699-713.	2.9	306

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91	Cloning and mapping of the ACLY gene to a chicken microchromosome. <i>Animal Genetics</i> , 2000, 31, 412-413.	1.7	2
92	The chicken LEP (OB) gene has not been mapped. <i>Animal Genetics</i> , 2000, 31, 281-281.	1.7	1
93	Mapping the Naked Neck (NA) and Polydactyly (PO) mutants of the chicken with microsatellite molecular markers. <i>Genetics Selection Evolution</i> , 2000, 32, 73-86.	3.0	31
94	First report on chicken genes and chromosomes 2000. <i>Cytogenetic and Genome Research</i> , 2000, 90, 169-218.	1.1	299
95	The chicken LEP (OB) gene has not been mapped. <i>Animal Genetics</i> , 2000, 31, 281-281.	1.7	34
96	A consensus linkage map of the chicken genome. <i>Genome Research</i> , 2000, 10, 137-47.	5.5	357
97	Characterisation of 33 chicken microsatellite loci: 20 new locations on reference maps. <i>Animal Genetics</i> , 1999, 30, 391-393.	1.7	1
98	Integrated chicken genetic and cytogenetic maps with fish identification of microchromosomes. <i>Animal Biotechnology</i> , 1999, 10, 87-91.	1.5	1
99	Mapping of the LEP(OB) gene to a chicken microchromosome. <i>Animal Genetics</i> , 1999, 30, 73-74.	1.7	7
100	Identification of 16 chicken microchromosomes by molecular markers using two-colour fluorescence in situ hybridization (FISH). <i>Chromosome Research</i> , 1998, 6, 307-313.	2.2	53
101	Mapping of FASN and ACACA on two chicken microchromosomes disrupts the human 17q syntenic group well conserved in mammals. <i>Mammalian Genome</i> , 1998, 9, 297-300.	2.2	14
102	Integration of chicken cytogenetic and genetic maps: 18 new polymorphic markers isolated from BAC and PAC clones. <i>Animal Genetics</i> , 1998, 29, 348-355.	1.7	21
103	Assignment of Stearoyl Coenzyme A Desaturase gene (SCD1) to chicken chromosome R-band 6q14 by in situ hybridization. <i>Cytogenetic and Genome Research</i> , 1997, 78, 229-230.	1.1	2
104	Genotyping Procedures in Linkage Mapping. <i>Methods</i> , 1996, 9, 91-97.	3.8	23
105	A comprehensive genetic map of the human genome based on 5,264 microsatellites. <i>Nature</i> , 1996, 380, 152-154.	27.8	2,916
106	Mapping of the genetically independent chicken major histocompatibility complexes <i>B²</i> and <i>RFP-Y²</i> to the same microchromosome by two-color fluorescent in situ hybridization. <i>Cytogenetic and Genome Research</i> , 1996, 75, 7-9.	1.1	51
107	Assignment of microsatellite sequences to the region duplicated in CMT1A (17p12): a useful tool for diagnosis. <i>Journal of Medical Genetics</i> , 1995, 32, 231-233.	3.2	25
108	Physical Mapping of 30 CA Repeats on Human Chromosome 22. <i>Genomics</i> , 1995, 27, 345-347.	2.9	4

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109	A comprehensive human linkage map with centimorgan density. Cooperative Human Linkage Center (CHLC). <i>Science</i> , 1994, 265, 2049-2054.	12.6	550
110	Apparent genetic homogeneity of the treacher Collins-Franceschetti syndrome. <i>American Journal of Medical Genetics Part A</i> , 1994, 52, 174-177.	2.4	21
111	The 1993-94 International human genetic linkage map. <i>Nature Genetics</i> , 1994, 7, 246-339.	21.4	2,015
112	Chromosome-specific microsatellite sets for fluorescence-based, semi-automated genome mapping. <i>Nature Genetics</i> , 1994, 7, 390-395.	21.4	323
113	A radiation hybrid map of 506 STS markers spanning human chromosome 11. <i>Nature Genetics</i> , 1994, 8, 70-76.	21.4	157
114	Assignment of 112 Microsatellite Markers to 23 Chromosome 11 Subregions Delineated by Somatic Hybrids: Comparison with the Genetic Map. <i>Genomics</i> , 1994, 21, 379-387.	2.9	26
115	Linkage analyses between dominant X-linked Charcot-Marie-Tooth disease, and 15 Xq11-Xq21 microsatellites in a new large family: Three new markers are closely linked to the gene. <i>Neuromuscular Disorders</i> , 1994, 4, 463-469.	0.6	10
116	A third locus for autosomal dominant cerebellar ataxia type I maps to chromosome 14q24.3-qter: evidence for the existence of a fourth locus. <i>American Journal of Human Genetics</i> , 1994, 54, 11-20.	6.2	88
117	Mapping of a novel gene for familial hypertrophic cardiomyopathy to chromosome 11. <i>Nature Genetics</i> , 1993, 4, 311-313.	21.4	184
118	Localization of Friedreich ataxia phenotype with selective vitamin E deficiency to chromosome 8q by homozygosity mapping. <i>Nature Genetics</i> , 1993, 5, 195-200.	21.4	215
119	Severe childhood autosomal recessive muscular dystrophy with the deficiency of the 50 kDa dystrophin-associated glycoprotein maps to chromosome 13q12. <i>Human Molecular Genetics</i> , 1993, 2, 1423-1428.	2.9	104
120	Relationship between Charcot - Marie-Tooth 1A and Smith - Magenis regions. snU3 may be a candidate gene for the Smith - Magenis syndrome. <i>Human Molecular Genetics</i> , 1993, 2, 1235-1243.	2.9	39
121	Continuum of overlapping clones spanning the entire human chromosome 21q. <i>Nature</i> , 1992, 359, 380-387.	27.8	436
122	A second-generation linkage map of the human genome. <i>Nature</i> , 1992, 359, 794-801.	27.8	1,795
123	Erythrocyte glycophorin B deficiency may occur by two distinct gene alterations. <i>American Journal of Hematology</i> , 1991, 37, 57-58.	4.1	23
124	A novel gene member of the human glycophorin A and B gene family. <i>Molecular cloning and expression</i> . <i>FEBS Journal</i> , 1990, 191, 619-625.	0.2	59
125	Promoter sequence and chromosomal organization of the genes encoding glycophorins A, B and E. <i>Gene</i> , 1990, 95, 289-293.	2.2	36
126	Molecular analysis of glycophorin A and B gene structure and expression in homozygous Miltenberger class V (Mi.V) human erythrocytes. <i>FEBS Journal</i> , 1989, 184, 337-344.	0.2	48

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127	Structure of the 5' flanking region of the gene encoding human glycophorin A and analysis of its multiple transcripts. <i>Gene</i> , 1989, 85, 471-477.	2.2	18
128	Alteration of the genes for glycoporphin A and B in glycoporphin-A-deficient individuals. <i>FEBS Journal</i> , 1988, 177, 605-614.	0.2	25
129	Reconstructing queen genotypes by pool sequencing colonies in eusocial insects: statistical methods and their application to honeybee. <i>Molecular Ecology Resources</i> , 0, , .	4.8	7