

Janet Kelso

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.

120
papers

23,311
citations

56
h-index

134
g-index

134
ext. papers

28,743
ext. citations

16.8
avg, IF

6.28
L-index

#	Paper	IF	Citations
120	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow.. <i>Science Advances</i> , 2022 , 8, eabl6496	14.3	0
119	The earliest Denisovans and their cultural adaptation. <i>Nature Ecology and Evolution</i> , 2021 ,	12.3	6
118	Detection of Neanderthal Adaptively Introgressed Genetic Variants that Modulate Reporter Gene Expression in Human Immune Cells. <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	5
117	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021 , 599, 41-46	50.4	9
116	Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. <i>Science</i> , 2021 , 372,	33.3	21
115	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. <i>Nature</i> , 2021 , 592, 253-257	50.4	29
114	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. <i>Nature</i> , 2021 , 595, 399-403	50.4	18
113	Reduced lipolysis in lipoma phenocopies lipid accumulation in obesity. <i>International Journal of Obesity</i> , 2021 , 45, 565-576	5.5	6
112	A novel compound heterozygous leptin receptor mutation causes more severe obesity than in Lepr mice. <i>Journal of Lipid Research</i> , 2021 , 62, 100105	6.3	1
111	A high-coverage Neanderthal 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
110	The Neanderthal Progesterone Receptor. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2655-2660	8.3	22
109	A Neanderthal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. <i>Current Biology</i> , 2020 , 30, 3465-3469.e4	6.3	10
108	Human Stem Cell Resources Are an Inroad to Neanderthal DNA Functions. <i>Stem Cell Reports</i> , 2020 , 15, 214-225	8	8
107	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. <i>Science</i> , 2020 , 370, 584-587	33.3	40
106	Denisovan ancestry and population history of early East Asians. <i>Science</i> , 2020 , 370, 579-583	33.3	27
105	The evolutionary history of Neanderthal and Denisovan Y chromosomes. <i>Science</i> , 2020 , 369, 1653-1656	33.3	35
104	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

103	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , 2019 , 5, eaaw5873	14.3	31
102	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
101	admixr-R package for reproducible analyses using ADMIXTOOLS. <i>Bioinformatics</i> , 2019 , 35, 3194-3195	7.2	43
100	Immune Gene Diversity in Archaic and Present-day Humans. <i>Genome Biology and Evolution</i> , 2019 , 11, 232-241	3.9	4
99	Limits of long-term selection against Neandertal introgression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1639-1644	11.5	83
98	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , 2019 , 29, 120-127.e5	6.3	44
97	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018 , 555, 652-656	50.4	138
96	RNA-seq analysis identifies different transcriptomic types and developmental trajectories of primary melanomas. <i>Oncogene</i> , 2018 , 37, 6136-6151	9.2	49
95	The genome of the offspring of a Neanderthal mother and a Denisovan father. <i>Nature</i> , 2018 , 561, 113-116	50.4	197
94	Expression signatures of early-stage and advanced medaka melanomas. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2018 , 208, 20-28	3.2	8
93	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018 , 9, 5018	17.4	43
92	Functional implications of Neandertal introgression in modern humans. <i>Genome Biology</i> , 2017 , 18, 61	18.3	55
91	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , 2017 , 356, 605-608	33.3	173
90	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017 , 358, 655-658	33.3	312
89	The Contribution of Neanderthals to Phenotypic Variation in Modern Humans. <i>American Journal of Human Genetics</i> , 2017 , 101, 578-589	11	82
88	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
87	A fourth Denisovan individual. <i>Science Advances</i> , 2017 , 3, e1700186	14.3	56
86	Palaeoproteomic evidence identifies archaic hominins associated with the Chelpepperronian 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

85	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016 , 538, 201-206	50.4	759
84	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , 2016 , 167, 643-656.e17	56.2	224
83	Genetic Evidence of Human Adaptation to a Cooked Diet. <i>Genome Biology and Evolution</i> , 2016 , 8, 1091-1093	19.3	21
82	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , 2016 , 352, 235-9	33.3	262
81	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. <i>Nature</i> , 2016 , 531, 504-7	50.4	319
80	Introgression of Neandertal- and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. <i>American Journal of Human Genetics</i> , 2016 , 98, 22-33	11	156
79	ABAEnrichment: an R package to test for gene set expression enrichment in the adult and developing human brain. <i>Bioinformatics</i> , 2016 , 32, 3201-3203	7.2	20
78	What we have learned from Neanderthals about genes involved in energy metabolism and adiposity. <i>Neuropeptides</i> , 2016 , 55, 9	3.3	
77	The genetic history of Ice Age Europe. <i>Nature</i> , 2016 , 534, 200-5	50.4	473
76	Human-specific gene ARHGAP11B promotes basal progenitor amplification and neocortex expansion. <i>Science</i> , 2015 , 347, 1465-70	33.3	347
75	Kiwi genome provides insights into evolution of a nocturnal lifestyle. <i>Genome Biology</i> , 2015 , 16, 147	18.3	52
74	An early modern human from Romania with a recent Neandertal ancestor. <i>Nature</i> , 2015 , 524, 216-9	50.4	446
73	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. <i>Genome Biology</i> , 2015 , 16, 224	18.3	193
72	deML: robust demultiplexing of Illumina sequences using a likelihood-based approach. <i>Bioinformatics</i> , 2015 , 31, 770-2	7.2	115
71	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
70	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , 2015 , 10, e0134548	3.7	5
69	Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. <i>Science</i> , 2014 , 344, 523-7	33.3	142
68	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

67	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , 2014 , 5, 3584	17.4	52
66	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014 , 505, 43-9	50.4	1339
65	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. <i>Nature</i> , 2014 , 506, 97-101	50.4	323
64	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014 , 507, 354-7	50.4	615
63	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014 , 514, 445-9	50.4	635
62	Ancient humans and the origin of modern humans. <i>Current Opinion in Genetics and Development</i> , 2014 , 29, 133-8	4.9	21
61	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014 , 513, 409-13	50.4	812
60	leeHom: adaptor trimming and merging for Illumina sequencing reads. <i>Nucleic Acids Research</i> , 2014 , 42, e141	20.1	143
59	The earliest transcribed zygotic genes are short, newly evolved, and different across species. <i>Cell Reports</i> , 2014 , 6, 285-92	10.6	121
58	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
57	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
56	High-throughput sequencing of the melanoma genome. <i>Experimental Dermatology</i> , 2013 , 22, 10-7	4	31
55	freelbis: an efficient basecaller with calibrated quality scores for Illumina sequencers. <i>Bioinformatics</i> , 2013 , 29, 1208-9	7.2	68
54	ISCB computational biology Wikipedia competition. <i>PLoS Computational Biology</i> , 2013 , 9, e1003242	5	3
53	Annotation of primate miRNAs by high throughput sequencing of small RNA libraries. <i>BMC Genomics</i> , 2012 , 13, 116	4.5	14
52	A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , 2012 , 338, 222-6	33.3	1276
51	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012 , 486, 527-31	50.4	350
50	Impact of ontology evolution on functional analyses. <i>Bioinformatics</i> , 2012 , 28, 2671-7	7.2	26

49	Analysis of human accelerated DNA regions using archaic hominin genomes. <i>PLoS ONE</i> , 2012 , 7, e32877	3.7	32
48	Transcription factors are targeted by differentially expressed miRNAs in primates. <i>Genome Biology and Evolution</i> , 2012 , 4, 552-64	3.9	27
47	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011 , 7, 548	12.2	723
46	OBML - Ontologies in Biomedicine and Life Sciences. <i>Journal of Biomedical Semantics</i> , 2011 , 2 Suppl 4, 11	2.2	1
45	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 13, S1	3.6	15
44	Addressing challenges in the production and analysis of illumina sequencing data. <i>BMC Genomics</i> , 2011 , 12, 382	4.5	99
43	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60	50.4	1169
42	Statistical tests for associations between two directed acyclic graphs. <i>PLoS ONE</i> , 2010 , 5, e10996	3.7	3
41	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010 , 11, R47	18.3	81
40	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
39	Relations as patterns: bridging the gap between OBO and OWL. <i>BMC Bioinformatics</i> , 2010 , 11, 441	3.6	42
38	Applying the functional abnormality ontology pattern to anatomical functions. <i>Journal of Biomedical Semantics</i> , 2010 , 1, 4	2.2	12
37	High-throughput DNA sequencing--concepts and limitations. <i>BioEssays</i> , 2010 , 32, 524-36	4.1	397
36	Ontologies in Biology 2010 , 347-371		1
35	DATABASE: A new forum for biological databases and curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap002	5	6
34	The ontology of biological sequences. <i>BMC Bioinformatics</i> , 2009 , 10, 377	3.6	10
33	BOWiki: an ontology-based wiki for annotation of data and integration of knowledge in biology. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 5, S5	3.6	11
32	Improved base calling for the Illumina Genome Analyzer using machine learning strategies. <i>Genome Biology</i> , 2009 , 10, R83	18.3	188

31	Transcriptional neoteny in the human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 5743-8	11.5	261
30	Population transcriptomics of life-history variation in the genus <i>Salmo</i> . <i>Molecular Ecology</i> , 2008 , 17, 3095-108	5.1	40
29	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , 2008 , 134, 416-26	56.2	405
28	GFO-Bio: A biological core ontology. <i>Applied Ontology</i> , 2008 , 3, 219-227	1.4	12
27	PatMaN: rapid alignment of short sequences to large databases. <i>Bioinformatics</i> , 2008 , 24, 1530-1	7.2	148
26	Identification and analysis of genomic regions with large between-population differentiation in humans. <i>Annals of Human Genetics</i> , 2008 , 72, 99-110	2.2	52
25	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
24	Comparison of protein and mRNA expression evolution in humans and chimpanzees. <i>PLoS ONE</i> , 2007 , 2, e216	3.7	59
23	Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. <i>BMC Bioinformatics</i> , 2007 , 8, 377	3.6	34
22	A splice variant of the human CCA-adding enzyme with modified activity. <i>Journal of Molecular Biology</i> , 2007 , 366, 1258-65	6.5	12
21	Identifying genes underlying skin pigmentation differences among human populations. <i>Human Genetics</i> , 2007 , 120, 613-21	6.3	101
20	Positive selection on gene expression in the human brain. <i>Current Biology</i> , 2006 , 16, R356-8	6.3	44
19	A top-level ontology of functions and its application in the Open Biomedical Ontologies. <i>Bioinformatics</i> , 2006 , 22, e66-73	7.2	32
18	Functionality of intergenic transcription: an evolutionary comparison. <i>PLoS Genetics</i> , 2006 , 2, e171	6	59
17	A Proposal for a Gene Functions Wiki. <i>Lecture Notes in Computer Science</i> , 2006 , 669-678	0.9	4
16	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
15	The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate technologies and platforms. <i>Nucleic Acids Research</i> , 2005 , 33, D567-72	20.1	16
14	Integration of text- and data-mining using ontologies successfully selects disease gene candidates. <i>Nucleic Acids Research</i> , 2005 , 33, 1544-52	20.1	140

13	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
12	Allele-specific transcript isoforms in human. <i>FEBS Letters</i> , 2004 , 577, 233-8	3.8	29
11	eVOC: a controlled vocabulary for unifying gene expression data. <i>Genome Research</i> , 2003 , 13, 1222-30	9.7	132
10	The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13418-23	11.5	93
9	Transcriptome analysis of mouse stem cells and early embryos. <i>PLoS Biology</i> , 2003 , 1, E74	9.7	135
8	Application of eVOC: controlled vocabularies for unifying gene expression data. <i>Comptes Rendus - Biologies</i> , 2003 , 326, 1089-96	1.4	7
7	Assembly, verification, and initial annotation of the NIA mouse 7.4K cDNA clone set. <i>Genome Research</i> , 2002 , 12, 1999-2003	9.7	39
6	Impact of the presence of paralogs on sequence divergence in a set of mouse-human orthologs. <i>Genome Research</i> , 2002 , 12, 1370-6	9.7	49
5	The contribution of exon-skipping events on chromosome 22 to protein coding diversity. <i>Genome Research</i> , 2001 , 11, 1848-53	9.7	39
4	Denisovan ancestry and population history of early East Asians		1
3	A high-coverage Neandertal genome from Chagyrskaya Cave		6
2	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe		2
1	The limits of long-term selection against Neandertal introgression		4