

# Svante PÃ¤Ã¤bo

## List of Publications by Year in descending order

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Version: 2024-02-01

214  
papers

57,342  
citations

1296

112  
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2402

204  
g-index

236  
all docs

236  
docs citations

236  
times ranked

39513  
citing authors

#	ARTICLE	IF	CITATIONS
1	The earliest Denisovans and their cultural adaptation. <i>Nature Ecology and Evolution</i> , 2022, 6, 28-35.	3.4	19
2	Improved gRNA secondary structures allow editing of target sites resistant to CRISPR-Cas9 cleavage. <i>Nature Communications</i> , 2022, 13, 489.	5.8	35
3	A substitution in the glutathione reductase lowers electron leakage and inflammation in modern humans. <i>Science Advances</i> , 2022, 8, eabm1148.	4.7	5
4	Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	41
5	The clinically relevant CYP2C8*3 and CYP2C9*2 haplotype is inherited from Neandertals. <i>Pharmacogenomics Journal</i> , 2022, 22, 247-249.	0.9	7
6	A genomic region associated with protection against severe COVID-19 is inherited from Neandertals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	167
7	Point-of-care bulk testing for SARS-CoV-2 by combining hybridization capture with improved colorimetric LAMP. <i>Nature Communications</i> , 2021, 12, 1467.	5.8	81
8	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. <i>Nature</i> , 2021, 592, 253-257.	13.7	119
9	Reduced purine biosynthesis in humans after their divergence from Neandertals. <i>ELife</i> , 2021, 10, .	2.8	12
10	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. <i>Nature</i> , 2021, 595, 399-403.	13.7	67
11	Comment on "Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment". <i>Science</i> , 2021, 374, eabi6060.	6.0	19
12	A Neanderthal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. <i>Current Biology</i> , 2020, 30, 3465-3469.e4.	1.8	33
13	Human Stem Cell Resources Are an Inroad to Neanderthal DNA Functions. <i>Stem Cell Reports</i> , 2020, 15, 214-225.	2.3	18
14	The major genetic risk factor for severe COVID-19 is inherited from Neanderthals. <i>Nature</i> , 2020, 587, 610-612.	13.7	437
15	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. <i>Science</i> , 2020, 370, 584-587.	6.0	129
16	Denisovan ancestry and population history of early East Asians. <i>Science</i> , 2020, 370, 579-583.	6.0	57
17	Single-cell-resolution transcriptome map of human, chimpanzee, bonobo, and macaque brains. <i>Genome Research</i> , 2020, 30, 776-789.	2.4	97
18	Initial Upper Palaeolithic <i>Homo sapiens</i> from Bacho Kiro Cave, Bulgaria. <i>Nature</i> , 2020, 581, 299-302.	13.7	188

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19	A high-coverage Neandertal genome from Chagyrskaya Cave. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15132-15136.	3.3	176
20	The Neandertal Progesterone Receptor. Molecular Biology and Evolution, 2020, 37, 2655-2660.	3.5	38
21	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. PLoS ONE, 2020, 15, e0244824.	1.1	12
22	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
23	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
24	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
25	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
26	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
27	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
28	Simultaneous precise editing of multiple genes in human cells. Nucleic Acids Research, 2019, 47, e116-e116.	6.5	85
29	A genetic analysis of the Gibraltar Neanderthals. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15610-15615.	3.3	30
30	Compound-specific radiocarbon dating and mitochondrial DNA analysis of the Pleistocene hominin from Salkhit Mongolia. Nature Communications, 2019, 10, 274.	5.8	39
31	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. Nature, 2019, 565, 640-644.	13.7	137
32	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. Science Advances, 2019, 5, eaaw5873.	4.7	52
33	FINDER project: collagen fingerprinting (ZooMS) for the identification of new human fossils. Antiquity, 2019, 93, .	0.5	8
34	Organoid single-cell genomic atlas uncovers human-specific features of brain development. Nature, 2019, 574, 418-422.	13.7	496
35	Limits of long-term selection against Neandertal introgression. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1639-1644.	3.3	151
36	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. Current Biology, 2019, 29, 120-127.e5.	1.8	86

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37	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018, 360, 548-552.	6.0	142
38	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	13.7	197
39	The Predecessors Within . . . <i>Cell</i> , 2018, 173, 6-7.	13.5	14
40	Molecular comparison of Neanderthal and Modern Human adenylosuccinate lyase. <i>Scientific Reports</i> , 2018, 8, 18008.	1.6	6
41	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018, 9, 5018.	5.8	86
42	The genome of the offspring of a Neanderthal mother and a Denisovan father. <i>Nature</i> , 2018, 561, 113-116.	13.7	323
43	Direct radiocarbon dating and DNA analysis of the Darra-i-Kur (Afghanistan) human temporal bone. <i>Journal of Human Evolution</i> , 2017, 107, 86-93.	1.3	19
44	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , 2017, 356, 605-608.	6.0	329
45	Lipidome determinants of maximal lifespan in mammals. <i>Scientific Reports</i> , 2017, 7, 5.	1.6	60
46	Expression of the human isoform of glutamate dehydrogenase, hGDH2, augments TCA cycle capacity and oxidative metabolism of glutamate during glucose deprivation in astrocytes. <i>Glia</i> , 2017, 65, 474-488.	2.5	30
47	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	6.0	501
48	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	13.5	308
49	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , 2017, 27, 3202-3208.e9.	1.8	191
50	A fourth Denisovan individual. <i>Science Advances</i> , 2017, 3, e1700186.	4.7	74
51	Direct dating of Neanderthal remains from the site of Vindija Cave and implications for the Middle to Upper Paleolithic transition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10606-10611.	3.3	100
52	Changes in Lipidome Composition during Brain Development in Humans, Chimpanzees, and Macaque Monkeys. <i>Molecular Biology and Evolution</i> , 2017, 34, 1155-1166.	3.5	28
53	Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism. <i>PLoS Biology</i> , 2016, 14, e1002558.	2.6	73
54	A single splice site mutation in human-specific <i>ARHGAP11B</i> causes basal progenitor amplification. <i>Science Advances</i> , 2016, 2, e1601941.	4.7	77

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55	Excess maternal transmission of variants in the THADA gene to offspring with type 2 diabetes. <i>Diabetologia</i> , 2016, 59, 1702-1713.	2.9	19
56	Mice carrying a human <i>GLUD2</i> gene recapitulate aspects of human transcriptome and metabolome development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5358-5363.	3.3	28
57	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	13.7	729
58	Genetic Time Travel. <i>Genetics</i> , 2016, 203, 9-12.	1.2	23
59	<i>Foxp2</i> controls synaptic wiring of corticostriatal circuits and vocal communication by opposing <i>Mef2c</i> . <i>Nature Neuroscience</i> , 2016, 19, 1513-1522.	7.1	99
60	Palaeoproteomic evidence identifies archaic hominins associated with the Châtelperronian at the Grotte du Renne. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11162-11167.	3.3	251
61	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
62	Identification of a new hominin bone from Denisova Cave, Siberia using collagen fingerprinting and mitochondrial DNA analysis. <i>Scientific Reports</i> , 2016, 6, 23559.	1.6	144
63	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , 2016, 352, 235-239.	6.0	391
64	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , 2016, 530, 429-433.	13.7	392
65	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. <i>Nature</i> , 2016, 531, 504-507.	13.7	436
66	Functional Analyses of Transcription Factor Binding Sites that Differ between Present-Day and Archaic Humans. <i>Molecular Biology and Evolution</i> , 2016, 33, 316-322.	3.5	19
67	Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. <i>ELife</i> , 2016, 5, .	2.8	200
68	Nuclear and mitochondrial DNA sequences from two Denisovan individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15696-15700.	3.3	154
69	Human cerebral organoids recapitulate gene expression programs of fetal neocortex development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15672-15677.	3.3	870
70	The contribution of ancient hominin genomes from Siberia to our understanding of human evolution. <i>Herald of the Russian Academy of Sciences</i> , 2015, 85, 392-396.	0.2	2
71	Organization and Evolution of Brain Lipidome Revealed by Large-Scale Analysis of Human, Chimpanzee, Macaque, and Mouse Tissues. <i>Neuron</i> , 2015, 85, 695-702.	3.8	123
72	Long-Term Balancing Selection in <i>LAD1</i> Maintains a Missense Trans-Species Polymorphism in Humans, Chimpanzees, and Bonobos. <i>Molecular Biology and Evolution</i> , 2015, 32, 1186-1196.	3.5	70

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73	Human-specific gene <i>ARHGAP11B</i> promotes basal progenitor amplification and neocortex expansion. <i>Science</i> , 2015, 347, 1465-1470.	6.0	487
74	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , 2015, 524, 216-219.	13.7	633
75	The diverse origins of the human gene pool. <i>Nature Reviews Genetics</i> , 2015, 16, 313-314.	7.7	70
76	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , 2015, 10, e0134548.	1.1	7
77	Exceptional Evolutionary Divergence of Human Muscle and Brain Metabolomes Parallels Human Cognitive and Physical Uniqueness. <i>PLoS Biology</i> , 2014, 12, e1001871.	2.6	80
78	Genetic Influences on Brain Gene Expression in Rats Selected for Tameness and Aggression. <i>Genetics</i> , 2014, 198, 1277-1290.	1.2	78
79	Primate iPS cells as tools for evolutionary analyses. <i>Stem Cell Research</i> , 2014, 12, 622-629.	0.3	61
80	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. <i>Science</i> , 2014, 344, 523-527.	6.0	188
81	The Human Condition—A Molecular Approach. <i>Cell</i> , 2014, 157, 216-226.	13.5	175
82	Patterns of coding variation in the complete exomes of three Neandertals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6666-6671.	3.3	223
83	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , 2014, 5, 3584.	5.8	70
84	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	13.7	1,830
85	Separating endogenous ancient DNA from modern day contamination in a Siberian Neanderthal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2229-2234.	3.3	349
86	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	13.7	877
87	A mitochondrial genome sequence of a hominin from Sima de los Huesos. <i>Nature</i> , 2014, 505, 403-406.	13.7	434
88	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	13.7	856
89	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
90	Humanized <i>Foxp2</i> accelerates learning by enhancing transitions from declarative to procedural performance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14253-14258.	3.3	156

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91	Analysis of Candidate Genes for Lineage-Specific Expression Changes in Humans and Primates. <i>Journal of Proteome Research</i> , 2014, 13, 3596-3606.	1.8	7
92	Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15758-15763.	3.3	1,097
93	DNA analysis of an early modern human from Tianyuan Cave, China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2223-2227.	3.3	484
94	A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene. <i>Molecular Biology and Evolution</i> , 2013, 30, 844-852.	3.5	205
95	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. <i>Current Biology</i> , 2013, 23, 553-559.	1.8	540
96	Ancient DNA Damage. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012567-a012567.	2.3	348
97	Identification of Putative Target Genes of the Transcription Factor RUNX2. <i>PLoS ONE</i> , 2013, 8, e83218.	1.1	27
98	A Comparison of Brain Gene Expression Levels in Domesticated and Wild Animals. <i>PLoS Genetics</i> , 2012, 8, e1002962.	1.5	130
99	Analysis of Human Accelerated DNA Regions Using Archaic Hominin Genomes. <i>PLoS ONE</i> , 2012, 7, e32877.	1.1	38
100	Temporal Patterns of Nucleotide Misincorporations and DNA Fragmentation in Ancient DNA. <i>PLoS ONE</i> , 2012, 7, e34131.	1.1	428
101	The Date of Interbreeding between Neandertals and Modern Humans. <i>PLoS Genetics</i> , 2012, 8, e1002947.	1.5	402
102	Extension of cortical synaptic development distinguishes humans from chimpanzees and macaques. <i>Genome Research</i> , 2012, 22, 611-622.	2.4	224
103	Generation times in wild chimpanzees and gorillas suggest earlier divergence times in great ape and human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15716-15721.	3.3	499
104	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	6.0	1,695
105	Complete Mitochondrial Genomes Reveal Neolithic Expansion into Europe. <i>PLoS ONE</i> , 2012, 7, e32473.	1.1	61
106	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012, 486, 527-531.	13.7	445
107	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011, 7, 548.	3.2	878
108	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011, 478, 343-348.	13.7	1,080

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109	Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania. <i>American Journal of Human Genetics</i> , 2011, 89, 516-528.	2.6	525
110	A Comprehensive Functional Analysis of Ancestral Human Signal Peptides. <i>Molecular Biology and Evolution</i> , 2011, 28, 25-28.	3.5	4
111	MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. <i>PLoS Biology</i> , 2011, 9, e1001214.	2.6	198
112	MicroRNA Expression and Regulation in Human, Chimpanzee, and Macaque Brains. <i>PLoS Genetics</i> , 2011, 7, e1002327.	1.5	126
113	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.	6.0	255
114	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	6.0	3,588
115	A Complete mtDNA Genome of an Early Modern Human from Kostenki, Russia. <i>Current Biology</i> , 2010, 20, 231-236.	1.8	252
116	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. <i>Nature</i> , 2010, 464, 894-897.	13.7	659
117	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	13.7	1,537
118	Multiplexed DNA Sequence Capture of Mitochondrial Genomes Using PCR Products. <i>PLoS ONE</i> , 2010, 5, e14004.	1.1	471
119	Intergenic and Repeat Transcription in Human, Chimpanzee and Macaque Brains Measured by RNA-Seq. <i>PLoS Computational Biology</i> , 2010, 6, e1000843.	1.5	62
120	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. <i>Nucleic Acids Research</i> , 2010, 38, e87-e87.	6.5	362
121	A functional test of Neandertal and modern human mitochondrial targeting sequences. <i>Biochemical and Biophysical Research Communications</i> , 2010, 402, 747-749.	1.0	1
122	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010, 11, R47.	13.9	135
123	Optimization of 454 sequencing library preparation from small amounts of DNA permits sequence determination of both DNA strands. <i>BioTechniques</i> , 2009, 46, 51-57.	0.8	40
124	Linkage Disequilibrium Extends Across Putative Selected Sites in FOXP2. <i>Molecular Biology and Evolution</i> , 2009, 26, 2181-2184.	3.5	51
125	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009, 28, 2494-2502.	3.5	170
126	A Humanized Version of Foxp2 Affects Cortico-Basal Ganglia Circuits in Mice. <i>Cell</i> , 2009, 137, 961-971.	13.5	555



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127	Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. <i>Science</i> , 2009, 325, 318-321.	6.0	456
128	Primer Extension Capture: Targeted Sequence Retrieval from Heavily Degraded DNA Sources. <i>Journal of Visualized Experiments</i> , 2009, , 1573.	0.2	22
129	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. <i>BMC Evolutionary Biology</i> , 2008, 8, 220.	3.2	261
130	Metabolic changes in schizophrenia and human brain evolution. <i>Genome Biology</i> , 2008, 9, R124.	13.9	89
131	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.	13.5	503
132	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2008, 36, e5-e5.	6.5	105
133	Human and Chimpanzee Gene Expression Differences Replicated in Mice Fed Different Diets. <i>PLoS ONE</i> , 2008, 3, e1504.	1.1	41
134	Patterns of damage in genomic DNA sequences from a Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14616-14621.	3.3	799
135	Molecular breeding of polymerases for amplification of ancient DNA. <i>Nature Biotechnology</i> , 2007, 25, 939-943.	9.4	115
136	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007, 449, 902-904.	13.7	293
137	FUNC: a package for detecting significant associations between gene sets and ontological annotations. <i>BMC Bioinformatics</i> , 2007, 8, 41.	1.2	180
138	The Derived FOXP2 Variant of Modern Humans Was Shared with Neandertals. <i>Current Biology</i> , 2007, 17, 1908-1912.	1.8	487
139	Sequencing and Analysis of Neandertal Genomic DNA. <i>Science</i> , 2006, 314, 1113-1118.	6.0	547
140	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. <i>Nature</i> , 2006, 439, 724-727.	13.7	194
141	Evolution of primate gene expression. <i>Nature Reviews Genetics</i> , 2006, 7, 693-702.	7.7	279
142	Analysis of one million base pairs of Neandertal DNA. <i>Nature</i> , 2006, 444, 330-336.	13.7	671
143	Aspm specifically maintains symmetric proliferative divisions of neuroepithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10438-10443.	3.3	379
144	Neandertals. <i>Current Biology</i> , 2006, 16, R113-R114.	1.8	10

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145	Positive selection on gene expression in the human brain. <i>Current Biology</i> , 2006, 16, R356-R358.	1.8	50
146	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. <i>Current Biology</i> , 2006, 16, R629-R630.	1.8	68
147	No Evidence of Neandertal mtDNA Contribution to Early Modern Humans. , 2006, , 491-503.		4
148	Analyses moléculaires de la spécificité humaine. , 2006, , 27-36.		0
149	A late Neandertal femur from Les Rochers-de-Villeneuve, France. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7085-7090.	3.3	90
150	Aging and Gene Expression in the Primate Brain. <i>PLoS Biology</i> , 2005, 3, e274.	2.6	160
151	The Population History of Extant and Extinct Hyenas. <i>Molecular Biology and Evolution</i> , 2005, 22, 2435-2443.	3.5	128
152	Toward a Neutral Evolutionary Model of Gene Expression. <i>Genetics</i> , 2005, 170, 929-939.	1.2	96
153	Why do human diversity levels vary at a megabase scale?. <i>Genome Research</i> , 2005, 15, 1222-1231.	2.4	156
154	Parallel Patterns of Evolution in the Genomes and Transcriptomes of Humans and Chimpanzees. <i>Science</i> , 2005, 309, 1850-1854.	6.0	550
155	Genomic Sequencing of Pleistocene Cave Bears. <i>Science</i> , 2005, 309, 597-599.	6.0	221
156	Functional analysis of human and chimpanzee promoters. <i>Genome Biology</i> , 2005, 6, R57.	13.9	19
157	A Neutral Model of Transcriptome Evolution. <i>PLoS Biology</i> , 2004, 2, e132.	2.6	294
158	Evidence for a Complex Demographic History of Chimpanzees. <i>Molecular Biology and Evolution</i> , 2004, 21, 799-808.	3.5	114
159	Evidence for Reproductive Isolation between Cave Bear Populations. <i>Current Biology</i> , 2004, 14, 40-43.	1.8	100
160	Differences in DNA methylation patterns between humans and chimpanzees. <i>Current Biology</i> , 2004, 14, R148-R149.	1.8	58
161	Lack of phylogeography in European mammals before the last glaciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12963-12968.	3.3	201
162	Genetic Analyses from Ancient DNA. <i>Annual Review of Genetics</i> , 2004, 38, 645-679.	3.2	1,084

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163	COMPARATIVE PRIMATE GENOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 351-378.	2.5	148
164	Regional Patterns of Gene Expression in Human and Chimpanzee Brains. Genome Research, 2004, 14, 1462-1473.	2.4	311
165	No Evidence of Neandertal mtDNA Contribution to Early Modern Humans. PLoS Biology, 2004, 2, e57.	2.6	327
166	Nuclear Gene Sequences from a Late Pleistocene Sloth Coprolite. Current Biology, 2003, 13, 1150-1152.	1.8	115
167	The mosaic that is our genome. Nature, 2003, 421, 409-412.	13.7	153
168	Selection on Human Genes as Revealed by Comparisons to Chimpanzee cDNA. Genome Research, 2003, 13, 831-837.	2.4	130
169	Early Allelic Selection in Maize as Revealed by Ancient DNA. Science, 2003, 302, 1206-1208.	6.0	287
170	The eternal molecule. , 2003, , 82-139.		0
171	The Neandertal type site revisited: Interdisciplinary investigations of skeletal remains from the Neander Valley, Germany. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13342-13347.	3.3	177
172	Inactivation of CMP-N-acetylneuraminic acid hydroxylase occurred prior to brain expansion during human evolution. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11736-11741.	3.3	313
173	Ancient DNA Analyses Reveal High Mitochondrial DNA Sequence Diversity and Parallel Morphological Evolution of Late Pleistocene Cave Bears. Molecular Biology and Evolution, 2002, 19, 1244-1250.	3.5	94
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