

# Hendrik-Jan Megens

## List of Publications by Year in descending order

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Version: 2024-02-01

111  
papers

8,644  
citations

57631

44  
h-index

48187

88  
g-index

113  
all docs

113  
docs citations

113  
times ranked

8340  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
2	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2009, 4, e6524.	1.1	568
3	Strong signatures of selection in the domestic pig genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19529-19536.	3.3	548
4	Multi-Platform Next-Generation Sequencing of the Domestic Turkey ( <i>Meleagris gallopavo</i> ): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	2.6	348
5	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. <i>PLoS Genetics</i> , 2012, 8, e1003100.	1.5	266
6	Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. <i>Nature Genetics</i> , 2015, 47, 1141-1148.	9.4	263
7	A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. <i>Genome Research</i> , 2009, 19, 510-519.	2.4	261
8	Genome-wide assessment of worldwide chicken SNP genetic diversity indicates significant absence of rare alleles in commercial breeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17312-17317.	3.3	230
9	Signatures of Diversifying Selection in European Pig Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003453.	1.5	228
10	Pig Domestication and Human-Mediated Dispersal in Western Eurasia Revealed through Ancient DNA and Geometric Morphometrics. <i>Molecular Biology and Evolution</i> , 2013, 30, 824-832.	3.5	196
11	The development and characterization of a 60K SNP chip for chicken. <i>BMC Genomics</i> , 2011, 12, 274.	1.2	185
12	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016, 7, 10474.	5.8	172
13	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. <i>BMC Genomics</i> , 2012, 13, 586.	1.2	150
14	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . <i>Genome Biology</i> , 2013, 14, R107.	13.9	137
15	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. <i>Nature Communications</i> , 2014, 5, 4392.	5.8	137
16	Genome-Wide Footprints of Pig Domestication and Selection Revealed through Massive Parallel Sequencing of Pooled DNA. <i>PLoS ONE</i> , 2011, 6, e14782.	1.1	135
17	Linkage Disequilibrium Decay and Haplotype Block Structure in the Pig. <i>Genetics</i> , 2008, 179, 569-579.	1.2	118
18	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. <i>BMC Genomics</i> , 2013, 14, 449.	1.2	118

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19	Genome-wide single nucleotide polymorphism analysis reveals recent genetic introgression from domestic pigs into Northwest European wild boar populations. <i>Molecular Ecology</i> , 2013, 22, 856-866.	2.0	117
20	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 71.	1.2	114
21	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17231-17238.	3.3	101
22	Deleterious alleles in the context of domestication, inbreeding, and selection. <i>Evolutionary Applications</i> , 2019, 12, 6-17.	1.5	94
23	Biodiversity of pig breeds from China and Europe estimated from pooled DNA samples: differences in microsatellite variation between two areas of domestication. <i>Genetics Selection Evolution</i> , 2008, 40, 103-128.	1.2	89
24	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. <i>BMC Genetics</i> , 2013, 14, 106.	2.7	87
25	Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. <i>BMC Genomics</i> , 2015, 16, 330.	1.2	85
26	Biodiversity of pig breeds from China and Europe estimated from pooled DNA samples: differences in microsatellite variation between two areas of domestication. <i>Genetics Selection Evolution</i> , 2008, 40, 103-128.	1.2	84
27	Atlantic salmon eggs favour sperm in competition that have similar major histocompatibility alleles. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 559-566.	1.2	83
28	Genetic origin, admixture and population history of aurochs ( <i>Bos primigenius</i> ) and primitive European cattle. <i>Heredity</i> , 2017, 118, 169-176.	1.2	80
29	Signatures of Selection in the Genomes of Commercial and Non-Commercial Chicken Breeds. <i>PLoS ONE</i> , 2012, 7, e32720.	1.1	77
30	Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations. <i>Genome Research</i> , 2015, 25, 970-981.	2.4	77
31	Comparison of linkage disequilibrium and haplotype diversity on macro- and microchromosomes in chicken. <i>BMC Genetics</i> , 2009, 10, 86.	2.7	72
32	The Genome of Winter Moth ( <i>Operophtera brumata</i> ) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. <i>Genome Biology and Evolution</i> , 2015, 7, 2321-2332.	1.1	70
33	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , 2017, 8, 108.	1.1	65
34	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , 2015, 6, 314.	1.1	64
35	Whole genome SNP discovery and analysis of genetic diversity in Turkey ( <i>Meleagris gallopavo</i> ). <i>BMC Genomics</i> , 2012, 13, 391.	1.2	63
36	Accuracy of genomic prediction using imputed whole-genome sequence data in white layers. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 167-179.	0.8	61

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37	Global lack of flyway structure in a cosmopolitan bird revealed by a genome wide survey of single nucleotide polymorphisms. <i>Molecular Ecology</i> , 2013, 22, 41-55.	2.0	59
38	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013, 110, 321-330.	1.2	58
39	Rapid Evolution of the MH Class I Locus Results in Different Allelic Compositions in Recently Diverged Populations of Atlantic Salmon. <i>Molecular Biology and Evolution</i> , 2005, 22, 1095-1106.	3.5	57
40	Hotspots of recent hybridization between pigs and wild boars in Europe. <i>Scientific Reports</i> , 2018, 8, 17372.	1.6	53
41	Untangling the hybrid nature of modern pig genomes: a mosaic derived from biogeographically distinct and highly divergent <i>Sus scrofa</i> populations. <i>Molecular Ecology</i> , 2014, 23, 4089-4102.	2.0	52
42	Identification of high utility SNPs for population assignment and traceability purposes in the pig using high-throughput sequencing. <i>Animal Genetics</i> , 2011, 42, 613-620.	0.6	49
43	Reintroductions and genetic introgression from domestic pigs have shaped the genetic population structure of Northwest European wild boar. <i>BMC Genetics</i> , 2013, 14, 43.	2.7	49
44	Extent of linkage disequilibrium in chicken. <i>Cytogenetic and Genome Research</i> , 2007, 117, 338-345.	0.6	47
45	A history of hybrids? Genomic patterns of introgression in the True Geese. <i>BMC Evolutionary Biology</i> , 2017, 17, 201.	3.2	47
46	Widespread horizontal genomic exchange does not erode species barriers among sympatric ducks. <i>BMC Evolutionary Biology</i> , 2012, 12, 45.	3.2	46
47	Loss of function mutations in essential genes cause embryonic lethality in pigs. <i>PLoS Genetics</i> , 2019, 15, e1008055.	1.5	46
48	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013, 14, 148.	1.2	45
49	Application of massive parallel sequencing to whole genome SNP discovery in the porcine genome. <i>BMC Genomics</i> , 2009, 10, 374.	1.2	44
50	Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. <i>BMC Genomics</i> , 2014, 15, 601.	1.2	44
51	Natural selection acts on Atlantic salmon major histocompatibility (MH) variability in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 861-869.	1.2	42
52	Genomic diversity and differentiation of a managed island wild boar population. <i>Heredity</i> , 2016, 116, 60-67.	1.2	41
53	Patterns of variability at the major histocompatibility class II alpha locus in Atlantic salmon contrast with those at the class I locus. <i>Immunogenetics</i> , 2005, 57, 16-24.	1.2	40
54	Preliminary insight into the age and origin of the Labeobarbus fish species flock from Lake Tana (Ethiopia) using the mtDNA cytochrome b gene. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 336-343.	1.2	40

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55	A tree of geese: A phylogenomic perspective on the evolutionary history of True Geese. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 303-313.	1.2	39
56	Balancing selection on a recessive lethal deletion with pleiotropic effects on two neighboring genes in the porcine genome. <i>PLoS Genetics</i> , 2018, 14, e1007661.	1.5	39
57	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <i>Nature Communications</i> , 2019, 10, 1992.	5.8	38
58	A systematic survey to identify lethal recessive variation in highly managed pig populations. <i>BMC Genomics</i> , 2017, 18, 858.	1.2	37
59	The type of bottleneck matters: Insights into the deleterious variation landscape of small managed populations. <i>Evolutionary Applications</i> , 2020, 13, 330-341.	1.5	36
60	A SNP based linkage map of the turkey genome reveals multiple intrachromosomal rearrangements between the Turkey and Chicken genomes. <i>BMC Genomics</i> , 2010, 11, 647.	1.2	35
61	Development of a genetic tool for product regulation in the diverse British pig breed market. <i>BMC Genomics</i> , 2012, 13, 580.	1.2	35
62	Systematic differences in the response of genetic variation to pedigree and genome-based selection methods. <i>Heredity</i> , 2014, 113, 503-513.	1.2	34
63	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. <i>Heredity</i> , 2010, 105, 290-298.	1.2	33
64	East Asian contributions to Dutch traditional and western commercial chickens inferred from mtDNA analysis. <i>Animal Genetics</i> , 2011, 42, 125-133.	0.6	32
65	Testing models of speciation from genome sequences: divergence and asymmetric admixture in <i>Sturnella</i> species during the Pliocene-Pleistocene climatic fluctuations. <i>Molecular Ecology</i> , 2014, 23, 5566-5574.	2.0	32
66	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. <i>Molecular Ecology</i> , 2020, 29, 1103-1119.	2.0	31
67	Review of the initial validation and characterization of a 3K chicken SNP array. <i>World's Poultry Science Journal</i> , 2008, 64, 219-226.	1.4	30
68	The effects of recent changes in breeding preferences on maintaining traditional Dutch chicken genomic diversity. <i>Heredity</i> , 2018, 121, 564-578.	1.2	29
69	Evolutionary origin of Lake Tana's (Ethiopia) small <i>Barbus</i> species: indications of rapid ecological divergence and speciation. <i>Animal Biology</i> , 2007, 57, 39-48.	0.6	28
70	A survey of functional genomic variation in domesticated chickens. <i>Genetics Selection Evolution</i> , 2018, 50, 17.	1.2	27
71	TRES: Identification of Discriminatory and Informative SNPs from Population Genomic Data: Figure 1.. <i>Journal of Heredity</i> , 2015, 106, 672-676.	1.0	26
72	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20152019.	1.2	25

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73	Tempo of speciation in a butterfly genus from the Southeast Asian tropics, inferred from mitochondrial and nuclear DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 1181-1196.	1.2	24
74	Shallow genetic divergence and species delineations in the endemic <i>Labeobarbus</i> species flock of Lake Tana, Ethiopia. <i>Journal of Fish Biology</i> , 2015, 87, 1191-1208.	0.7	24
75	Phylogenetic patterns in larval host plant and ant association of Indo-Australian Arhopalini butterflies (Lycaenidae: Theclinae). <i>Biological Journal of the Linnean Society</i> , 2005, 84, 225-241.	0.7	22
76	Adaptive Evolution of Toll-Like Receptors (TLRs) in the Family Suidae. <i>PLoS ONE</i> , 2015, 10, e0124069.	1.1	22
77	Farm analysis of microsatellite, mtDNA and SNP genotype data reveals inbreeding and crossbreeding as threats to the survival of a native Spanish pig breed. <i>Animal Genetics</i> , 2013, 44, 259-266.	0.6	21
78	The impact of genome editing on the introduction of monogenic traits in livestock. <i>Genetics Selection Evolution</i> , 2018, 50, 18.	1.2	21
79	pCADD: SNV prioritisation in <i>Sus scrofa</i> . <i>Genetics Selection Evolution</i> , 2020, 52, 4.	1.2	21
80	Gene Expression in Chicken Reveals Correlation with Structural Genomic Features and Conserved Patterns of Transcription in the Terrestrial Vertebrates. <i>PLoS ONE</i> , 2010, 5, e11990.	1.1	20
81	Hybrid origin of European commercial pigs examined by an in-depth haplotype analysis on chromosome 1. <i>Frontiers in Genetics</i> , 2014, 5, 442.	1.1	19
82	Parallel Genetic Origin of Foot Feathering in Birds. <i>Molecular Biology and Evolution</i> , 2020, 37, 2465-2476.	3.5	19
83	Genetic consequences of long-term small effective population size in the critically endangered pygmy hog. <i>Evolutionary Applications</i> , 2021, 14, 710-720.	1.5	19
84	Impact of merging commercial breeding lines on the genetic diversity of Landrace pigs. <i>Genetics Selection Evolution</i> , 2019, 51, 60.	1.2	18
85	A Novel Loss-of-Function Variant in Transmembrane Protein 263 (TMEM263) of Autosomal Dwarfism in Chicken. <i>Frontiers in Genetics</i> , 2018, 9, 193.	1.1	17
86	Accelerated discovery of functional genomic variation in pigs. <i>Genomics</i> , 2021, 113, 2229-2239.	1.3	16
87	Varying disease-mediated selection at different life-history stages of Atlantic salmon in fresh water. <i>Evolutionary Applications</i> , 2011, 4, 749-762.	1.5	15
88	Fragmentation and Translocation Distort the Genetic Landscape of Ungulates: Red Deer in the Netherlands. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	15
89	Molecular phylogeny of the Oriental butterfly genus <i>Arhopala</i> (Lycaenidae, Theclinae) inferred from mitochondrial and nuclear genes. <i>Systematic Entomology</i> , 2004, 29, 115-131.	1.7	14
90	Distinguishing migration events of different timing for wild boar in the Balkans. <i>Journal of Biogeography</i> , 2017, 44, 259-270.	1.4	14

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91	The Use of Genomics in Conservation Management of the Endangered Visayan Warty Pig ( <i>Sus</i> ) Tj ETQq1 1 0.784314 rgBT/Overlook	0.8	12
92	Increased <i>Mycoplasma hyopneumoniae</i> Disease Prevalence in Domestic Hybrids Among Free-Living Wild Boar. <i>EcoHealth</i> , 2015, 12, 571-579.	0.9	11
93	Early and late feathering in turkey and chicken: same gene but different mutations. <i>Genetics Selection Evolution</i> , 2018, 50, 7.	1.2	11
94	Genomic analysis of a Nile tilapia strain selected for salinity tolerance shows signatures of selection and hybridization with blue tilapia ( <i>Oreochromis aureus</i> ). <i>Aquaculture</i> , 2022, 560, 738527.	1.7	11
95	Evolution of Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 188-189.	9.4	10
96	Domesticated species form a treasure-trove for molecular characterization of Mendelian traits by exploiting the specific genetic structure of these species in across-breed genome wide association studies. <i>Heredity</i> , 2012, 109, 1-3.	1.2	9
97	Evolutionary patterns of Toll-like receptor signaling pathway genes in the Suidae. <i>BMC Evolutionary Biology</i> , 2016, 16, 33.	3.2	8
98	Regional regulation of transcription in the chicken genome. <i>BMC Genomics</i> , 2010, 11, 28.	1.2	7
99	Genome-wide candidate regions for selective sweeps revealed through massive parallel sequencing of DNA across ten turkey populations. <i>BMC Genetics</i> , 2014, 15, 117.	2.7	7
100	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of <i>SULT2A1</i> in the testis. <i>BMC Genetics</i> , 2014, 15, 4.	2.7	7
101	Evidence for adaptation of porcine Toll-like receptors. <i>Immunogenetics</i> , 2016, 68, 179-189.	1.2	7
102	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. <i>PLoS Genetics</i> , 2020, 16, e1009027.	1.5	7
103	Detection of a Frameshift Deletion in the <i>SPTBN4</i> Gene Leads to Prevention of Severe Myopathy and Postnatal Mortality in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 1226.	1.1	6
104	Host genetic heterozygosity and age are important determinants of porcine circovirus type 2 disease prevalence in European wild boar. <i>European Journal of Wildlife Research</i> , 2014, 60, 803-810.	0.7	4
105	A Genomic Perspective on Wild Boar Demography and Evolution. , 0, , 376-387.		3
106	The Visayan Warty Pig ( <i>Sus cebifrons</i> ) Genome Provides Insight Into Chromosome Evolution and Sensory Adaptation in Pigs. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
107	Genomic consequences of a century of inbreeding and isolation in the Danish wild boar population. <i>Evolutionary Applications</i> , 2022, 15, 954-966.	1.5	0
108	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0

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109	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
110	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
111	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0