Stephen Obrien

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.

40,587 187 98 443 h-index g-index citations papers 6.87 458 10.2 45,071 L-index avg, IF ext. papers ext. citations

#	Paper	IF	Citations
443	A decade of GigaScience: A perspective on conservation genetics. <i>GigaScience</i> , 2022 , 11,	7.6	2
442	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
441	GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. <i>GigaScience</i> , 2020 , 9,	7.6	16
440	A Beautiful Life: High Risk-High Payoff in Genetic Science. <i>Annual Review of Animal Biosciences</i> , 2020 , 8, 1-24	13.7	3
439	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. <i>Current Biology</i> , 2020 , 30, 5018-5025.e5	6.3	18
438	Draft genome of Bugula neritina, a colonial animal packing powerful symbionts and potential medicines. <i>Scientific Data</i> , 2020 , 7, 356	8.2	1
437	Are pangolins scapegoats of the COVID-19 outbreak-CoV transmission and pathology evidence?. <i>Conservation Letters</i> , 2020 , 13, e12754	6.9	8
436	Genome-wide sequence analyses of ethnic populations across Russia. <i>Genomics</i> , 2020 , 112, 442-458	4.3	8
435	New Gene Variants Associated with the Risk of Chronic HBV Infection. <i>Virologica Sinica</i> , 2020 , 35, 378-3	38 7 .4	3
434	Precision nomenclature for the new genomics. <i>GigaScience</i> , 2019 , 8,	7.6	9
433	Integrated analysis of competing endogenous RNA network revealing potential prognostic biomarkers of hepatocellular carcinoma. <i>Journal of Cancer</i> , 2019 , 10, 3267-3283	4.5	17
432	Whole Genome Sequencing and Re-sequencing of the Sable Antelope (): A Resource for Monitoring Diversity in and Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1785-1793	3.2	14
431	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
430	The Vertebrate TLR Supergene Family Evolved Dynamically by Gene Gain/Loss and Positive Selection Revealing a HostPathogen Arms Race in Birds. <i>Diversity</i> , 2019 , 11, 131	2.5	9
429	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
428	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
427	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

426	Comparative Chromosome Mapping of Musk Ox and the X Chromosome among Some Bovidae Species. <i>Genes</i> , 2019 , 10,	4.2	3
425	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
424	Robust forensic matching of confiscated horns to individual poached African rhinoceros. <i>Current Biology</i> , 2018 , 28, R13-R14	6.3	20
423	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered Solenodon paradoxus from the island of Hispaniola. <i>GigaScience</i> , 2018 , 7,	7.6	10
422	New high copy tandem repeat in the content of the chicken W chromosome. <i>Chromosoma</i> , 2018 , 127, 73-83	2.8	5
421	Whole-Genome Analysis of Mycobacterium tuberculosis from Patients with Tuberculous Spondylitis, Russia. <i>Emerging Infectious Diseases</i> , 2018 , 24, 579-583	10.2	4
420	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
419	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
418	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
417	Life table estimator revisited. Communications in Statistics - Theory and Methods, 2018, 47, 2126-2133	0.5	1
416	Genome-Wide Evolutionary Analysis of Natural History and Adaptation in the WorldN Tigers. <i>Current Biology</i> , 2018 , 28, 3840-3849.e6	6.3	32
415	Adaptive genomic evolution of opsins reveals that early mammals flourished in nocturnal environments. <i>BMC Genomics</i> , 2018 , 19, 121	4.5	11
414	Conservation Genetics of the Cheetah: Genetic History and Implications for Conservation 2018, 71-92		4
413	Mitogenomic sequences support a north-south subspecies subdivision within Solenodon paradoxus. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017 , 28, 662-670	1.3	8
412	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
411	Signal localization: a new approach in signal discovery. <i>Biometrical Journal</i> , 2017 , 59, 126-144	1.5	O
410	Aldehyde dehydrogenase 1 (ALDH1) isoform expression and potential clinical implications in hepatocellular carcinoma. <i>PLoS ONE</i> , 2017 , 12, e0182208	3.7	20
409	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017 , 3, e1700299	14.3	67

408	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
407	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. <i>Journal of Heredity</i> , 2017 , 108, 671-677	2.4	15
406	X Chromosome Evolution in Cetartiodactyla. <i>Genes</i> , 2017 , 8,	4.2	16
405	Preoperative transcatheter arterial chemotherapy may suppress oxidative stress in hepatocellular carcinoma cells and reduce the risk of short-term relapse. <i>Oncotarget</i> , 2017 , 8, 54402-54415	3.3	
404	Positive Selection Linked with Generation of Novel Mammalian Dentition Patterns. <i>Genome Biology and Evolution</i> , 2016 , 8, 2748-59	3.9	6
403	Primary cultures of human colon cancer as a model to study cancer stem cells. <i>Tumor Biology</i> , 2016 , 37, 12833-12842	2.9	3
402	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016 , 17, 211	18.3	61
401	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016 , 6, 28199	4.9	9
400	Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. <i>GigaScience</i> , 2016 , 5, 38	7.6	40
399	PGD: a pangolin genome hub for the research community. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	5
398	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, 160	7 ³ 1 ² 6	32
397	Continued decline in genetic diversity among wild cheetahs (Acinonyx jubatus) without further loss of semen quality. <i>Biological Conservation</i> , 2016 , 200, 192-199	6.2	14
396	The Population Origins and Expansion of Feral Cats in Australia. <i>Journal of Heredity</i> , 2016 , 107, 104-14	2.4	14
395	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
394	Genetic Evidence for Contrasting Wetland and Savannah Habitat Specializations in Different Populations of Lions (Panthera leo). <i>Journal of Heredity</i> , 2016 , 107, 101-3	2.4	4
393	Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application. <i>Trends in Ecology and Evolution</i> , 2016 , 31, 81-83	10.9	115
392	Response to Comment by Faurby, Werdelin and Svenning. <i>Genome Biology</i> , 2016 , 17, 90	18.3	2
391	A Mutation in LTBP2 Causes Congenital Glaucoma in Domestic Cats (Felis catus). <i>PLoS ONE</i> , 2016 , 11, e0154412	3.7	14

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390	The Genome-Wide Analysis of Carcinoembryonic Antigen Signaling by Colorectal Cancer Cells Using RNA Sequencing. <i>PLoS ONE</i> , 2016 , 11, e0161256	3.7	11
389	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
388	Bone-associated gene evolution and the origin of flight in birds. BMC Genomics, 2016, 17, 371	4.5	5
387	Contrasting origin of B chromosomes in two cervids (Siberian roe deer and grey brocket deer) unravelled by chromosome-specific DNA sequencing. <i>BMC Genomics</i> , 2016 , 17, 618	4.5	36
386	The Asian arowana (Scleropages formosus) genome provides new insights into the evolution of an early lineage of teleosts. <i>Scientific Reports</i> , 2016 , 6, 24501	4.9	66
385	Koalas (Phascolarctos cinereus) From Queensland Are Genetically Distinct From 2 Populations in Victoria. <i>Journal of Heredity</i> , 2016 , 107, 573-580	2.4	3
384	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016 , 26, 1312-1322	9.7	54
383	The Genome 10K Project: a way forward. <i>Annual Review of Animal Biosciences</i> , 2015 , 3, 57-111	13.7	223
382	Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2832-43	8.3	47
381	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015 , 25, 2158-65	6.3	118
380	Recurrent evolution of melanism in South American felids. <i>PLoS Genetics</i> , 2015 , 11, e1004892	6	24
379	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
378	Genetic ancestry of the extinct Javan and Bali tigers. Journal of Heredity, 2015, 106, 247-57	2.4	12
377	The Genome Russia project: closing the largest remaining omission on the world Genome map. <i>GigaScience</i> , 2015 , 4, 53	7.6	13
376	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
375	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
374	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). <i>PLoS Genetics</i> , 2015 , 11, e1005352	6	84
373	Genomic legacy of the African cheetah, Acinonyx jubatus. <i>Genome Biology</i> , 2015 , 16, 277	18.3	99

372	Putting Russia on the genome map. <i>Science</i> , 2015 , 350, 747	33.3	7
371	Phylogeography and population history of Leopardus guigna, the smallest American felid. <i>Conservation Genetics</i> , 2014 , 15, 631-653	2.6	27
370	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014 , 46, 88-92	36.3	186
369	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
368	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
367	Annotated features of domestic cat - Felis catus genome. <i>GigaScience</i> , 2014 , 3, 13	7.6	26
366	Genome-wide Mycobacterium tuberculosis variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. <i>BMC Genomics</i> , 2014 , 15, 308	4.5	61
365	Sympatric Asian felid phylogeography reveals a major Indochinese-Sundaic divergence. <i>Molecular Ecology</i> , 2014 , 23, 2072-92	5.7	38
364	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
363	Genetic variations affecting serum carcinoembryonic antigen levels and status of regional lymph nodes in patients with sporadic colorectal cancer from Southern China. <i>PLoS ONE</i> , 2014 , 9, e97923	3.7	9
362	GWATCH: a web platform for automated gene association discovery analysis. <i>GigaScience</i> , 2014 , 3, 18	7.6	2
361	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
360	The dynamic proliferation of CanSINEs mirrors the complex evolution of Feliforms. <i>BMC Evolutionary Biology</i> , 2014 , 14, 137	3	7
359	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
358	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
357	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
356	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
355	Evolution: a new cat species emerges. <i>Current Biology</i> , 2013 , 23, R1103-5	6.3	

354	Host genomic influences on HIV/AIDS. <i>Genome Biology</i> , 2013 , 14, 201	18.3	16
353	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
352	The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013 , 4, 2433	17.4	147
351	Molecular evidence for a recent demographic expansion in the puma (Puma concolor) (Mammalia, Felidae). <i>Genetics and Molecular Biology</i> , 2013 , 36, 586-97	2	12
350	Genome-wide and differential proteomic analysis of hepatitis B virus and aflatoxin B1 related hepatocellular carcinoma in Guangxi, China. <i>PLoS ONE</i> , 2013 , 8, e83465	3.7	24
349	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
348	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
347	Does genetic introgression improve female reproductive performance? A test on the endangered Florida panther. <i>Oecologia</i> , 2012 , 168, 289-300	2.9	10
346	Specifying and sustaining pigmentation patterns in domestic and wild cats. <i>Science</i> , 2012 , 337, 1536-41	33.3	84
345	Tissue sampling methods and standards for vertebrate genomics. <i>GigaScience</i> , 2012 , 1, 8	7.6	35
344	The fishes of Genome 10K. <i>Marine Genomics</i> , 2012 , 7, 3-6	1.9	34
343	How the leopard hides its spots: ASIP mutations and melanism in wild cats. <i>PLoS ONE</i> , 2012 , 7, e50386	3.7	26
342	Emerging viruses in the Felidae: shifting paradigms. Viruses, 2012, 4, 236-57	6.2	37
341	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
340	Evolution of CRISPs associated with toxicoferan-reptilian venom and mammalian reproduction. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1807-22	8.3	75
339	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	7 ²
338	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
337	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

336	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
335	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.	.e4 ⁹	13
334	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
333	A molecular phylogeny of living primates. <i>PLoS Genetics</i> , 2011 , 7, e1001342	6	916
332	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
331	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
330	Adaptive evolution of the matrix extracellular phosphoglycoprotein in mammals. <i>BMC Evolutionary Biology</i> , 2011 , 11, 342	3	15
329	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
328	Reply:. <i>Hepatology</i> , 2011 , 54, 375-376	11.2	
327	A suite of genetic markers useful in assessing wildcat (Felis silvestris ssp.)-domestic cat (Felis silvestris catus) admixture. <i>Journal of Heredity</i> , 2011 , 102 Suppl 1, S87-90	2.4	13
326	Genome-wide association study implicates PARD3B-based AIDS restriction. <i>Journal of Infectious Diseases</i> , 2011 , 203, 1491-502	7	45
325	Restoring tigers to the Caspian region. <i>Science</i> , 2011 , 333, 822-3	33.3	5
324	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. <i>Genome Research</i> , 2011 , 21, 137-45	9.7	59
323	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
322	A common HLA-DPA1 variant is a major determinant of hepatitis B virus clearance in Han Chinese. Journal of Infectious Diseases, 2011 , 203, 943-7	7	70
321	Genetic variants in nuclear-encoded mitochondrial genes influence AIDS progression. <i>PLoS ONE</i> , 2010 , 5, e12862	3.7	35
320	What Is a Tiger? Genetics and Phylogeography 2010 , 35-51		3
319	Effect of host genetics on the development of cytomegalovirus retinitis in patients with AIDS. Journal of Infectious Diseases, 2010 , 202, 606-13	7	27

318	Mutation discovered in a feline model of human congenital retinal blinding disease 2010 , 51, 2852-9		47
317	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
316	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
315	Genetic Future for Florida PanthersResponse. <i>Science</i> , 2010 , 330, 1744-1744	33.3	1
314	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
313	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
312	Genetic Introgression and the Survival of Florida Panther Kittens. <i>Biological Conservation</i> , 2010 , 143, 2789-2796	6.2	31
311	Feline immunodeficiency virus (FIV) in wild Pallas Ntats. <i>Veterinary Immunology and Immunopathology</i> , 2010 , 134, 90-5	2	18
310	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
309	Mitochondrial haplogroups are associated with risk of neuroretinal disorder in HIV-positive patients. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010 , 53, 451-5	3.1	22
308	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
307	Genetic restoration of the Florida panther. <i>Science</i> , 2010 , 329, 1641-5	33.3	349
306	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
305	Light whole genome sequence for SNP discovery across domestic cat breeds. <i>BMC Genomics</i> , 2010 , 11, 406	4.5	48
304	Accounting for multiple comparisons in a genome-wide association study (GWAS). <i>BMC Genomics</i> , 2010 , 11, 724	4.5	191
303	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
302	Applying molecular genetic tools to tiger conservation. <i>Integrative Zoology</i> , 2010 , 5, 351-362	1.9	9
301	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

300	Comparative genomics in vertebrates: a role for the platypus. Introduction. <i>Reproduction, Fertility and Development</i> , 2009 , 21, vii-ix	1.8	2
299	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
298	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
297	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
296	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
295	Mitochondrial DNA haplogroups influence lipoatrophy after highly active antiretroviral therapy. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2009 , 51, 111-6	3.1	67
294	Genetics and pathogenesis of feline infectious peritonitis virus. <i>Emerging Infectious Diseases</i> , 2009 , 15, 1445-52	10.2	79
293	Guidelines for naming nonprimate APOBEC3 genes and proteins. <i>Journal of Virology</i> , 2009 , 83, 494-7	6.6	182
292	Common genetic variation and the control of HIV-1 in humans. PLoS Genetics, 2009, 5, e1000791	6	310
291	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
2 90	Every genome sequence needs a good map. <i>Genome Research</i> , 2009 , 19, 1925-8	9.7	122
289	Molecular genetic evidence for social group disruption of wild vicu l s Vicugna vicugna captured for wool harvest in Chile. <i>Small Ruminant Research</i> , 2009 , 84, 28-34	1.7	7
288	Pathological manifestations of feline immunodeficiency virus (FIV) infection in wild African lions. <i>Virology</i> , 2009 , 390, 1-12	3.6	48
287	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
286	Association of Y chromosome haplogroup I with HIV progression, and HAART outcome. <i>Human Genetics</i> , 2009 , 125, 281-94	6.3	25
285	CCL3L1 and HIV/AIDS susceptibility. <i>Nature Medicine</i> , 2009 , 15, 1110-2	50.5	60
284	The Taming of the Cat. Scientific American, 2009, 300, 68-75	0.5	70
283	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

(2008-2009)

282	An autosomal genetic linkage map of the domestic cat, Felis silvestris catus. <i>Genomics</i> , 2009 , 93, 305-1	3 4.3	33
281	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
280	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
279	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
278	The adaptive evolution of the mammalian mitochondrial genome. BMC Genomics, 2008, 9, 119	4.5	234
277	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
276	Subspecies genetic assignments of worldwide captive tigers increase conservation value of captive populations. <i>Current Biology</i> , 2008 , 18, 592-6	6.3	49
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74 73 7 ² 7 ¹	Genomic prospecting. <i>Nature Medicine</i> , 1995 , 1, 742-4 Hypervariable genomic variation to reconstruct the natural history of populations: lessons from the big cats. <i>Electrophoresis</i> , 1995 , 16, 1771-4 Exchanges of short polymorphic DNA segments predating speciation in feline major histocompatibility complex class I genes. <i>Journal of Molecular Evolution</i> , 1994 , 39, 22-33 Polymorphisms in the 3Nuntranslated region of the I kappa B/MAD-3 (NFKBI) gene located on chromosome 14. <i>Human Genetics</i> , 1994 , 93, 694-6 Nucleotide sequence analysis of puma lentivirus (PLV-14): genomic organization and relationship to	50.5 3.6 3.1 6.3	10 12 23 13
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