

Martien A M Groenen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

289 papers	16,325 citations	62 h-index	119 g-index
303 ext. papers	19,105 ext. citations	5.5 avg, IF	6.52 L-index

#	Paper	IF	Citations
289	Organoids: a promising new in vitro platform in livestock and veterinary research. <i>Veterinary Research</i> , 2021 , 52, 43	3.8	9
288	A natural knockout of the MYO7A gene leads to pre-weaning mortality in pigs. <i>Animal Genetics</i> , 2021 , 52, 514-517	2.5	0
287	Deleterious Mutations in the TPO Gene Associated with Familial Thyroid Follicular Cell Carcinoma in Dutch German Longhaired Pointers. <i>Genes</i> , 2021 , 12,	4.2	1
286	Genetic consequences of long-term small effective population size in the critically endangered pygmy hog. <i>Evolutionary Applications</i> , 2021 , 14, 710-720	4.8	7
285	Heterogeneity of a dwarf phenotype in Dutch traditional chicken breeds revealed by genomic analyses. <i>Evolutionary Applications</i> , 2021 , 14, 1095-1108	4.8	2
284	Parallel Genomic Changes Drive Repeated Evolution of Placentas in Live-Bearing Fish. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2627-2638	8.3	2
283	Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021 , 49, 1859-1871	17.1	7
282	Accelerated discovery of functional genomic variation in pigs. <i>Genomics</i> , 2021 , 113, 2229-2239	4.3	2
281	A 12 kb multi-allelic copy number variation encompassing a GC gene enhancer is associated with mastitis resistance in dairy cattle. <i>PLoS Genetics</i> , 2021 , 17, e1009331	6	3
280	Familial follicular cell thyroid carcinomas in a large number of Dutch German longhaired pointers. <i>Veterinary and Comparative Oncology</i> , 2021 ,	2.5	1
279	Introgression contributes to distribution of structural variations in cattle. <i>Genomics</i> , 2021 , 113, 3092-3102	4.3	0
278	Time Course Transcriptomic Study Reveals the Gene Regulation During Liver Development and the Correlation With Abdominal Fat Weight in Chicken. <i>Frontiers in Genetics</i> , 2021 , 12, 723519	4.5	2
277	Quantitative genetics of wing morphology in the parasitoid wasp <i>Nasonia vitripennis</i> : hosts increase sibling similarity. <i>Heredity</i> , 2020 , 125, 40-49	3.6	4
276	pCADD: SNV prioritisation in <i>Sus scrofa</i> . <i>Genetics Selection Evolution</i> , 2020 , 52, 4	4.9	7
275	Altered Hippocampal Epigenetic Regulation Underlying Reduced Cognitive Development in Response to Early Life Environmental Insults. <i>Genes</i> , 2020 , 11,	4.2	4
274	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. <i>Molecular Ecology</i> , 2020 , 29, 1103-1119	5.7	10
273	Impact of genotype, body weight and sex on the prenatal muscle transcriptome of Iberian pigs. <i>PLoS ONE</i> , 2020 , 15, e0227861	3.7	5

272	Parallel Genetic Origin of Foot Feathering in Birds. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2465-2476	8.3	6
271	CNVRanger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020 , 36, 972-973	7.2	2
270	Functional and population genetic features of copy number variations in two dairy cattle populations. <i>BMC Genomics</i> , 2020 , 21, 89	4.5	12
269	Developments in genetic modification of cattle and implications for regulation, safety and traceability. <i>Frontiers of Agricultural Science and Engineering</i> , 2020 , 7, 136	1.7	3
268	The Genomes of the Livebearing Fish Species <i>Poeciliopsis retropinna</i> and <i>Poeciliopsis turrubarensis</i> Reflect Their Different Reproductive Strategies. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1376-1386	8.3	6
267	The type of bottleneck matters: Insights into the deleterious variation landscape of small managed populations. <i>Evolutionary Applications</i> , 2020 , 13, 330-341	4.8	15
266	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. <i>PLoS Genetics</i> , 2020 , 16, e1009027	6	2
265	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020 , 21, 285	18.3	21
264	RNA-Seq Analysis Reveals Hub Genes Involved in Chicken Intramuscular Fat and Abdominal Fat Deposition During Development. <i>Frontiers in Genetics</i> , 2020 , 11, 1009	4.5	9
263	Genome-Wide Assessment of DNA Methylation in Chicken Cardiac Tissue Exposed to Different Incubation Temperatures and CO Levels. <i>Frontiers in Genetics</i> , 2020 , 11, 558189	4.5	5
262	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD 2020 , 16, e1009027		
261	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD 2020 , 16, e1009027		
260	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD 2020 , 16, e1009027		
259	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD 2020 , 16, e1009027		
258	Genomic relatedness and diversity of Swedish native cattle breeds. <i>Genetics Selection Evolution</i> , 2019 , 51, 56	4.9	17
257	Response to Perrier and Charmantier: On the importance of time scales when studying adaptive evolution. <i>Evolution Letters</i> , 2019 , 3, 248-253	5.3	
256	The Genomic Complexity of a Large Inversion in Great Tits. <i>Genome Biology and Evolution</i> , 2019 , 11, 1870-1881	5.1	6
255	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <i>Nature Communications</i> , 2019 , 10, 1992	17.4	16

254	Loss of function mutations in essential genes cause embryonic lethality in pigs. <i>PLoS Genetics</i> , 2019 , 15, e1008055	6	24
253	Deciphering the patterns of genetic admixture and diversity in southern European cattle using genome-wide SNPs. <i>Evolutionary Applications</i> , 2019 , 12, 951-963	4.8	14
252	Deleterious alleles in the context of domestication, inbreeding, and selection. <i>Evolutionary Applications</i> , 2019 , 12, 6-17	4.8	36
251	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	11.5	42
250	The genome of the live-bearing fish <i>Heterandria formosa</i> implicates a role of conserved vertebrate genes in the evolution of placental fish. <i>BMC Evolutionary Biology</i> , 2019 , 19, 156	3	5
249	Detection of a Frameshift Deletion in the Gene Leads to Prevention of Severe Myopathy and Postnatal Mortality in Pigs. <i>Frontiers in Genetics</i> , 2019 , 10, 1226	4.5	4
248	Exploring the unmapped DNA and RNA reads in a songbird genome. <i>BMC Genomics</i> , 2019 , 20, 19	4.5	12
247	The effects of recent changes in breeding preferences on maintaining traditional Dutch chicken genomic diversity. <i>Heredity</i> , 2018 , 121, 564-578	3.6	17
246	A high-density SNP chip for genotyping great tit (<i>Parus major</i>) populations and its application to studying the genetic architecture of exploration behaviour. <i>Molecular Ecology Resources</i> , 2018 , 18, 877-891	8.4	25
245	Genome-wide population structure and admixture analysis reveals weak differentiation among Ugandan goat breeds. <i>Animal Genetics</i> , 2018 , 49, 59-70	2.5	10
244	The impact of genome editing on the introduction of monogenic traits in livestock. <i>Genetics Selection Evolution</i> , 2018 , 50, 18	4.9	13
243	A survey of functional genomic variation in domesticated chickens. <i>Genetics Selection Evolution</i> , 2018 , 50, 17	4.9	21
242	CNVs are associated with genomic architecture in a songbird. <i>BMC Genomics</i> , 2018 , 19, 195	4.5	8
241	A Novel Loss-of-Function Variant in Transmembrane Protein 263 (TMEM263) of Autosomal Dwarfism in Chicken. <i>Frontiers in Genetics</i> , 2018 , 9, 193	4.5	9
240	Early and late feathering in turkey and chicken: same gene but different mutations. <i>Genetics Selection Evolution</i> , 2018 , 50, 7	4.9	9
239	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	6	14
238	Genome-Wide Characterization of Selection Signatures and Runs of Homozygosity in Ugandan Goat Breeds. <i>Frontiers in Genetics</i> , 2018 , 9, 318	4.5	46
237	Gene networks for total number born in pigs across divergent environments. <i>Mammalian Genome</i> , 2017 , 28, 426-435	3.2	2

236	Recent natural selection causes adaptive evolution of an avian polygenic trait. <i>Science</i> , 2017 , 358, 365-368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000	101	
235	A history of hybrids? Genomic patterns of introgression in the True Geese. <i>BMC Evolutionary Biology</i> , 2017 , 17, 201	3	27
234	A systematic survey to identify lethal recessive variation in highly managed pig populations. <i>BMC Genomics</i> , 2017 , 18, 858	4.5	26
233	Oncopig Soft-Tissue Sarcomas Recapitulate Key Transcriptional Features of Human Sarcomas. <i>Scientific Reports</i> , 2017 , 7, 2624	4.9	17
232	Genetic origin, admixture and population history of aurochs (<i>Bos primigenius</i>) and primitive European cattle. <i>Heredity</i> , 2017 , 118, 169-176	3.6	54
231	Distinguishing migration events of different timing for wild boar in the Balkans. <i>Journal of Biogeography</i> , 2017 , 44, 259-270	4.1	6
230	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017 , 49, 71	4.9	63
229	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , 2017 , 8, 108	4.5	34
228	Genomic diversity and differentiation of a managed island wild boar population. <i>Heredity</i> , 2016 , 116, 60-7	3.6	28
227	GO-FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016 , 47, 528-33	2.5	37
226	Evidence for adaptation of porcine Toll-like receptors. <i>Immunogenetics</i> , 2016 , 68, 179-89	3.2	4
225	A decade of pig genome sequencing: a window on pig domestication and evolution. <i>Genetics Selection Evolution</i> , 2016 , 48, 23	4.9	58
224	Evolutionary patterns of Toll-like receptor signaling pathway genes in the Suidae. <i>BMC Evolutionary Biology</i> , 2016 , 16, 33	3	4
223	Accuracy of genomic prediction using imputed whole-genome sequence data in white layers. <i>Journal of Animal Breeding and Genetics</i> , 2016 , 133, 167-79	2.9	38
222	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016 , 7, 10474	17.4	125
221	The Evolution of Suidae. <i>Annual Review of Animal Biosciences</i> , 2016 , 4, 61-85	13.7	58
220	The Use of Genomics in Conservation Management of the Endangered Visayan Warty Pig (<i>Sus cebifrons</i>). <i>International Journal of Genomics</i> , 2016 , 2016, 5613862	2.5	9
219	Impact of neonatal iron deficiency on hippocampal DNA methylation and gene transcription in a porcine biomedical model of cognitive development. <i>BMC Genomics</i> , 2016 , 17, 856	4.5	29

218	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations. <i>Journal of Animal Science</i> , 2016 , 94, 1446-58	0.7	8
217	A tree of geese: A phylogenomic perspective on the evolutionary history of True Geese. <i>Molecular Phylogenetics and Evolution</i> , 2016 , 101, 303-313	4.1	28
216	Genome-wide single nucleotide polymorphism (SNP) identification and characterization in a non-model organism, the African buffalo (<i>Syncerus caffer</i>), using next generation sequencing. <i>Mammalian Biology</i> , 2016 , 81, 595-603	1.6	8
215	Evolution of Tibetan wild boars. <i>Nature Genetics</i> , 2015 , 47, 188-9	36.3	8
214	TRES: Identification of Discriminatory and Informative SNPs from Population Genomic Data. <i>Journal of Heredity</i> , 2015 , 106, 672-6	2.4	17
213	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015 , 145, 78-179	1.9	57
212	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015 , 16, 130	4.5	47
211	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
210	Accuracy of imputation using the most common sires as reference population in layer chickens. <i>BMC Genetics</i> , 2015 , 16, 101	2.6	10
209	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, 2321-32	3.9	53
208	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, 1141-8	36.3	151
207	Replicated analysis of the genetic architecture of quantitative traits in two wild great tit populations. <i>Molecular Ecology</i> , 2015 , 24, 6148-62	5.7	48
206	Adult porcine genome-wide DNA methylation patterns support pigs as a biomedical model. <i>BMC Genomics</i> , 2015 , 16, 743	4.5	61
205	Accuracy of Predicted Genomic Breeding Values in Purebred and Crossbred Pigs. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1575-83	3.2	29
204	Adaptive Evolution of Toll-Like Receptors (TLRs) in the Family Suidae. <i>PLoS ONE</i> , 2015 , 10, e0124069	3.7	17
203	Accuracy of genomic prediction using deregressed breeding values estimated from purebred and crossbred offspring phenotypes in pigs. <i>Journal of Animal Science</i> , 2015 , 93, 3313-21	0.7	9
202	Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. <i>BMC Genomics</i> , 2015 , 16, 330	4.5	51
201	Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations. <i>Genome Research</i> , 2015 , 25, 970-81	9.7	53

200	Population-level consequences of complementary sex determination in a solitary parasitoid. <i>BMC Evolutionary Biology</i> , 2015 , 15, 98	3	11
199	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	4.4	18
198	Hybrid origin of European commercial pigs examined by an in-depth haplotype analysis on chromosome 1. <i>Frontiers in Genetics</i> , 2014 , 5, 442	4.5	11
197	Systematic differences in the response of genetic variation to pedigree and genome-based selection methods. <i>Heredity</i> , 2014 , 113, 503-13	3.6	16
196	Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. <i>BMC Genomics</i> , 2014 , 15, 601	4.5	33
195	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, 4089-102	5.7	32
194	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. <i>Nature Communications</i> , 2014 , 5, 4392	17.4	97
193	Asian low-androstenone haplotype on pig chromosome 6 does not unfavorably affect production and reproduction traits. <i>Animal Genetics</i> , 2014 , 45, 874-7	2.5	1
192	A genetic linkage map of sole (<i>Solea solea</i>): a tool for evolutionary and comparative analyses of exploited (flat)fishes. <i>PLoS ONE</i> , 2014 , 9, e115040	3.7	10
191	Replicated high-density genetic maps of two great tit populations reveal fine-scale genomic departures from sex-equal recombination rates. <i>Heredity</i> , 2014 , 112, 307-16	3.6	37
190	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. <i>Physiological Genomics</i> , 2014 , 46, 195-206	3.6	19
189	Identification of species-specific novel transcripts in pig reproductive tissues using RNA-seq. <i>Animal Genetics</i> , 2014 , 45, 198-204	2.5	19
188	Testing models of speciation from genome sequences: divergence and asymmetric admixture in Island South-East Asian <i>Sus</i> species during the Plio-Pleistocene climatic fluctuations. <i>Molecular Ecology</i> , 2014 , 23, 5566-74	5.7	23
187	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of SULT2A1 in the testis. <i>BMC Genetics</i> , 2014 , 15, 4	2.6	6
186	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, 856-66	5.7	84
185	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. <i>BMC Genomics</i> , 2013 , 14, 449	4.5	92
184	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013 , 14, 148	4.5	40
183	Large scale variation in DNA copy number in chicken breeds. <i>BMC Genomics</i> , 2013 , 14, 398	4.5	39

182	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013 , 110, 321-30	3.6	42
181	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013 , 45, 776-783	36.3	240
180	Signatures of diversifying selection in European pig breeds. <i>PLoS Genetics</i> , 2013 , 9, e1003453	6	131
179	Pig domestication and human-mediated dispersal in western Eurasia revealed through ancient DNA and geometric morphometrics. <i>Molecular Biology and Evolution</i> , 2013 , 30, 824-32	8.3	155
178	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . <i>Genome Biology</i> , 2013 , 14, R107	18.3	97
177	Genetic consequences of breaking migratory traditions in barnacle geese <i>Branta leucopsis</i> . <i>Molecular Ecology</i> , 2013 , 22, 5835-47	5.7	34
176	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. <i>BMC Genetics</i> , 2013 , 14, 106	2.6	63
175	The design and cross-population application of a genome-wide SNP chip for the great tit <i>Parus major</i> . <i>Molecular Ecology Resources</i> , 2012 , 12, 753-70	8.4	46
174	SNP marker detection and genotyping in tilapia. <i>Molecular Ecology Resources</i> , 2012 , 12, 932-41	8.4	28
173	Centromere positions in chicken and Japanese quail chromosomes: de novo centromere formation versus pericentric inversions. <i>Chromosome Research</i> , 2012 , 20, 1017-32	4.4	26
172	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
171	Widespread horizontal genomic exchange does not erode species barriers among sympatric ducks. <i>BMC Evolutionary Biology</i> , 2012 , 12, 45	3	39
170	Whole genome SNP discovery and analysis of genetic diversity in Turkey (<i>Meleagris gallopavo</i>). <i>BMC Genomics</i> , 2012 , 13, 391	4.5	49
169	Development of a genetic tool for product regulation in the diverse British pig breed market. <i>BMC Genomics</i> , 2012 , 13, 580	4.5	25
168	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	4.5	113
167	Identification of Nucleotide Variation in Genomes Using Next-Generation Sequencing 2012 , 257-276		
166	Signatures of selection in the genomes of commercial and non-commercial chicken breeds. <i>PLoS ONE</i> , 2012 , 7, e32720	3.7	51
165	Regions of homozygosity in the porcine genome: consequence of demography and the recombination landscape. <i>PLoS Genetics</i> , 2012 , 8, e1003100	6	178

164	Genetic correlation between heart ratio and body weight as a function of ascites frequency in broilers split up into sex and health status. <i>Poultry Science</i> , 2012 , 91, 556-64	3.9	9
163	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, 19529-36	11.5	367
162	The imprinted gene DIO3 is a candidate gene for litter size in pigs. <i>PLoS ONE</i> , 2012 , 7, e31825	3.7	28
161	The development of a genome wide SNP set for the Barnacle goose <i>Branta leucopsis</i> . <i>PLoS ONE</i> , 2012 , 7, e38412	3.7	19
160	Prediction of altered 3S UTR miRNA-binding sites from RNA-Seq data: the swine leukocyte antigen complex (SLA) as a model region. <i>PLoS ONE</i> , 2012 , 7, e48607	3.7	14
159	The distal end of porcine chromosome 6p is involved in the regulation of skatole levels in boars. <i>BMC Genetics</i> , 2011 , 12, 35	2.6	20
158	Genome wide SNP discovery, analysis and evaluation in mallard (<i>Anas platyrhynchos</i>). <i>BMC Genomics</i> , 2011 , 12, 150	4.5	55
157	Genome-wide footprints of pig domestication and selection revealed through massive parallel sequencing of pooled DNA. <i>PLoS ONE</i> , 2011 , 6, e14782	3.7	103
156	Regional regulation of transcription in the bovine genome. <i>PLoS ONE</i> , 2011 , 6, e20413	3.7	1
155	East Asian contributions to Dutch traditional and western commercial chickens inferred from mtDNA analysis. <i>Animal Genetics</i> , 2011 , 42, 125-33	2.5	27
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