

Stephen J O brien

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.

417
papers

39,576
citations

95
h-index

186
g-index

426
ext. papers

44,244
ext. citations

10.1
avg, IF

6.85
L-index

#	Paper	IF	Citations
417	A decade of GigaScience: A perspective on conservation genetics. <i>GigaScience</i> , 2022 , 11,	7.6	2
416	Ultracontinuous Single Haplotype Genome Assemblies for the Domestic Cat (<i>Felis catus</i>) and Asian Leopard Cat (<i>Prionailurus bengalensis</i>). <i>Journal of Heredity</i> , 2021 , 112, 165-173	2.4	5
415	Genome-wide association study identifies new loci associated with risk of HBV infection and disease progression. <i>BMC Medical Genomics</i> , 2021 , 14, 84	3.7	3
414	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746.	36.4	161
413	Draft de novo Genome Assembly of the Elusive Jaguarundi, <i>Puma yagouaroundi</i> . <i>Journal of Heredity</i> , 2021 , 112, 540-548	2.4	0
412	Genomic evidence for the Chinese mountain cat as a wildcat conspecific () and its introgression to domestic cats. <i>Science Advances</i> , 2021 , 7,	14.3	4
411	Commentary: Unbiasing Genome-Based Analyses of Selection: An Example Using Iconic Shark Species. <i>Frontiers in Marine Science</i> , 2021 , 8,	4.5	
410	Karyotype Evolution in 10 Pinniped Species: Variability of Heterochromatin versus High Conservatism of Euchromatin as Revealed by Comparative Molecular Cytogenetics. <i>Genes</i> , 2020 , 11,	4.2	4
409	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 10927-10934	11.5	31
408	GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. <i>GigaScience</i> , 2020 , 9,	7.6	16
407	A Beautiful Life: High Risk-High Payoff in Genetic Science. <i>Annual Review of Animal Biosciences</i> , 2020 , 8, 1-24	13.7	3
406	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020 , 30, 5018-5025.e5	6.3	18
405	Draft genome of <i>Bugula neritina</i> , a colonial animal packing powerful symbionts and potential medicines. <i>Scientific Data</i> , 2020 , 7, 356	8.2	1
404	Are pangolins scapegoats of the COVID-19 outbreak-CoV transmission and pathology evidence?. <i>Conservation Letters</i> , 2020 , 13, e12754	6.9	8
403	Genome-wide sequence analyses of ethnic populations across Russia. <i>Genomics</i> , 2020 , 112, 442-458	4.3	8
402	New Gene Variants Associated with the Risk of Chronic HBV Infection. <i>Virologica Sinica</i> , 2020 , 35, 378-386.	3.4	3
401	Precision nomenclature for the new genomics. <i>GigaScience</i> , 2019 , 8,	7.6	9

400	Avian Binocularity and Adaptation to Nocturnal Environments: Genomic Insights from a Highly Derived Visual Phenotype. <i>Genome Biology and Evolution</i> , 2019 , 11, 2244-2255	3.9	6
399	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. <i>Nature Communications</i> , 2019 , 10, 4769	17.4	24
398	White shark genome reveals ancient elasmobranch adaptations associated with wound healing and the maintenance of genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 4446-4455	11.5	51
397	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019 , 29, 576-589	9.7	15
396	Comparative Chromosome Mapping of Musk Ox and the X Chromosome among Some Bovidae Species. <i>Genes</i> , 2019 , 10,	4.2	3
395	The Complete Phylogeny of Pangolins: Scaling Up Resources for the Molecular Tracing of the Most Trafficked Mammals on Earth. <i>Journal of Heredity</i> , 2018 , 109, 347-359	2.4	42
394	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered <i>Solenodon paradoxus</i> from the island of Hispaniola. <i>GigaScience</i> , 2018 , 7,	7.6	10
393	New high copy tandem repeat in the content of the chicken W chromosome. <i>Chromosoma</i> , 2018 , 127, 73-83	2.8	5
392	Whole-Genome Analysis of <i>Mycobacterium tuberculosis</i> from Patients with Tuberculous Spondylitis, Russia. <i>Emerging Infectious Diseases</i> , 2018 , 24, 579-583	10.2	4
391	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1479-1491	12.3	74
390	Marker of proliferation Ki-67 expression is associated with transforming growth factor beta 1 and can predict the prognosis of patients with hepatic B virus-related hepatocellular carcinoma. <i>Cancer Management and Research</i> , 2018 , 10, 679-696	3.6	18
389	Analytical "bake-off" of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. <i>PLoS ONE</i> , 2018 , 13, e0200423	3.7	4
388	Genome-Wide Evolutionary Analysis of Natural History and Adaptation in the World's Tigers. <i>Current Biology</i> , 2018 , 28, 3840-3849.e6	6.3	32
387	Adaptive genomic evolution of opsins reveals that early mammals flourished in nocturnal environments. <i>BMC Genomics</i> , 2018 , 19, 121	4.5	11
386	Mitogenomic sequences support a north-south subspecies subdivision within <i>Solenodon paradoxus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017 , 28, 662-670	1.3	8
385	Genome-Wide Analyses Reveal Gene Influence on HIV Disease Progression and HIV-1C Acquisition in Southern Africa. <i>AIDS Research and Human Retroviruses</i> , 2017 , 33, 597-609	1.6	7
384	Signal localization: a new approach in signal discovery. <i>Biometrical Journal</i> , 2017 , 59, 126-144	1.5	0
383	Aldehyde dehydrogenase 1 (ALDH1) isoform expression and potential clinical implications in hepatocellular carcinoma. <i>PLoS ONE</i> , 2017 , 12, e0182208	3.7	20

382	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017 , 3, e1700299	14.3	67
381	Genome-Wide Association Study of MKI67 Expression and its Clinical Implications in HBV-Related Hepatocellular Carcinoma in Southern China. <i>Cellular Physiology and Biochemistry</i> , 2017 , 42, 1342-1357	3.9	19
380	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. <i>Journal of Heredity</i> , 2017 , 108, 671-677	2.4	15
379	X Chromosome Evolution in Cetartiodactyla. <i>Genes</i> , 2017 , 8,	4.2	16
378	Positive Selection Linked with Generation of Novel Mammalian Dentition Patterns. <i>Genome Biology and Evolution</i> , 2016 , 8, 2748-59	3.9	6
377	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016 , 17, 211	18.3	61
376	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016 , 6, 28199	4.9	9
375	Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. <i>GigaScience</i> , 2016 , 5, 38	7.6	40
374	PGD: a pangolin genome hub for the research community. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	5
373	A High-Resolution SNP Array-Based Linkage Map Anchors a New Domestic Cat Draft Genome Assembly and Provides Detailed Patterns of Recombination. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1607-16	3.2	32
372	Continued decline in genetic diversity among wild cheetahs (<i>Acinonyx jubatus</i>) without further loss of semen quality. <i>Biological Conservation</i> , 2016 , 200, 192-199	6.2	14
371	The Population Origins and Expansion of Feral Cats in Australia. <i>Journal of Heredity</i> , 2016 , 107, 104-14	2.4	14
370	Whole-Genome Identification, Phylogeny, and Evolution of the Cytochrome P450 Family 2 (CYP2) Subfamilies in Birds. <i>Genome Biology and Evolution</i> , 2016 , 8, 1115-31	3.9	15
369	Genetic Evidence for Contrasting Wetland and Savannah Habitat Specializations in Different Populations of Lions (<i>Panthera leo</i>). <i>Journal of Heredity</i> , 2016 , 107, 101-3	2.4	4
368	Response to Comment by Faurby, Werdelin and Svenning. <i>Genome Biology</i> , 2016 , 17, 90	18.3	2
367	A Mutation in LTBP2 Causes Congenital Glaucoma in Domestic Cats (<i>Felis catus</i>). <i>PLoS ONE</i> , 2016 , 11, e0154412	3.7	14
366	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016 , 12, e1005954	6	77
365	Bone-associated gene evolution and the origin of flight in birds. <i>BMC Genomics</i> , 2016 , 17, 371	4.5	5

364	Koalas (<i>Phascolarctos cinereus</i>) From Queensland Are Genetically Distinct From 2 Populations in Victoria. <i>Journal of Heredity</i> , 2016 , 107, 573-580	2.4	3
363	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016 , 26, 1312-1322	9.7	54
362	The Genome 10K Project: a way forward. <i>Annual Review of Animal Biosciences</i> , 2015 , 3, 57-111	13.7	223
361	Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2832-43	8.3	47
360	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015 , 25, 2158-65	6.3	118
359	Recurrent evolution of melanism in South American felids. <i>PLoS Genetics</i> , 2015 , 11, e1004892	6	24
358	SmileFinder: a resampling-based approach to evaluate signatures of selection from genome-wide sets of matching allele frequency data in two or more diploid populations. <i>GigaScience</i> , 2015 , 4, 1	7.6	87
357	Genetic ancestry of the extinct Javan and Bali tigers. <i>Journal of Heredity</i> , 2015 , 106, 247-57	2.4	12
356	The Genome Russia project: closing the largest remaining omission on the world Genome map. <i>GigaScience</i> , 2015 , 4, 53	7.6	13
355	The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. <i>Genome Biology</i> , 2015 , 16, 215	18.3	32
354	Gene loss, adaptive evolution and the co-evolution of plumage coloration genes with opsins in birds. <i>BMC Genomics</i> , 2015 , 16, 751	4.5	37
353	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015 , 16, 277	18.3	99
352	Putting Russia on the genome map. <i>Science</i> , 2015 , 350, 747	33.3	7
351	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014 , 46, 88-92	36.3	186
350	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17230-5	11.5	184
349	Endogenous retrovirus insertion in the KIT oncogene determines white and white spotting in domestic cats. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1881-91	3.2	38
348	Annotated features of domestic cat - <i>Felis catus</i> genome. <i>GigaScience</i> , 2014 , 3, 13	7.6	26
347	Sympatric Asian felid phylogeography reveals a major Indochinese-Sundaic divergence. <i>Molecular Ecology</i> , 2014 , 23, 2072-92	5.7	38

346	Evolutionary genomics and adaptive evolution of the Hedgehog gene family (Shh, Ihh and Dhh) in vertebrates. <i>PLoS ONE</i> , 2014 , 9, e74132	3.7	18
345	GWATCH: a web platform for automated gene association discovery analysis. <i>GigaScience</i> , 2014 , 3, 18	7.6	2
344	Evaluation and integration of genetic signature for prediction risk of nasopharyngeal carcinoma in Southern China. <i>BioMed Research International</i> , 2014 , 2014, 434072	3	9
343	The dynamic proliferation of CanSINEs mirrors the complex evolution of Feliforms. <i>BMC Evolutionary Biology</i> , 2014 , 14, 137	3	7
342	Mammalian keratin associated proteins (KRTAPs) subgenomes: disentangling hair diversity and adaptation to terrestrial and aquatic environments. <i>BMC Genomics</i> , 2014 , 15, 779	4.5	37
341	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
340	Development of MHC-Linked Microsatellite Markers in the Domestic Cat and Their Use to Evaluate MHC Diversity in Domestic Cats, Cheetahs, and Gir Lions. <i>Journal of Heredity</i> , 2014 , 105, 493-505	2.4	7
339	The Global Invertebrate Genomics Alliance (GIGA): developing community resources to study diverse invertebrate genomes. <i>Journal of Heredity</i> , 2014 , 105, 1-18	2.4	70
338	Evolution: a new cat species emerges. <i>Current Biology</i> , 2013 , 23, R1103-5	6.3	
337	Host genomic influences on HIV/AIDS. <i>Genome Biology</i> , 2013 , 14, 201	18.3	16
336	Association study of common genetic variants and HIV-1 acquisition in 6,300 infected cases and 7,200 controls. <i>PLoS Pathogens</i> , 2013 , 9, e1003515	7.6	86
335	The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013 , 4, 2433	17.4	147
334	Molecular evidence for a recent demographic expansion in the puma (<i>Puma concolor</i>) (Mammalia, Felidae). <i>Genetics and Molecular Biology</i> , 2013 , 36, 586-97	2	12
333	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013 , 2, e01123	8.9	85
332	A population genetic database of cat breeds developed in coordination with a domestic cat STR multiplex. <i>Journal of Forensic Sciences</i> , 2012 , 57, 596-601	1.8	11
331	Does genetic introgression improve female reproductive performance? A test on the endangered Florida panther. <i>Oecologia</i> , 2012 , 168, 289-300	2.9	10
330	Specifying and sustaining pigmentation patterns in domestic and wild cats. <i>Science</i> , 2012 , 337, 1536-41	33.3	84
329	Tissue sampling methods and standards for vertebrate genomics. <i>GigaScience</i> , 2012 , 1, 8	7.6	35

328	The fishes of Genome 10K. <i>Marine Genomics</i> , 2012 , 7, 3-6	1.9	34
327	How the leopard hides its spots: ASIP mutations and melanism in wild cats. <i>PLoS ONE</i> , 2012 , 7, e50386	3.7	26
326	Emerging viruses in the Felidae: shifting paradigms. <i>Viruses</i> , 2012 , 4, 236-57	6.2	37
325	Fish lateral line innovation: insights into the evolutionary genomic dynamics of a unique mechanosensory organ. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3887-98	8.3	10
324	The principal genetic determinants for nasopharyngeal carcinoma in China involve the HLA class I antigen recognition groove. <i>PLoS Genetics</i> , 2012 , 8, e1003103	6	72
323	Multicohort genomewide association study reveals a new signal of protection against HIV-1 acquisition. <i>Journal of Infectious Diseases</i> , 2012 , 205, 1155-62	7	21
322	Risk factors for symptomatic hyperlactatemia and lactic acidosis among combination antiretroviral therapy-treated adults in Botswana: results from a clinical trial. <i>AIDS Research and Human Retroviruses</i> , 2012 , 28, 759-65	1.6	13
321	The role of gene duplication and unconstrained selective pressures in the melanopsin gene family evolution and vertebrate circadian rhythm regulation. <i>PLoS ONE</i> , 2012 , 7, e52413	3.7	17
320	Association of host genetic risk factors with the course of cytomegalovirus retinitis in patients infected with human immunodeficiency virus. <i>American Journal of Ophthalmology</i> , 2011 , 151, 999-1006.e49	4.9	13
319	FIV diversity: FIV Ple subtype composition may influence disease outcome in African lions. <i>Veterinary Immunology and Immunopathology</i> , 2011 , 143, 338-46	2	24
318	A molecular phylogeny of living primates. <i>PLoS Genetics</i> , 2011 , 7, e1001342	6	916
317	Evolution of a major drug metabolizing enzyme defect in the domestic cat and other felidae: phylogenetic timing and the role of hypercarnivory. <i>PLoS ONE</i> , 2011 , 6, e18046	3.7	59
316	Intentional genetic introgression influences survival of adults and subadults in a small, inbred felid population. <i>Journal of Animal Ecology</i> , 2011 , 80, 958-67	4.7	35
315	Adaptive evolution of the matrix extracellular phosphoglycoprotein in mammals. <i>BMC Evolutionary Biology</i> , 2011 , 11, 342	3	15
314	Strong influence of human leukocyte antigen (HLA)-DP gene variants on development of persistent chronic hepatitis B virus carriers in the Han Chinese population. <i>Hepatology</i> , 2011 , 53, 422-8	11.2	106
313	Reply:. <i>Hepatology</i> , 2011 , 54, 375-376	11.2	
312	A suite of genetic markers useful in assessing wildcat (<i>Felis silvestris</i> ssp.)-domestic cat (<i>Felis silvestris catus</i>) admixture. <i>Journal of Heredity</i> , 2011 , 102 Suppl 1, S87-90	2.4	13
311	Genome-wide association study implicates PARD3B-based AIDS restriction. <i>Journal of Infectious Diseases</i> , 2011 , 203, 1491-502	7	45

310	Restoring tigers to the Caspian region. <i>Science</i> , 2011 , 333, 822-3	33.3	5
309	Role of exonic variation in chemokine receptor genes on AIDS: CCRL2 F167Y association with pneumocystis pneumonia. <i>PLoS Genetics</i> , 2011 , 7, e1002328	6	16
308	A common HLA-DPA1 variant is a major determinant of hepatitis B virus clearance in Han Chinese. <i>Journal of Infectious Diseases</i> , 2011 , 203, 943-7	7	70
307	Genetic variants in nuclear-encoded mitochondrial genes influence AIDS progression. <i>PLoS ONE</i> , 2010 , 5, e12862	3.7	35
306	Effect of host genetics on the development of cytomegalovirus retinitis in patients with AIDS. <i>Journal of Infectious Diseases</i> , 2010 , 202, 606-13	7	27
305	Mutation discovered in a feline model of human congenital retinal blinding disease 2010 , 51, 2852-9		47
304	Multistage genomewide association study identifies a locus at 1q41 associated with rate of HIV-1 disease progression to clinical AIDS. <i>Journal of Infectious Diseases</i> , 2010 , 201, 618-26	7	60
303	Genetic associations of variants in genes encoding HIV-dependency factors required for HIV-1 infection. <i>Journal of Infectious Diseases</i> , 2010 , 202, 1836-45	7	22
302	Examination of disease-based selection, demographic history and population structure in European Y-chromosome haplogroup I. <i>Journal of Human Genetics</i> , 2010 , 55, 613-20	4.3	3
301	Genome-wide scans for footprints of natural selection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010 , 365, 185-205	5.8	225
300	Genetic Introgression and the Survival of Florida Panther Kittens. <i>Biological Conservation</i> , 2010 , 143, 2789-2796	6.2	31
299	Feline immunodeficiency virus (FIV) in wild PallasCats. <i>Veterinary Immunology and Immunopathology</i> , 2010 , 134, 90-5	2	18
298	Defining and mapping mammalian coat pattern genes: multiple genomic regions implicated in domestic cat stripes and spots. <i>Genetics</i> , 2010 , 184, 267-75	4	34
297	Effect of host genetics on incidence of HIV neuroretinal disorder in patients with AIDS. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010 , 54, 343-51	3.1	14
296	Genetic restoration of the Florida panther. <i>Science</i> , 2010 , 329, 1641-5	33.3	349
295	Molecular evolution and the role of oxidative stress in the expansion and functional diversification of cytosolic glutathione transferases. <i>BMC Evolutionary Biology</i> , 2010 , 10, 281	3	59
294	Light whole genome sequence for SNP discovery across domestic cat breeds. <i>BMC Genomics</i> , 2010 , 11, 406	4.5	48
293	Accounting for multiple comparisons in a genome-wide association study (GWAS). <i>BMC Genomics</i> , 2010 , 11, 724	4.5	191

292	Genetic Polymorphisms of CYP2E1, GSTP1, NQO1 and MPO and the Risk of Nasopharyngeal Carcinoma in a Han Chinese Population of Southern China. <i>BMC Research Notes</i> , 2010 , 3, 212	2.3	30
291	Applying molecular genetic tools to tiger conservation. <i>Integrative Zoology</i> , 2010 , 5, 351-362	1.9	9
290	Pattern and timing of diversification of the mammalian order Carnivora inferred from multiple nuclear gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010 , 56, 49-63	4.1	173
289	Comparative genomics in vertebrates: a role for the platypus. Introduction. <i>Reproduction, Fertility and Development</i> , 2009 , 21, vii-ix	1.8	2
288	A domestic cat X chromosome linkage map and the sex-linked orange locus: mapping of orange, multiple origins and epistasis over nonagouti. <i>Genetics</i> , 2009 , 181, 1415-25	4	21
287	Mapping of the domestic cat "SILVER" coat color locus identifies a unique genomic location for silver in mammals. <i>Journal of Heredity</i> , 2009 , 100 Suppl 1, S8-13	2.4	9
286	From wild animals to domestic pets, an evolutionary view of domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106 Suppl 1, 9971-8	11.5	295
285	Artifacts of the 1.9x feline genome assembly derived from the feline-specific satellite sequence. <i>Journal of Heredity</i> , 2009 , 100 Suppl 1, S14-8	2.4	4
284	Mitochondrial DNA haplogroups influence lipotrophy after highly active antiretroviral therapy. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2009 , 51, 111-6	3.1	67
283	Genetics and pathogenesis of feline infectious peritonitis virus. <i>Emerging Infectious Diseases</i> , 2009 , 15, 1445-52	10.2	79
282	Guidelines for naming nonprimate APOBEC3 genes and proteins. <i>Journal of Virology</i> , 2009 , 83, 494-7	6.6	182
281	Common genetic variation and the control of HIV-1 in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000791	6	310
280	Analyses of sweet receptor gene (Tas1r2) and preference for sweet stimuli in species of Carnivora. <i>Journal of Heredity</i> , 2009 , 100 Suppl 1, S90-100	2.4	35
279	Every genome sequence needs a good map. <i>Genome Research</i> , 2009 , 19, 1925-8	9.7	122
278	Pathological manifestations of feline immunodeficiency virus (FIV) infection in wild African lions. <i>Virology</i> , 2009 , 390, 1-12	3.6	48
277	Evaluation of nonviral risk factors for nasopharyngeal carcinoma in a high-risk population of Southern China. <i>International Journal of Cancer</i> , 2009 , 124, 2942-7	7.5	109
276	Association of Y chromosome haplogroup I with HIV progression, and HAART outcome. <i>Human Genetics</i> , 2009 , 125, 281-94	6.3	25
275	CCL3L1 and HIV/AIDS susceptibility. <i>Nature Medicine</i> , 2009 , 15, 1110-2	50.5	60

274	The Taming of the Cat. <i>Scientific American</i> , 2009 , 300, 68-75	0.5	70
273	Stewardship of human biospecimens, DNA, genotype, and clinical data in the GWAS era. <i>Annual Review of Genomics and Human Genetics</i> , 2009 , 10, 193-209	9.7	34
272	An autosomal genetic linkage map of the domestic cat, <i>Felis silvestris catus</i> . <i>Genomics</i> , 2009 , 93, 305-13	4.3	33
271	Mitochondrial phylogeography illuminates the origin of the extinct caspian tiger and its relationship to the amur tiger. <i>PLoS ONE</i> , 2009 , 4, e4125	3.7	42
270	The Taming of the cat. Genetic and archaeological findings hint that wildcats became housecats earlier--and in a different place--than previously thought. <i>Scientific American</i> , 2009 , 300, 68-75	0.5	25
269	Ecological and biogeographical inferences on two sympatric and enigmatic Andean cat species using genetic identification of faecal samples. <i>Molecular Ecology</i> , 2008 , 17, 678-90	5.7	47
268	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. <i>BMC Evolutionary Biology</i> , 2008 , 8, 220	3	207
267	The adaptive evolution of the mammalian mitochondrial genome. <i>BMC Genomics</i> , 2008 , 9, 119	4.5	234
266	Genomic organization, sequence divergence, and recombination of feline immunodeficiency virus from lions in the wild. <i>BMC Genomics</i> , 2008 , 9, 66	4.5	25
265	Subspecies genetic assignments of worldwide captive tigers increase conservation value of captive populations. <i>Current Biology</i> , 2008 , 18, 592-6	6.3	49
264	State of cat genomics. <i>Trends in Genetics</i> , 2008 , 24, 268-79	8.5	68
263	Functions, structure, and read-through alternative splicing of feline APOBEC3 genes. <i>Genome Biology</i> , 2008 , 9, R48	18.3	103
262	Evolution of feline immunodeficiency virus in Felidae: implications for human health and wildlife ecology. <i>Veterinary Immunology and Immunopathology</i> , 2008 , 123, 32-44	2	55
261	FIV cross-species transmission: an evolutionary prospective. <i>Veterinary Immunology and Immunopathology</i> , 2008 , 123, 159-66	2	44
260	Patterns of molecular genetic variation among cat breeds. <i>Genomics</i> , 2008 , 91, 1-11	4.3	51
259	The platypus genome unraveled. <i>Cell</i> , 2008 , 133, 953-5	56.2	9
258	Molecular genetic insights on cheetah (<i>Acinonyx jubatus</i>) ecology and conservation in Namibia. <i>Journal of Heredity</i> , 2008 , 99, 2-13	2.4	25
257	Host genetic influences on highly active antiretroviral therapy efficacy and AIDS-free survival. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008 , 48, 263-71	3.1	39

256	Mitochondrial DNA haplogroups influence AIDS progression. <i>Aids</i> , 2008 , 22, 2429-39	3.5	74
255	GSTM1 and GSTT1 gene deletions and the risk for nasopharyngeal carcinoma in Han Chinese. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008 , 17, 1760-3	4	36
254	The evolutionary dynamics of the lion <i>Panthera leo</i> revealed by host and viral population genomics. <i>PLoS Genetics</i> , 2008 , 4, e1000251	6	86
253	The ancestral carnivore karyotype (2n = 38) lives today in ringtails. <i>Journal of Heredity</i> , 2008 , 99, 241-53	2.4	13
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