

# Janet Kelso

## List of Publications by Citations

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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	The transcriptional landscape of the mammalian genome. <i>Science</i> , <b>2005</b> , 309, 1559-63	33.3	2807
119	A draft sequence of the Neandertal genome. <i>Science</i> , <b>2010</b> , 328, 710-722	33.3	2599
118	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , <b>2014</b> , 505, 43-9	50.4	1339
117	A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , <b>2012</b> , 338, 222-6	33.3	1276
116	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , <b>2010</b> , 468, 1053-60	50.4	1169
115	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , <b>2014</b> , 513, 409-13	50.4	812
114	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , <b>2016</b> , 538, 201-206	50.4	759
113	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 548	12.2	723
112	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , <b>2014</b> , 514, 445-9	50.4	635
111	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , <b>2014</b> , 507, 354-7	50.4	615
110	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> , <b>2007</b> , 104, 14616-21	11.5	610
109	The genetic history of Ice Age Europe. <i>Nature</i> , <b>2016</b> , 534, 200-5	50.4	473
108	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , <b>2015</b> , 524, 216-9	50.4	446
107	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , <b>2008</b> , 134, 416-26	56.2	405
106	High-throughput DNA sequencing--concepts and limitations. <i>BioEssays</i> , <b>2010</b> , 32, 524-36	4.1	397
105	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> , <b>2013</b> , 110, 2223-7	11.5	353
104	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , <b>2012</b> , 486, 527-31	50.4	350

103	Human-specific gene ARHGAP11B promotes basal progenitor amplification and neocortex expansion. <i>Science</i> , <b>2015</b> , 347, 1465-70	33.3	347
102	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. <i>Nature</i> , <b>2014</b> , 506, 97-101	50.4	323
101	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. <i>Nature</i> , <b>2016</b> , 531, 504-7	50.4	319
100	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , <b>2017</b> , 358, 655-658	33.3	312
99	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , <b>2016</b> , 352, 235-9	33.3	262
98	Transcriptional neoteny in the human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 5743-8	11.5	261
97	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , <b>2004</b> , 2, e162	9.7	255
96	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , <b>2016</b> , 167, 643-656.e17	56.2	224
95	The genome of the offspring of a Neanderthal mother and a Denisovan father. <i>Nature</i> , <b>2018</b> , 561, 113-116	56.4	197
94	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. <i>Genome Biology</i> , <b>2015</b> , 16, 224	18.3	193
93	Improved base calling for the Illumina Genome Analyzer using machine learning strategies. <i>Genome Biology</i> , <b>2009</b> , 10, R83	18.3	188
92	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> , <b>2014</b> , 111, 6666-71	11.5	175
91	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , <b>2017</b> , 356, 605-608	33.3	173
90	Palaeoproteomic evidence identifies archaic hominins associated with the Chelpperronian at the Grotte du Renne. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 11162-11167	11.5	172
89	A recent evolutionary change affects a regulatory element in the human FOXP2 gene. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 844-52	8.3	163
88	Introgression of Neandertal- and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 22-33	11	156
87	PatMaN: rapid alignment of short sequences to large databases. <i>Bioinformatics</i> , <b>2008</b> , 24, 1530-1	7.2	148
86	leeHom: adaptor trimming and merging for Illumina sequencing reads. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e141	20.1	143

85	Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. <i>Science</i> , <b>2014</b> , 344, 523-7	33.3	142
84	Integration of text- and data-mining using ontologies successfully selects disease gene candidates. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 1544-52	20.1	140
83	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , <b>2018</b> , 555, 652-656	50.4	138
82	Transcriptome analysis of mouse stem cells and early embryos. <i>PLoS Biology</i> , <b>2003</b> , 1, E74	9.7	135
81	eVOC: a controlled vocabulary for unifying gene expression data. <i>Genome Research</i> , <b>2003</b> , 13, 1222-30	9.7	132
80	Nuclear and mitochondrial DNA sequences from two Denisovan individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 15696-700	11.5	124
79	The earliest transcribed zygotic genes are short, newly evolved, and different across species. <i>Cell Reports</i> , <b>2014</b> , 6, 285-92	10.6	121
78	deML: robust demultiplexing of Illumina sequences using a likelihood-based approach. <i>Bioinformatics</i> , <b>2015</b> , 31, 770-2	7.2	115
77	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , <b>2017</b> , 27, 3202-3208.e9	6.3	108
76	Identifying genes underlying skin pigmentation differences among human populations. <i>Human Genetics</i> , <b>2007</b> , 120, 613-21	6.3	101
75	Addressing challenges in the production and analysis of Illumina sequencing data. <i>BMC Genomics</i> , <b>2011</b> , 12, 382	4.5	99
74	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. <i>Nature</i> , <b>2019</b> , 565, 640-644	50.4	97
73	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> , <b>2003</b> , 100, 13418-23	11.5	93
72	Limits of long-term selection against Neandertal introgression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 1639-1644	11.5	83
71	The Contribution of Neanderthals to Phenotypic Variation in Modern Humans. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 578-589	11	82
70	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , <b>2010</b> , 11, R47	18.3	81
69	A high-coverage Neandertal genome from Chagyrskaya Cave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 15132-15136	11.5	76
68	freelb: an efficient basecaller with calibrated quality scores for Illumina sequencers. <i>Bioinformatics</i> , <b>2013</b> , 29, 1208-9	7.2	68

67	Comparison of protein and mRNA expression evolution in humans and chimpanzees. <i>PLoS ONE</i> , <b>2007</b> , 2, e216	3.7	59
66	Functionality of intergenic transcription: an evolutionary comparison. <i>PLoS Genetics</i> , <b>2006</b> , 2, e171	6	59
65	A fourth Denisovan individual. <i>Science Advances</i> , <b>2017</b> , 3, e1700186	14.3	56
64	Functional implications of Neandertal introgression in modern humans. <i>Genome Biology</i> , <b>2017</b> , 18, 61	18.3	55
63	Kiwi genome provides insights into evolution of a nocturnal lifestyle. <i>Genome Biology</i> , <b>2015</b> , 16, 147	18.3	52
62	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , <b>2014</b> , 5, 3584	17.4	52
61	Identification and analysis of genomic regions with large between-population differentiation in humans. <i>Annals of Human Genetics</i> , <b>2008</b> , 72, 99-110	2.2	52
60	RNA-seq analysis identifies different transcriptomic types and developmental trajectories of primary melanomas. <i>Oncogene</i> , <b>2018</b> , 37, 6136-6151	9.2	49
59	Impact of the presence of paralogs on sequence divergence in a set of mouse-human orthologs. <i>Genome Research</i> , <b>2002</b> , 12, 1370-6	9.7	49
58	Positive selection on gene expression in the human brain. <i>Current Biology</i> , <b>2006</b> , 16, R356-8	6.3	44
57	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , <b>2019</b> , 29, 120-127.e5	6.3	44
56	admixr-R package for reproducible analyses using ADMIXTOOLS. <i>Bioinformatics</i> , <b>2019</b> , 35, 3194-3195	7.2	43
55	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , <b>2018</b> , 9, 5018	17.4	43
54	Relations as patterns: bridging the gap between OBO and OWL. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 441	3.6	42
53	Population transcriptomics of life-history variation in the genus <i>Salmo</i> . <i>Molecular Ecology</i> , <b>2008</b> , 17, 3095-1108	5.1	40
52	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. <i>Science</i> , <b>2020</b> , 370, 584-587	33.3	40
51	Assembly, verification, and initial annotation of the NIA mouse 7.4K cDNA clone set. <i>Genome Research</i> , <b>2002</b> , 12, 1999-2003	9.7	39
50	The contribution of exon-skipping events on chromosome 22 to protein coding diversity. <i>Genome Research</i> , <b>2001</b> , 11, 1848-53	9.7	39

49	The evolutionary history of Neanderthal and Denisovan Y chromosomes. <i>Science</i> , <b>2020</b> , 369, 1653-1656	33.3	35
48	Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 377	3.6	34
47	Analysis of human accelerated DNA regions using archaic hominin genomes. <i>PLoS ONE</i> , <b>2012</b> , 7, e32877	3.7	32
46	A top-level ontology of functions and its application in the Open Biomedical Ontologies. <i>Bioinformatics</i> , <b>2006</b> , 22, e66-73	7.2	32
45	Nuclear DNA from two early Neanderthals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , <b>2019</b> , 5, eaaw5873	14.3	31
44	High-throughput sequencing of the melanoma genome. <i>Experimental Dermatology</i> , <b>2013</b> , 22, 10-7	4	31
43	Allele-specific transcript isoforms in human. <i>FEBS Letters</i> , <b>2004</b> , 577, 233-8	3.8	29
42	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. <i>Nature</i> , <b>2021</b> , 592, 253-257	50.4	29
41	Transcription factors are targeted by differentially expressed miRNAs in primates. <i>Genome Biology and Evolution</i> , <b>2012</b> , 4, 552-64	3.9	27
40	Denisovan ancestry and population history of early East Asians. <i>Science</i> , <b>2020</b> , 370, 579-583	33.3	27
39	Impact of ontology evolution on functional analyses. <i>Bioinformatics</i> , <b>2012</b> , 28, 2671-7	7.2	26
38	The Neanderthal Progesterone Receptor. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 2655-2660	8.3	22
37	Genetic Evidence of Human Adaptation to a Cooked Diet. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 1091-1093	10.3	21
36	Ancient humans and the origin of modern humans. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 29, 133-8	4.9	21
35	Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. <i>Science</i> , <b>2021</b> , 372,	33.3	21
34	ABAEnrichment: an R package to test for gene set expression enrichment in the adult and developing human brain. <i>Bioinformatics</i> , <b>2016</b> , 32, 3201-3203	7.2	20
33	A genetic analysis of the Gibraltar Neanderthals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 15610-15615	11.5	19
32	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. <i>Nature</i> , <b>2021</b> , 595, 399-403	50.4	18

31	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> , <b>2005</b> , 33, D567-72	20.1	16
30	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 13, S1	3.6	15
29	Annotation of primate miRNAs by high throughput sequencing of small RNA libraries. <i>BMC Genomics</i> , <b>2012</b> , 13, 116	4.5	14
28	Applying the functional abnormality ontology pattern to anatomical functions. <i>Journal of Biomedical Semantics</i> , <b>2010</b> , 1, 4	2.2	12
27	GFO-Bio: A biological core ontology. <i>Applied Ontology</i> , <b>2008</b> , 3, 219-227	1.4	12
26	A splice variant of the human CCA-adding enzyme with modified activity. <i>Journal of Molecular Biology</i> , <b>2007</b> , 366, 1258-65	6.5	12
25	BOWiki: an ontology-based wiki for annotation of data and integration of knowledge in biology. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 5, S5	3.6	11
24	The ontology of biological sequences. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 377	3.6	10
23	A Neanderthal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. <i>Current Biology</i> , <b>2020</b> , 30, 3465-3469.e4	6.3	10
22	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , <b>2021</b> , 599, 41-46	50.4	9
21	Human Stem Cell Resources Are an Inroad to Neanderthal DNA Functions. <i>Stem Cell Reports</i> , <b>2020</b> , 15, 214-225	8	8
20	Expression signatures of early-stage and advanced medaka melanomas. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , <b>2018</b> , 208, 20-28	3.2	8
19	Application of eVOC: controlled vocabularies for unifying gene expression data. <i>Comptes Rendus - Biologies</i> , <b>2003</b> , 326, 1089-96	1.4	7
18	DATABASE: A new forum for biological databases and curation. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2009</b> , 2009, bap002	5	6
17	The earliest Denisovans and their cultural adaptation. <i>Nature Ecology and Evolution</i> , <b>2021</b> ,	12.3	6
16	A high-coverage Neanderthal genome from Chagyrskaya Cave		6
15	Reduced lipolysis in lipoma phenocopies lipid accumulation in obesity. <i>International Journal of Obesity</i> , <b>2021</b> , 45, 565-576	5.5	6
14	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134548	3.7	5

13	Detection of Neanderthal Adaptively Introgressed Genetic Variants that Modulate Reporter Gene Expression in Human Immune Cells. <i>Molecular Biology and Evolution</i> , <b>2021</b> ,	8.3	5
12	The limits of long-term selection against Neandertal introgression		4
11	Immune Gene Diversity in Archaic and Present-day Humans. <i>Genome Biology and Evolution</i> , <b>2019</b> , 11, 232-241	3.9	4
10	A Proposal for a Gene Functions Wiki. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 669-678	0.9	4
9	ISCB computational biology Wikipedia competition. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003242	5	3
8	Statistical tests for associations between two directed acyclic graphs. <i>PLoS ONE</i> , <b>2010</b> , 5, e10996	3.7	3
7	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe		2
6	OBML - Ontologies in Biomedicine and Life Sciences. <i>Journal of Biomedical Semantics</i> , <b>2011</b> , 2 Suppl 4, I1	2.2	1
5	Denisovan ancestry and population history of early East Asians		1
4	Ontologies in Biology <b>2010</b> , 347-371		1
3	A novel compound heterozygous leptin receptor mutation causes more severe obesity than in Lepr mice. <i>Journal of Lipid Research</i> , <b>2021</b> , 62, 100105	6.3	1
2	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow.. <i>Science Advances</i> , <b>2022</b> , 8, eabl6496	14.3	0
1	What we have learned from Neanderthals about genes involved in energy metabolism and adiposity. <i>Neuropeptides</i> , <b>2016</b> , 55, 9	3.3	