Stephen Obrien

List of Publications by Year in descending order

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450 papers 49,076 citations

105 h-index 201 g-index

458 all docs

458 docs citations

458 times ranked

42910 citing authors

#	Article	IF	CITATIONS
1	Molecular phylogenetics and the origins of placental mammals. Nature, 2001, 409, 614-618.	13.7	1,292
2	Resolution of the Early Placental Mammal Radiation Using Bayesian Phylogenetics. Science, 2001, 294, 2348-2351.	6.0	1,215
3	HLA and HIV-1: Heterozygote Advantage and B*35-Cw*04 Disadvantage. Science, 1999, 283, 1748-1752.	6.0	1,151
4	A Molecular Phylogeny of Living Primates. PLoS Genetics, 2011, 7, e1001342.	1.5	1,130
5	Epistatic interaction between KIR3DS1 and HLA-B delays the progression to AIDS. Nature Genetics, 2002, 31, 429-434.	9.4	1,090
6	HLA and NK Cell Inhibitory Receptor Genes in Resolving Hepatitis C Virus Infection. Science, 2004, 305, 872-874.	6.0	1,086
7	A Molecular Phylogeny for Bats Illuminates Biogeography and the Fossil Record. Science, 2005, 307, 580-584.	6.0	988
8	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
9	Contrasting Genetic Influence of CCR2 and CCR5 Variants on HIV-1 Infection and Disease Progression. Science, 1997, 277, 959-965.	6.0	860
10	Placental mammal diversification and the Cretaceous-Tertiary boundary. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1056-1061.	3.3	767
11	Innate partnership of HLA-B and KIR3DL1 subtypes against HIV-1. Nature Genetics, 2007, 39, 733-740.	9.4	691
12	The Influence of HLAGenotype on AIDS. Annual Review of Medicine, 2003, 54, 535-551.	5.0	690
13	Genetic Restriction of AIDS Pathogenesis by an SDF-1 Chemokine Gene Variant. Science, 1998, 279, 389-393.	6.0	674
14	A canine distemper virus epidemic in Serengeti lions (Panthera leo). Nature, 1996, 379, 441-445.	13.7	671
15	The Late Miocene Radiation of Modern Felidae: A Genetic Assessment. Science, 2006, 311, 73-77.	6.0	596
16	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. Science, 2005, 309, 613-617.	6.0	542
17	Numt, a recent transfer and tandem amplification of mitochondrial DNA to the nuclear genome of the domestic cat. Journal of Molecular Evolution, 1994, 39, 174-190.	0.8	528
18	Mechanism of met oncogene activation. Cell, 1986, 45, 895-904.	13.5	523

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19	Dating the Origin of the CCR5-î"32 AIDS-Resistance Allele by the Coalescence of Haplotypes. American Journal of Human Genetics, 1998, 62, 1507-1515.	2.6	507
20	Anchored reference loci for comparative genome mapping in mammals. Nature Genetics, 1993, 3, 103-112.	9.4	499
21	Genetic Restoration of the Florida Panther. Science, 2010, 329, 1641-1645.	6.0	467
22	Effect of a Single Amino Acid Change in MHC Class I Molecules on the Rate of Progression to AIDS. New England Journal of Medicine, 2001, 344, 1668-1675.	13.9	456
23	Interactive influence of infectious disease and genetic diversity in natural populations. Trends in Ecology and Evolution, 1988, 3, 254-259.	4.2	452
24	Methods for High-Density Admixture Mapping of Disease Genes. American Journal of Human Genetics, 2004, 74, 979-1000.	2.6	437
25	The Promise of Comparative Genomics in Mammals. Science, 1999, 286, 458-481.	6.0	423
26	A High-Density Admixture Map for Disease Gene Discovery in African Americans. American Journal of Human Genetics, 2004, 74, 1001-1013.	2.6	416
27	The Near Eastern Origin of Cat Domestication. Science, 2007, 317, 519-523.	6.0	414
28	From wild animals to domestic pets, an evolutionary view of domestication. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9971-9978.	3.3	397
29	Bureaucratic Mischief: Recognizing Endangered Species and Subspecies. Science, 1991, 251, 1187-1188.	6.0	392
30	A Genetic Linkage Map of Microsatellites in the Domestic Cat (Felis catus). Genomics, 1999, 57, 9-23.	1.3	377
31	Common Genetic Variation and the Control of HIV-1 in Humans. PLoS Genetics, 2009, 5, e1000791.	1.5	377
32	Detecting single base substitutions as heteroduplex polymorphisms. Genomics, 1992, 12, 301-306.	1.3	369
33	Genetic fingerprinting reflects population differentiation in the California Channel Island fox. Nature, 1990, 344, 764-767.	13.7	355
34	Genome-wide scans for footprints of natural selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 185-205.	1.8	343
35	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. Nature Genetics, 2006, 38, 68-74.	9.4	339
36	Comparative anchor tagged sequences (CATS) for integrative mapping of mammalian genomes. Nature Genetics, 1997, 15, 47-56.	9.4	338

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37	The consequences of demographic reduction and genetic depletion in the endangered Florida panther. Current Biology, 1993, 3, 340-350.	1.8	336
38	Mammalian phylogenomics comes of age. Trends in Genetics, 2004, 20, 631-639.	2.9	327
39	Initial sequence and comparative analysis of the cat genome. Genome Research, 2007, 17, 1675-1689.	2.4	311
40	The adaptive evolution of the mammalian mitochondrial genome. BMC Genomics, 2008, 9, 119.	1.2	303
41	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	3.6	294
42	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17230-17235.	3.3	281
43	Genetic Evidence for Two Species of Elephant in Africa. Science, 2001, 293, 1473-1477.	6.0	280
44	Human genes that limit AIDS. Nature Genetics, 2004, 36, 565-574.	9.4	278
45	Molecular Genetics and Evolution of Melanism in the Cat Family. Current Biology, 2003, 13, 448-453.	1.8	274
46	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. BMC Evolutionary Biology, 2008, 8, 220.	3.2	261
47	Accounting for multiple comparisons in a genome-wide association study (GWAS). BMC Genomics, 2010, 11, 724.	1.2	256
48	Complete Nucleotide Sequences of the Domestic Cat (Felis catus) Mitochondrial Genome and a Transposed mtDNA Tandem Repeat (Numt) in the Nuclear Genome. Genomics, 1996, 33, 229-246.	1.3	244
49	The effect of genetic variation in chemokines and their receptorson HIV transmission and progression to AIDS. Immunological Reviews, 2000, 177, 99-111.	2.8	244
50	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. GigaScience, 2015, 4, 1.	3.3	241
51	Minke whale genome and aquatic adaptation in cetaceans. Nature Genetics, 2014, 46, 88-92.	9.4	227
52	A molecular solution to the riddle of the giant panda's phylogeny. Nature, 1985, 317, 140-144.	13.7	221
53	Guidelines for Naming Nonprimate APOBEC3 Genes and Proteins. Journal of Virology, 2009, 83, 494-497.	1.5	217
54	The tiger genome and comparative analysis with lion and snow leopard genomes. Nature Communications, 2013, 4, 2433.	5.8	217

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55	Canine and Feline Parvoviruses Can Use Human or Feline Transferrin Receptors To Bind, Enter, and Infect Cells. Journal of Virology, 2001, 75, 3896-3902.	1.5	209
56	Pattern and timing of diversification of the mammalian order Carnivora inferred from multiple nuclear gene sequences. Molecular Phylogenetics and Evolution, 2010, 56, 49-63.	1.2	206
57	HLA and AIDS: a cautionary tale. Trends in Molecular Medicine, 2001, 7, 379-381.	3.5	202
58	Phylogeography and Genetic Ancestry of Tigers (Panthera tigris). PLoS Biology, 2004, 2, e442.	2.6	197
59	Mapping by admixture linkage disequilibrium: advances, limitations and guidelines. Nature Reviews Genetics, 2005, 6, 623-632.	7.7	197
60	Modulating influence on HIV/AIDS by interacting RANTES gene variants. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10002-10007.	3.3	196
61	AIDS restriction HLA allotypes target distinct intervals of HIV-1 pathogenesis. Nature Medicine, 2005, 11, 1290-1292.	15.2	192
62	Cytonuclear genomic dissociation in African elephant species. Nature Genetics, 2005, 37, 96-100.	9.4	185
63	Phylogenetic reconstruction of the felidae using 16S rRNA and NADH-5 mitochondrial genes. Journal of Molecular Evolution, 1997, 44, S98-S116.	0.8	182
64	Expression of the human c-fms proto-oncogene in hematopoietic cells and its deletion in the 5qâ^' syndrome. Cell, 1985, 42, 421-428.	13.5	181
65	Phylogeography, population history and conservation genetics of jaguars (Panthera onca, Mammalia,) Tj ETQq $1\ 1$	0,7,84314	· rgBT /Over
66	APOBEC3G Genetic Variants and Their Influence on the Progression to AIDS. Journal of Virology, 2004, 78, 11070-11076.	1.5	178
67	HLA-Cw*04 and Hepatitis C Virus Persistence. Journal of Virology, 2002, 76, 4792-4797.	1.5	176
68	A Family Matter: Conclusive Resolution of the Taxonomic Position of the Long-Fingered Bats, Miniopterus. Molecular Biology and Evolution, 2007, 24, 1553-1561.	3. 5	176
69	Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application. Trends in Ecology and Evolution, 2016, 31, 81-83.	4.2	173
70	Phylogenetics, genome diversity and origin of modern leopard, Panthera pardus. Molecular Ecology, 2001, 10, 2617-2633.	2.0	168
71	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.	3.8	167
72	Exclusive and Persistent Use of the Entry Coreceptor CXCR4 by Human Immunodeficiency Virus Type 1 from a Subject Homozygous for <i>CCR5</i> Î"32. Journal of Virology, 1998, 72, 6040-6047.	1.5	163

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73	Immunologic and virologic response to highly active antiretroviral therapy in the Multicenter AIDS Cohort Study. Aids, 2001, 15, 735-746.	1.0	159
74	Genetic variance of laboratory outbred Swiss mice. Nature, 1980, 283, 157-161.	13.7	157
75	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. Current Biology, 2015, 25, 2158-2165.	1.8	156
76	Dispersion of the ras family of transforming genes to four different chromosomes in man. Nature, 1983, 302, 839-842.	13.7	155
77	Molecular analysis of integrated human papillomavirus 16 sequences in the cervical cancer cell line SiHa. Virology, 1987, 159, 389-398.	1.1	153
78	Transactivation induced by human T-lymphotropic virus type III (HTLV III) maps to a viral sequence encoding 58 amino acids and lacks tissue specificity. Virology, 1986, 148, 226-231.	1.1	152
79	Novel Alleles of the Chemokine-Receptor Gene CCR5. American Journal of Human Genetics, 1997, 61, 1261-1267.	2.6	152
80	Unusual Polymorphisms in Human Immunodeficiency Virus Type 1 Associated with Nonprogressive Infection. Journal of Virology, 2000, 74, 4361-4376.	1.5	152
81	BALANCEDPOLYMORPHISMSELECTED BYGENETICVERSUSINFECTIOUSHUMANDISEASE. Annual Review of Genomics and Human Genetics, 2002, 3, 263-292.	2.5	150
82	Mesozoic origin for West Indian insectivores. Nature, 2004, 429, 649-651.	13.7	149
83	KIR/HLA Pleiotropism: Protection against Both HIV and Opportunistic Infections. PLoS Pathogens, 2006, 2, e79.	2.1	149
84	Origin of the HIV-Susceptible Human CD4+ Cell Line H9. AIDS Research and Human Retroviruses, 1989, 5, 253-255.	0.5	148
85	Every genome sequence needs a good map. Genome Research, 2009, 19, 1925-1928.	2.4	148
86	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. Science Advances, 2017, 3, e1700299.	4.7	142
87	Influence of the <i>CCR2-V64I</i> Polymorphism on Human Immunodeficiency Virus Type 1 Coreceptor Activity and on Chemokine Receptor Function of CCR2b, CCR3, CCR5, and CXCR4. Journal of Virology, 1998, 72, 7450-7458.	1.5	138
88	Comprehensive Analysis of Class I and Class II HLA Antigens and Chronic Hepatitis B Virus Infection. Journal of Virology, 2003, 77, 12083-12087.	1.5	133
89	Seroprevalence and Genomic Divergence of Circulating Strains of Feline Immunodeficiency Virus among Felidae and Hyaenidae Species. Journal of Virology, 2005, 79, 8282-8294.	1.5	132
90	Markers for Mapping by Admixture Linkage Disequilibrium in African American and Hispanic Populations. American Journal of Human Genetics, 2001, 69, 1080-1094.	2.6	130

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91	Evaluation of nonviral risk factors for nasopharyngeal carcinoma in a highâ€risk population of Southern China. International Journal of Cancer, 2009, 124, 2942-2947.	2.3	130
92	Strong influence of human leukocyte antigen (HLA)-DP gene variants on development of persistent chronic hepatitis B virus carriers in the Han Chinese population. Hepatology, 2011, 53, 422-428.	3.6	129
93	Comparative genomics: lessons from cats. Trends in Genetics, 1997, 13, 393-399.	2.9	128
94	Patterns of Genetic Diversity in Remaining Giant Panda Populations. Conservation Biology, 2001, 15, 1596-1607.	2.4	128
95	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	2.8	126
96	Rapid evolution of a heteroplasmic repetitive sequence in the mitochondrial DNA control region of carnivores. Journal of Molecular Evolution, 1994, 39, 191-199.	0.8	121
97	Mammalian genome mapping: lessons and prospects. Current Opinion in Genetics and Development, 1991, 1, 105-111.	1.5	120
98	Phylogeographic Subspecies Recognition in Leopards (Panthera pardus): Molecular Genetic Variation. Conservation Biology, 1996, 10, 1115-1132.	2.4	118
99	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). PLoS Genetics, 2015, 11, e1005352.	1.5	118
100	Allozyme Divergence Within the Canidae. Systematic Zoology, 1987, 36, 339.	1.6	117
101	A Radiation Hybrid Map of the Cat Genome: Implications for Comparative Mapping. Genome Research, 2000, 10, 691-702.	2.4	116
101		2.4	116
	2000, 10, 691-702. Cytotoxic T-Lymphocyte Antigen 4 Gene and Recovery from Hepatitis B Virus Infection. Journal of		
102	2000, 10, 691-702. Cytotoxic T-Lymphocyte Antigen 4 Gene and Recovery from Hepatitis B Virus Infection. Journal of Virology, 2004, 78, 11258-11262. Effects of human TRIM5î± polymorphisms on antiretroviral function and susceptibility to human	1.5	116
102	2000, 10, 691-702. Cytotoxic T-Lymphocyte Antigen 4 Gene and Recovery from Hepatitis B Virus Infection. Journal of Virology, 2004, 78, 11258-11262. Effects of human TRIM5î± polymorphisms on antiretroviral function and susceptibility to human immunodeficiency virus infection. Virology, 2006, 354, 15-27. Functions, structure, and read-through alternative splicing of feline APOBEC3 genes. Genome Biology,	1.5	116
102 103 104	Cytotoxic T-Lymphocyte Antigen 4 Gene and Recovery from Hepatitis B Virus Infection. Journal of Virology, 2004, 78, 11258-11262. Effects of human TRIM5α polymorphisms on antiretroviral function and susceptibility to human immunodeficiency virus infection. Virology, 2006, 354, 15-27. Functions, structure, and read-through alternative splicing of feline APOBEC3 genes. Genome Biology, 2008, 9, R48. Isolation of HTLV-transformed B-lymphocyte clone from a patient with HTLV-associated adult T-cell	1.5 1.1 13.9	116 116 116
102 103 104	Cytotoxic T-Lymphocyte Antigen 4 Gene and Recovery from Hepatitis B Virus Infection. Journal of Virology, 2004, 78, 11258-11262. Effects of human TRIM5α polymorphisms on antiretroviral function and susceptibility to human immunodeficiency virus infection. Virology, 2006, 354, 15-27. Functions, structure, and read-through alternative splicing of feline APOBEC3 genes. Genome Biology, 2008, 9, R48. Isolation of HTLV-transformed B-lymphocyte clone from a patient with HTLV-associated adult T-cell leukaemia. Nature, 1984, 310, 505-506. Association of DC-SIGN Promoter Polymorphism with Increased Risk for Parenteral, but Not Mucosal, Acquisition of Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2004, 78,	1.5 1.1 13.9	116 116 116

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109	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. Nature Ecology and Evolution, 2018, 2, 1479-1491.	3.4	113
110	Specifying and Sustaining Pigmentation Patterns in Domestic and Wild Cats. Science, 2012, 337, 1536-1541.	6.0	110
111	Association Study of Common Genetic Variants and HIV-1 Acquisition in 6,300 Infected Cases and 7,200 Controls. PLoS Pathogens, 2013, 9, e1003515.	2.1	109
112	The linkage disequilibrium maps of three human chromosomes across four populations reflect their demographic history and a common underlying recombination pattern. Genome Research, 2005, 15, 454-462.	2.4	107
113	The Adequacy of Morphology for Reconstructing the Early History of Placental Mammals. Systematic Biology, 2007, 56, 673-684.	2.7	107
114	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954.	1.5	105
115	The α-glycerophosphate cycle inDrosophila melanogaster. I. Biochemical and developmental aspects. Biochemical Genetics, 1972, 7, 141-161.	0.8	104
116	An STR Forensic Typing System for Genetic Individualization of Domestic Cat (Felis catus) Samples. Journal of Forensic Sciences, 2005, 50, 1-10.	0.9	103
117	Extensive Conservation of Sex Chromosome Organization Between Cat and Human Revealed by Parallel Radiation Hybrid Mapping. Genome Research, 1999, 9, 1223-1230.	2.4	101
118	Comparative Genome Organization of Human, Murine, and Feline MHC Class II Region. Genome Research, 2003, 13, 1169-1179.	2.4	101
119	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211.	3.8	101
120	Non-Hodgkin's B cell lymphoma in persons with acquired immunodeficiency syndrome is associated with increased serum levels of IL10, or the IL10 promoter â^592 C/C genotype. Clinical Immunology, 2003, 109, 119-129.	1.4	99
121	Molecular Evidence for Species-Level Distinctions in Clouded Leopards. Current Biology, 2006, 16, 2371-2376.	1.8	98
122	Genetics and Pathogenesis of Feline Infectious Peritonitis Virus. Emerging Infectious Diseases, 2009, 15, 1445-1452.	2.0	98
123	The Taming of the Cat. Scientific American, 2009, 300, 68-75.	1.0	98
124	Patterns of molecular genetic variation among African elephant populations. Molecular Ecology, 2002, 11, 2489-2498.	2.0	96
125	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. Journal of Heredity, 2014, 105, 1-18.	1.0	96
126	Genomic differentiation among natural populations of orang-utan (Pongo pygmaeus). Current Biology, 1996, 6, 1326-1336.	1.8	95

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127	Pangolin genomes and the evolution of mammalian scales and immunity. Genome Research, 2016, 26, 1312-1322.	2.4	95
128	Significant Admixture Linkage Disequilibrium across 30 cM around the FY Locus in African Americans. American Journal of Human Genetics, 2000, 66, 969-978.	2.6	93
129	Mapping of the gene encoding the \hat{l}_{\pm} subunit of the stimulatory G protein of adenylyl cyclase (GNAS1) to 20q13.2 \hat{a}_{\pm} q13.3 in human by in situ hybridization. Genomics, 1991, 11, 478-479.	1.3	92
130	Mutation in CEP290 Discovered for Cat Model of Human Retinal Degeneration. Journal of Heredity, 2007, 98, 211-220.	1.0	92
131	White shark genome reveals ancient elasmobranch adaptations associated with wound healing and the maintenance of genome stability. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4446-4455.	3.3	92
132	Pet cat hair implicates murder suspect. Nature, 1997, 386, 774-774.	13.7	91
133	The Evolutionary Dynamics of the Lion Panthera leo Revealed by Host and Viral Population Genomics. PLoS Genetics, 2008, 4, e1000251.	1.5	91
134	The Principal Genetic Determinants for Nasopharyngeal Carcinoma in China Involve the HLA Class I Antigen Recognition Groove. PLoS Genetics, 2012, 8, e1003103.	1.5	91
135	Genomic Microsatellites as Evolutionary Chronometers: A Test in Wild Cats. Genome Research, 2002, 12, 414-423.	2.4	90
136	The Evolution Cats. Scientific American, 2007, 297, 68-75.	1.0	90
137	A homozygous single-base deletion in MLPH causes the dilute coat color phenotype in the domestic cat. Genomics, 2006, 88, 698-705.	1.3	89
138	Evolution of CRISPs Associated with Toxicoferan-Reptilian Venom and Mammalian Reproduction. Molecular Biology and Evolution, 2012, 29, 1807-1822.	3. 5	89
139	Genome-wide Mycobacterium tuberculosis variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. BMC Genomics, 2014, 15, 308.	1.2	89
140	The Asian arowana (Scleropages formosus) genome provides new insights into the evolution of an early lineage of teleosts. Scientific Reports, 2016, 6, 24501.	1.6	89
141	A molecular approach to the identification and individualization of human and animal cells in culture: Isozyme and allozyme genetic signatures. In Vitro, 1980, 16, 119-135.	1.2	87
142	Phylogeographic Patterns and Evolution of the Mitochondrial DNA Control Region in Two Neotropical Cats (Mammalia, Felidae). Journal of Molecular Evolution, 1998, 47, 613-624.	0.8	87
143	Elevated male European and female African contributions to the genomes of African American individuals. Human Genetics, 2006, 120, 713-722.	1.8	84
144	Pandas, people and policy. Nature, 1994, 369, 179-180.	13.7	83

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145	Genetic Protection against Hepatitis B Virus Conferred by CCR51"32: Evidence that CCR5 Contributes to Viral Persistence. Journal of Virology, 2007, 81, 441-445.	1.5	83
146	Mapping of an endogenous retroviral sequence to human chromosome 18. Nature, 1983, 303, 74-77.	13.7	80
147	Polygenic and Multifactorial Disease Gene Association in Man: Lessons from AIDS. Annual Review of Genetics, 2000, 34, 563-591.	3.2	80
148	Evolutionary analysis of a large mtDNA translocation (numt) into the nuclear genome of the Panthera genus species. Gene, 2006, 366, 292-302.	1.0	79
149	State of cat genomics. Trends in Genetics, 2008, 24, 268-279.	2.9	79
150	Mitochondrial DNA haplogroups influence AIDS progression. Aids, 2008, 22, 2429-2439.	1.0	78
151	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. Genome Research, 2011, 21, 137-145.	2.4	78
152	Evidence of Natural Bluetongue Virus Infection among African Carnivores. American Journal of Tropical Medicine and Hygiene, 1994, 51, 568-576.	0.6	78
153	Chromosomal localization of the genes encoding two forms of the G protein \hat{l}^2 polypeptide, \hat{l}^21 and \hat{l}^23 , in man. Genomics, 1990, 8, 380-386.	1.3	77
154	A Common HLA–DPA1 Variant is a Major Determinant of Hepatitis B Virus Clearance in Han Chinese. Journal of Infectious Diseases, 2011, 203, 943-947.	1.9	76
155	Mannose Binding Lectin Genotypes Influence Recovery from Hepatitis B Virus Infection. Journal of Virology, 2005, 79, 9192-9196.	1.5	73
156	Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. Molecular Biology and Evolution, 2015, 32, 2832-2843.	3.5	73
157	Safety issues in cell-based intervention trials. Fertility and Sterility, 2003, 80, 1077-1085.	0.5	72
158	Four Independent Mutations in the Feline Fibroblast Growth Factor 5 Gene Determine the Long-Haired Phenotype in Domestic Cats. Journal of Heredity, 2007, 98, 555-566.	1.0	71
159	Molecular evolution and the role of oxidative stress in the expansion and functional diversification of cytosolic glutathione transferases. BMC Evolutionary Biology, 2010, 10, 281.	3.2	71
160	Evolution of a Major Drug Metabolizing Enzyme Defect in the Domestic Cat and Other Felidae: Phylogenetic Timing and the Role of Hypercarnivory. PLoS ONE, 2011, 6, e18046.	1.1	71
161	Influence of CCR5 promoter haplotypes on AIDS progression in African–Americans. Aids, 2000, 14, 2117-2122.	1.0	70
162	The Origin of Human Chromosome 1 and Its Homologs in Placental Mammals. Genome Research, 2003, 13, 1880-8.	2.4	70

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163	CCL3L1 and HIV/AIDS susceptibility. Nature Medicine, 2009, 15, 1110-1112.	15.2	70
164	The evolutionary history of extinct and living lions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10927-10934.	3.3	70
165	Disparate phylogeographic patterns of molecular genetic variation in four closely related South American small cat species. Molecular Ecology, 1999, 8, S79-S94.	2.0	69
166	Ancestral primate viewed. Nature, 1999, 402, 365-366.	13.7	69
167	Mitochondrial DNA Haplogroups Influence Lipoatrophy After Highly Active Antiretroviral Therapy. Journal of Acquired Immune Deficiency Syndromes (1999), 2009, 51, 111-116.	0.9	69
168	Rapid Radiation Events in the Family Ursidae Indicated by Likelihood Phylogenetic Estimation from Multiple Fragments of mtDNA. Molecular Phylogenetics and Evolution, 1999, 13, 82-92.	1.2	68
169	Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. GigaScience, 2016, 5, 38.	3.3	68
170	Considering genetic profiles in functional studies of immune responsiveness to HIV-1. Immunology Letters, 2001, 79, 131-140.	1.1	67
171	EPIZOOTIOLOGY AND MANAGEMENT OF FELINE LEUKEMIA VIRUS IN THE FLORIDA PUMA. Journal of Wildlife Diseases, 2008, 44, 537-552.	0.3	67
172	Multistage Genomewide Association Study Identifies a Locus at 1q41 Associated with Rate of HIVâ€1 Disease Progression to Clinical AIDS. Journal of Infectious Diseases, 2010, 201, 618-626.	1.9	67
173	Public Stem Cell Banks: Considerations of Justice in Stem Cell Research and Therapy. Hastings Center Report, 2003, 33, 13.	0.7	66
174	Endogenous Retrovirus Insertion in the <i> KIT </i> Oncogene Determines <i> White </i> and <i> White spotting </i> in Domestic Cats. G3: Genes, Genomes, Genetics, 2014, 4, 1881-1891.	0.8	66
175	Captive breeding of the cheetah (Acinonyx jubatus) in North American zoos (1871-1986). Zoo Biology, 1989, 8, 3-16.	0.5	65
176	Association of Polymorphisms in Human Leukocyte Antigen Class I and Transporter Associated with Antigen Processing Genes with Resistance to Human Immunodeficiency Virus Type 1 Infection. Journal of Infectious Diseases, 2003, 187, 1404-1410.	1.9	65
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