

Svante Pbo

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.

224
papers

42,579
citations

104
h-index

206
g-index

236
ext. papers

51,617
ext. citations

20.9
avg, IF

7.14
L-index

#	Paper	IF	Citations
224	Improved gRNA secondary structures allow editing of target sites resistant to CRISPR-Cas9 cleavage.. <i>Nature Communications</i> , 2022 , 13, 489	17.4	1
223	A substitution in the glutathione reductase lowers electron leakage and inflammation in modern humans.. <i>Science Advances</i> , 2022 , 8, eabm1148	14.3	0
222	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,	11.5	6
221	The earliest Denisovans and their cultural adaptation. <i>Nature Ecology and Evolution</i> , 2021 ,	12.3	6
220	Comment on "Reintroduction of the archaic variant of in cortical organoids alters neurodevelopment". <i>Science</i> , 2021 , 374, eabi6060	33.3	6
219	Point-of-care bulk testing for SARS-CoV-2 by combining hybridization capture with improved colorimetric LAMP. <i>Nature Communications</i> , 2021 , 12, 1467	17.4	36
218	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. <i>Nature</i> , 2021 , 592, 253-257	50.4	29
217	Reduced purine biosynthesis in humans after their divergence from Neandertals. <i>ELife</i> , 2021 , 10,	8.9	2
216	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. <i>Nature</i> , 2021 , 595, 399-403	50.4	18
215	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,	11.5	53
214	Single-cell-resolution transcriptome map of human, chimpanzee, bonobo, and macaque brains. <i>Genome Research</i> , 2020 , 30, 776-789	9.7	32
213	Initial Upper Palaeolithic Homo sapiens from Bacho Kiro Cave, Bulgaria. <i>Nature</i> , 2020 , 581, 299-302	50.4	92
212	A high-coverage Neandertal genome from Chagyrskaya Cave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15132-15136	11.5	76
211	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. <i>PLoS ONE</i> , 2020 , 15, e0244824	3.7	4
210	The Neandertal Progesterone Receptor. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2655-2660	8.3	22
209	A Neandertal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. <i>Current Biology</i> , 2020 , 30, 3465-3469.e4	6.3	10
208	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. <i>Stem Cell Reports</i> , 2020 , 15, 214-225	8	8

207	The major genetic risk factor for severe COVID-19 is inherited from Neanderthals. <i>Nature</i> , 2020 , 587, 610-612	50.4	212
206	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. <i>Science</i> , 2020 , 370, 584-587	33.3	40
205	Denisovan ancestry and population history of early East Asians. <i>Science</i> , 2020 , 370, 579-583	33.3	27
204	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2 2020 , 15, e0244824		
203	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2 2020 , 15, e0244824		
202	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2 2020 , 15, e0244824		
201	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2 2020 , 15, e0244824		
200	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2 2020 , 15, e0244824		
199	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2 2020 , 15, e0244824		
198	Compound-specific radiocarbon dating and mitochondrial DNA analysis of the Pleistocene hominin from Salkhit Mongolia. <i>Nature Communications</i> , 2019 , 10, 274	17.4	29
197	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. <i>Nature</i> , 2019 , 565, 640-644	50.4	97
196	Nuclear DNA from two early Neanderthals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , 2019 , 5, eaaw5873	14.3	31
195	Simultaneous precise editing of multiple genes in human cells. <i>Nucleic Acids Research</i> , 2019 , 47, e116	20.1	44
194	A genetic analysis of the Gibraltar Neanderthals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15610-15615	11.5	19
193	FINDER project: collagen fingerprinting (ZoomS) for the identification of new human fossils. <i>Antiquity</i> , 2019 , 93,	1	4
192	Organoid single-cell genomic atlas uncovers human-specific features of brain development. <i>Nature</i> , 2019 , 574, 418-422	50.4	233
191	Limits of long-term selection against Neanderthal introgression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1639-1644	11.5	83
190	Neanderthal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , 2019 , 29, 120-127.e5	6.3	44

189	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018 , 360, 548-552	33.3	83
188	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018 , 555, 652-656	50.4	138
187	The Predecessors Within ... <i>Cell</i> , 2018 , 173, 6-7	56.2	4
186	The genome of the offspring of a Neanderthal mother and a Denisovan father. <i>Nature</i> , 2018 , 561, 113-116	56.4	197
185	Molecular comparison of Neanderthal and Modern Human adenylosuccinate lyase. <i>Scientific Reports</i> , 2018 , 8, 18008	4.9	3
184	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018 , 9, 5018	17.4	43
183	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	3.1	10
182	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , 2017 , 356, 605-608	33.3	173
181	Lipidome determinants of maximal lifespan in mammals. <i>Scientific Reports</i> , 2017 , 7, 5	4.9	37
180	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	9	22
179	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017 , 358, 655-658	33.3	312
178	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017 , 171, 59-71.e21	56.2	201
177	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , 2017 , 27, 3202-3208.e9	6.3	108
176	A fourth Denisovan individual. <i>Science Advances</i> , 2017 , 3, e1700186	14.3	56
175	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	11.5	67
174	Changes in Lipidome Composition during Brain Development in Humans, Chimpanzees, and Macaque Monkeys. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1155-1166	8.3	20
173	Functional Analyses of Transcription Factor Binding Sites that Differ between Present-Day and Archaic Humans. <i>Molecular Biology and Evolution</i> , 2016 , 33, 316-22	8.3	14
172	Palaeoproteomic evidence identifies archaic hominins associated with the Chelperronian at the Grotte du Renne. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11162-11167	11.5	172

171	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016 , 538, 201-206	50.4	759
170	Identification of a new hominin bone from Denisova Cave, Siberia using collagen fingerprinting and mitochondrial DNA analysis. <i>Scientific Reports</i> , 2016 , 6, 23559	4.9	99
169	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , 2016 , 352, 235-9	33.3	262
168	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , 2016 , 530, 429-33	50.4	269
167	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. <i>Nature</i> , 2016 , 531, 504-7	50.4	319
166	Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. <i>ELife</i> , 2016 , 5,	8.9	128
165	Author response: Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development 2016 ,		5
164	Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism. <i>PLoS Biology</i> , 2016 , 14, e1002558	9.7	45
163	A single splice site mutation in human-specific causes basal progenitor amplification. <i>Science Advances</i> , 2016 , 2, e1601941	14.3	43
162	Excess maternal transmission of variants in the THADA gene to offspring with type 2 diabetes. <i>Diabetologia</i> , 2016 , 59, 1702-13	10.3	13
161	Mice carrying a human GLUD2 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, 5358-63	11.5	21
160	The genetic history of Ice Age Europe. <i>Nature</i> , 2016 , 534, 200-5	50.4	473
159	Genetic Time Travel. <i>Genetics</i> , 2016 , 203, 9-12	4	18
158	Foxp2 controls synaptic wiring of corticostriatal circuits and vocal communication by opposing Mef2c. <i>Nature Neuroscience</i> , 2016 , 19, 1513-1522	25.5	65
157	Human-specific gene ARHGAP11B promotes basal progenitor amplification and neocortex expansion. <i>Science</i> , 2015 , 347, 1465-70	33.3	347
156	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , 2015 , 524, 216-9	50.4	446
155	The diverse origins of the human gene pool. <i>Nature Reviews Genetics</i> , 2015 , 16, 313-4	30.1	60
154	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, 15696-700	11.5	124

153	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, 15672-7	11.5	579
152	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	0.7	1
151	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	13.9	94
150	Long-Term Balancing Selection in LAD1 Maintains a Missense Trans-Species Polymorphism in Humans, Chimpanzees, and Bonobos. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1186-96	8.3	47
149	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , 2015 , 10, e0134548	3.7	5
148	Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. <i>Science</i> , 2014 , 344, 523-7	33.3	142
147	The human condition-a molecular approach. <i>Cell</i> , 2014 , 157, 216-26	56.2	117
146	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, 6666-71	11.5	175
145	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , 2014 , 5, 3584	17.4	52
144	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014 , 505, 43-9	50.4	1339
143	Separating endogenous ancient DNA from modern day contamination in a Siberian Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2229-34	11.5	244
142	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014 , 507, 354-7	50.4	615
141	A mitochondrial genome sequence of a hominin from Sima de los Huesos. <i>Nature</i> , 2014 , 505, 403-6	50.4	341
140	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014 , 514, 445-9	50.4	635
139	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014 , 513, 409-13	50.4	812
138	Humanized Foxp2 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, 14253-8	11.5	128
137	Analysis of candidate genes for lineage-specific expression changes in humans and primates. <i>Journal of Proteome Research</i> , 2014 , 13, 3596-606	5.6	5
136	Exceptional evolutionary divergence of human muscle and brain metabolomes parallels human cognitive and physical uniqueness. <i>PLoS Biology</i> , 2014 , 12, e1001871	9.7	63

135	Genetic influences on brain gene expression in rats selected for tameness and aggression. <i>Genetics</i> , 2014 , 198, 1277-90	4	53
134	Primate iPS cells as tools for evolutionary analyses. <i>Stem Cell Research</i> , 2014 , 12, 622-9	1.6	41
133	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, 15758-63	11.5	759
132	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, 2223-7	11.5	353
131	A recent evolutionary change affects a regulatory element in the human FOXP2 gene. <i>Molecular Biology and Evolution</i> , 2013 , 30, 844-52	8.3	163
130	A revised timescale for human evolution based on ancient mitochondrial genomes. <i>Current Biology</i> , 2013 , 23, 553-559	6.3	387
129	Ancient DNA damage. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5,	10.2	208
128	Identification of putative target genes of the transcription factor RUNX2. <i>PLoS ONE</i> , 2013 , 8, e83218	3.7	21
127	The date of interbreeding between Neandertals and modern humans. <i>PLoS Genetics</i> , 2012 , 8, e1002947	6	317
126	Extension of cortical synaptic development distinguishes humans from chimpanzees and macaques. <i>Genome Research</i> , 2012 , 22, 611-22	9.7	157
125	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, 15716-21	11.5	365
124	A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , 2012 , 338, 222-6	33.3	1276
123	Complete mitochondrial genomes reveal neolithic expansion into Europe. <i>PLoS ONE</i> , 2012 , 7, e32473	3.7	49
122	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012 , 486, 527-31	50.4	350
121	A comparison of brain gene expression levels in domesticated and wild animals. <i>PLoS Genetics</i> , 2012 , 8, e1002962	6	91
120	Analysis of human accelerated DNA regions using archaic hominin genomes. <i>PLoS ONE</i> , 2012 , 7, e32877	3.7	32
119	Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. <i>PLoS ONE</i> , 2012 , 7, e34131	3.7	325
118	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011 , 7, 548	12.2	723

117	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011 , 478, 343-8	50.4	787
116	Denisova admixture and the first modern human dispersals into Southeast Asia and Oceania. <i>American Journal of Human Genetics</i> , 2011 , 89, 516-28	11	390
115	A comprehensive functional analysis of ancestral human signal peptides. <i>Molecular Biology and Evolution</i> , 2011 , 28, 25-8	8.3	3
114	MicroRNA-driven developmental remodeling in the brain distinguishes humans from other primates. <i>PLoS Biology</i> , 2011 , 9, e1001214	9.7	159
113	MicroRNA expression and regulation in human, chimpanzee, and macaque brains. <i>PLoS Genetics</i> , 2011 , 7, e1002327	6	101
112	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. <i>Nature</i> , 2010 , 464, 894-7	50.4	521
111	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60	50.4	1169
110	Multiplexed DNA sequence capture of mitochondrial genomes using PCR products. <i>PLoS ONE</i> , 2010 , 5, e14004	3.7	387
109	Intergenic and repeat transcription in human, chimpanzee and macaque brains measured by RNA-Seq. <i>PLoS Computational Biology</i> , 2010 , 6, e1000843	5	48
108	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. <i>Nucleic Acids Research</i> , 2010 , 38, e87	20.1	283
107	A functional test of Neandertal and modern human mitochondrial targeting sequences. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 402, 747-9	3.4	0
106	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010 , 11, R47	18.3	81
105	Targeted investigation of the Neandertal genome by array-based sequence capture. <i>Science</i> , 2010 , 328, 723-5	33.3	224
104	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
103	A complete mtDNA genome of an early modern human from Kostenki, Russia. <i>Current Biology</i> , 2010 , 20, 231-6	6.3	213
102	Optimization of 454 sequencing library preparation from small amounts of DNA permits sequence determination of both DNA strands. <i>BioTechniques</i> , 2009 , 46, 51-2, 54-7	2.5	37
101	Linkage disequilibrium extends across putative selected sites in FOXP2. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2181-4	8.3	33
100	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009 , 28, 2494-502	13	118

99	A humanized version of Foxp2 affects cortico-basal ganglia circuits in mice. <i>Cell</i> , 2009 , 137, 961-71	56.2	427
98	Targeted retrieval and analysis of five Neandertal mtDNA genomes. <i>Science</i> , 2009 , 325, 318-21	33.3	387
97	Primer extension capture: targeted sequence retrieval from heavily degraded DNA sources. <i>Journal of Visualized Experiments</i> , 2009 , 1573	1.6	16
96	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
95	Metabolic changes in schizophrenia and human brain evolution. <i>Genome Biology</i> , 2008 , 9, R124	18.3	77
94	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , 2008 , 134, 416-26	56.2	405
93	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2008 , 36, e5	20.1	100
92	Human and chimpanzee gene expression differences replicated in mice fed different diets. <i>PLoS ONE</i> , 2008 , 3, e1504	3.7	36
91	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, 14616-21	11.5	610
90	Molecular breeding of polymerases for amplification of ancient DNA. <i>Nature Biotechnology</i> , 2007 , 25, 939-43	44.5	99
89	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007 , 449, 902-4	50.4	243
88	FUNC: a package for detecting significant associations between gene sets and ontological annotations. <i>BMC Bioinformatics</i> , 2007 , 8, 41	3.6	137
87	The derived FOXP2 variant of modern humans was shared with Neandertals. <i>Current Biology</i> , 2007 , 17, 1908-12	6.3	376
86	Neandertals. <i>Current Biology</i> , 2006 , 16, R113-4	6.3	9
85	Positive selection on gene expression in the human brain. <i>Current Biology</i> , 2006 , 16, R356-8	6.3	44
84	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. <i>Current Biology</i> , 2006 , 16, R629-30	6.3	63
83	Sequencing and analysis of Neanderthal genomic DNA. <i>Science</i> , 2006 , 314, 1113-8	33.3	415
82	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. <i>Nature</i> , 2006 , 439, 724-7	50.4	167

81	Evolution of primate gene expression. <i>Nature Reviews Genetics</i> , 2006 , 7, 693-702	30.1	224
80	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006 , 444, 330-6	50.4	511
79	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	11.5	315
78	Analyses moléculaires de la spécificité humaine 2006 , 27-36		
77	No Evidence of Neanderthal mtDNA Contribution to Early Modern Humans 2006 , 491-503		2
76	Why do human diversity levels vary at a megabase scale?. <i>Genome Research</i> , 2005 , 15, 1222-31	9.7	125
75	Parallel patterns of evolution in the genomes and transcriptomes of humans and chimpanzees. <i>Science</i> , 2005 , 309, 1850-4	33.3	460
74	Genomic sequencing of Pleistocene cave bears. <i>Science</i> , 2005 , 309, 597-9	33.3	191
73	Functional analysis of human and chimpanzee promoters. <i>Genome Biology</i> , 2005 , 6, R57	18.3	17
72	A late Neanderthal femur from Les Rochers-de-Villeneuve, France. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7085-90	11.5	78
71	Aging and gene expression in the primate brain. <i>PLoS Biology</i> , 2005 , 3, e274	9.7	131
70	The population history of extant and extinct hyenas. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2435-43	8.3	105
69	Toward a neutral evolutionary model of gene expression. <i>Genetics</i> , 2005 , 170, 929-39	4	80
68	A neutral model of transcriptome evolution. <i>PLoS Biology</i> , 2004 , 2, E132	9.7	251
67	Evidence for a complex demographic history of chimpanzees. <i>Molecular Biology and Evolution</i> , 2004 , 21, 799-808	8.3	104
66	Evidence for reproductive isolation between cave bear populations. <i>Current Biology</i> , 2004 , 14, 40-3	6.3	88
65	Differences in DNA methylation patterns between humans and chimpanzees. <i>Current Biology</i> , 2004 , 14, R148-R149	6.3	50
64	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, 12963-8	11.5	187

63	Genetic analyses from ancient DNA. <i>Annual Review of Genetics</i> , 2004 , 38, 645-79	14.5	904
62	Comparative primate genomics. <i>Annual Review of Genomics and Human Genetics</i> , 2004 , 5, 351-78	9.7	132
61	Regional patterns of gene expression in human and chimpanzee brains. <i>Genome Research</i> , 2004 , 14, 1462-73	24.5	245
60	No evidence of Neandertal mtDNA contribution to early modern humans. <i>PLoS Biology</i> , 2004 , 2, E57	9.7	261
59	Early allelic selection in maize as revealed by ancient DNA. <i>Science</i> , 2003 , 302, 1206-8	33.3	224
58	Nuclear gene sequences from a late pleistocene sloth coprolite. <i>Current Biology</i> , 2003 , 13, 1150-2	6.3	108
57	The mosaic that is our genome. <i>Nature</i> , 2003 , 421, 409-12	50.4	118
56	Selection on human genes as revealed by comparisons to chimpanzee cDNA. <i>Genome Research</i> , 2003 , 13, 831-7	9.7	112
55	The eternal molecule 2003 , 82-139		
54	Molecular evolution of FOXP2, a gene involved in speech and language. <i>Nature</i> , 2002 , 418, 869-72	50.4	1128
53	The Neandertal type site revisited: interdisciplinary investigations of skeletal remains from the Neander Valley, Germany. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13342-7	11.5	155
52	Inactivation of CMP-N-acetylneuraminic acid hydroxylase occurred prior to brain expansion during human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 11736-41	11.5	239
51	Ancient DNA analyses reveal high mitochondrial DNA sequence diversity and parallel morphological evolution of late pleistocene cave bears. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1244-50	8.3	88
50	Intra- and interspecific variation in primate gene expression patterns. <i>Science</i> , 2002 , 296, 340-3	33.3	680
49	A molecular phylogeny of two extinct sloths. <i>Molecular Phylogenetics and Evolution</i> , 2001 , 18, 94-103	4.1	54
48	Great ape DNA sequences reveal a reduced diversity and an expansion in humans. <i>Nature Genetics</i> , 2001 , 27, 155-6	36.3	191
47	Ancient DNA. <i>Nature Reviews Genetics</i> , 2001 , 2, 353-9	30.1	667
46	Evidence for import of a lysyl-tRNA into marsupial mitochondria. <i>Molecular Biology of the Cell</i> , 2001 , 12, 2688-98	3.5	75

45	A view of Neandertal genetic diversity. <i>Nature Genetics</i> , 2000 , 26, 144-6	36.3	277
44	Mitochondrial genome variation and the origin of modern humans. <i>Nature</i> , 2000 , 408, 708-13	50.4	1062
43	Nuclear insertion sequences of mitochondrial DNA predominate in hair but not in blood of elephants. <i>Molecular Ecology</i> , 1999 , 8, 133-7	5.7	79
42	DNA sequence variation in a non-coding region of low recombination on the human X chromosome. <i>Nature Genetics</i> , 1999 , 22, 78-81	36.3	202
41	Human evolution. <i>Trends in Genetics</i> , 1999 , 15, M13-M16	8.5	11
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10	Single-cell-resolution transcriptome map of human, chimpanzee, bonobo, and macaque brains		1

9	Denisovan ancestry and population history of early East Asians	1
8	A high-coverage Neandertal genome from Chagyrskaya Cave	6
7	The major genetic risk factor for severe COVID-19 is inherited from Neandertals	15
6	A genetic variant protective against severe COVID-19 is inherited from Neandertals	4
5	The MERS-CoV receptor gene is among COVID-19 risk factors inherited from Neandertals	2
4	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe	2
3	The limits of long-term selection against Neandertal introgression	4
2	Single-cell genomic atlas of great ape cerebral organoids uncovers human-specific features of brain development	
1	Longer metaphase and fewer chromosome segregation errors in modern human than Neandertal brain development	1