Janet Kelso

List of Publications by Year
in descending order

123 papers	32,077 citations	17440 63 h-index	18647 119 g-index
134 all docs	134 docs citations	134 times ranked	30136 citing authors

#	Article	IF	Citations
1	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	12.6	3,588
2	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
3	The complete genome sequence of a Neanderthal from the Altai Mountains. Nature, 2014, 505, 43-49.	27.8	1,830
4	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	12.6	1,695
5	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	27.8	1,537
6	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
7	Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 2014, 513, 409-413.	27.8	1,179
8	Deep proteome and transcriptome mapping of a human cancer cell line. Molecular Systems Biology, 2011, 7, 548.	7.2	878
9	The genomic landscape of Neanderthal ancestry in present-day humans. Nature, 2014, 507, 354-357.	27.8	877
10	Genome sequence of a 45,000-year-old modern human from western Siberia. Nature, 2014, 514, 445-449.	27.8	856
11	Patterns of damage in genomic DNA sequences from a Neandertal. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14616-14621.	7.1	799
12	The genetic history of Ice Age Europe. Nature, 2016, 534, 200-205.	27.8	729
13	An early modern human from Romania with a recent Neanderthal ancestor. Nature, 2015, 524, 216-219.	27.8	633
14	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. Cell, 2008, 134, 416-426.	28.9	503
15	A high-coverage Neandertal genome from Vindija Cave in Croatia. Science, 2017, 358, 655-658.	12.6	501
16	High‐throughput DNA sequencing – concepts and limitations. BioEssays, 2010, 32, 524-536.	2.5	490
17	Human-specific gene *ARHGAP11B* promotes basal progenitor amplification and neocortex expansion. Science, 2015, 347, 1465-1470.	12.6	487
18	DNA analysis of an early modern human from Tianyuan Cave, China. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2223-2227.	7.1	484

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19	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	27.8	445
20	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. Nature, 2014, 506, 97-101.	27.8	439
21	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. Nature, 2016, 531, 504-507.	27.8	436
22	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. Science, 2016, 352, 235-239.	12.6	391
23	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. Cell, 2016, 167, 643-656.e17.	28.9	373
24	Transcriptional neoteny in the human brain. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5743-5748.	7.1	347
25	Neandertal and Denisovan DNA from Pleistocene sediments. Science, 2017, 356, 605-608.	12.6	329
26	The genome of the offspring of a Neanderthal mother and a Denisovan father. Nature, 2018, 561, 113-116.	27.8	323
27	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. Genome Biology, 2015, 16, 224.	8.8	307
28	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
29	Palaeoproteomic evidence identifies archaic hominins associated with the ChÃ¢telperronian at the Grotte du Renne. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11162-11167.	7.1	251
30	Introgression of Neandertal- and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. American Journal of Human Genetics, 2016, 98, 22-33.	6.2	226
31	Patterns of coding variation in the complete exomes of three Neandertals. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6666-6671.	7.1	223
32	Improved base calling for the Illumina Genome Analyzer using machine learning strategies. Genome Biology, 2009, 10, R83.	9.6	212
33	A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene. Molecular Biology and Evolution, 2013, 30, 844-852.	8.9	205
34	leeHom: adaptor trimming and merging for Illumina sequencing reads. Nucleic Acids Research, 2014, 42, e141-e141.	14.5	200
35	Reconstructing the genetic history of late Neanderthals. Nature, 2018, 555, 652-656.	27.8	197
36	PatMaN: rapid alignment of short sequences to large databases. Bioinformatics, 2008, 24, 1530-1531.	4.1	193

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37	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. Current Biology, 2017, 27, 3202-3208.e9.	3.9	191
38	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. Science, 2014, 344, 523-527.	12.6	188
39	deML: robust demultiplexing of Illumina sequences using a likelihood-based approach. Bioinformatics, 2015, 31, 770-772.	4.1	184
40	The Earliest Transcribed Zygotic Genes Are Short, Newly Evolved, and Different across Species. Cell Reports, 2014, 6, 285-292.	6.4	179
41	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.	7.1	176
42	Integration of text- and data-mining using ontologies successfully selects disease gene candidates. Nucleic Acids Research, 2005, 33, 1544-1552.	14.5	167
43	Transcriptome Analysis of Mouse Stem Cells and Early Embryos. PLoS Biology, 2003, 1, e74.	5.6	156
44	Nuclear and mitochondrial DNA sequences from two Denisovan individuals. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15696-15700.	7.1	154
45	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.	7.1	151
46	eVOC: A Controlled Vocabulary for Unifying Gene Expression Data. Genome Research, 2003, 13, 1222-1230.	5.5	144
47	The Contribution of Neanderthals to Phenotypic Variation in Modern Humans. American Journal of Human Genetics, 2017, 101, 578-589.	6.2	140
48	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. Nature, 2019, 565, 640-644.	27.8	137
49	Computational challenges in the analysis of ancient DNA. Genome Biology, 2010, 11, R47.	9.6	135
50	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. Science, 2020, 370, 584-587.	12.6	129
51	Identifying genes underlying skin pigmentation differences among human populations. Human Genetics, 2006, 120, 613-621.	3.8	128
52	Addressing challenges in the production and analysis of illumina sequencing data. BMC Genomics, 2011, 12, 382.	2.8	126
53	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. Nature, 2021, 592, 253-257.	27.8	119
54	*admixr*—R package for reproducible analyses using ADMIXTOOLS. Bioinformatics, 2019, 35, 3194-3195.	4.1	111

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55	The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13418-13423.	7.1	105
56	RNA-seq analysis identifies different transcriptomic types and developmental trajectories of primary melanomas. Oncogene, 2018, 37, 6136-6151.	5.9	91
57	The evolutionary history of Neanderthal and Denisovan Y chromosomes. Science, 2020, 369, 1653-1656.	12.6	90
58	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. Nature Communications, 2018, 9, 5018.	12.8	86
59	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. Current Biology, 2019, 29, 120-127.e5.	3.9	86
60	Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. Science, 2021, 372, .	12.6	86
61	Functional implications of Neandertal introgression in modern humans. Genome Biology, 2017, 18, 61.	8.8	81
62	A fourth Denisovan individual. Science Advances, 2017, 3, e1700186.	10.3	74
63	Functionality of Intergenic Transcription: An Evolutionary Comparison. PLoS Genetics, 2006, 2, e171.	3.5	73
64	freeIbis: an efficient basecaller with calibrated quality scores for Illumina sequencers. Bioinformatics, 2013, 29, 1208-1209.	4.1	71
65	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. Nature Communications, 2014, 5, 3584.	12.8	70
66	Kiwi genome provides insights into evolution of a nocturnal lifestyle. Genome Biology, 2015, 16, 147.	8.8	68
67	Comparison of Protein and mRNA Expression Evolution in Humans and Chimpanzees. PLoS ONE, 2007, 2, e216.	2.5	67
68	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. Nature, 2021, 595, 399-403.	27.8	67
69	Identification and Analysis of Genomic Regions with Large Betweenâ€Population Differentiation in Humans. Annals of Human Genetics, 2008, 72, 99-110.	0.8	62
70	Impact of the Presence of Paralogs on Sequence Divergence in a Set of Mouse-Human Orthologs. Genome Research, 2002, 12, 1370-1376.	5.5	59
71	Denisovan ancestry and population history of early East Asians. Science, 2020, 370, 579-583.	12.6	57
72	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. Science Advances, 2019, 5, eaaw5873.	10.3	52

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73	Positive selection on gene expression in the human brain. Current Biology, 2006, 16, R356-R358.	3.9	50
74	Assembly, Verification, and Initial Annotation of the NIA Mouse 7.4K cDNA Clone Set. Genome Research, 2002, 12, 1999-2003.	5.5	49
75	Ethics of DNA research on human remains: five globally applicable guidelines. Nature, 2021, 599, 41-46.	27.8	49
76	The Contribution of Exon-Skipping Events on Chromosome 22 to Protein Coding Diversity. Genome Research, 2001, 11, 1848-1853.	5.5	46
77	Relations as patterns: bridging the gap between OBO and OWL. BMC Bioinformatics, 2010, 11, 441.	2.6	44
78	ABAEnrichment: an R package to test for gene set expression enrichment in the adult and developing human brain. Bioinformatics, 2016, 32, 3201-3203.	4.1	43
79	Population transcriptomics of life‐history variation in the genus *Salmo*. Molecular Ecology, 2008, 17, 3095-3108.	3.9	41
80	A top-level ontology of functions and its application in the Open Biomedical Ontologies. Bioinformatics, 2006, 22, e66-e73.	4.1	40
81	Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. BMC Bioinformatics, 2007, 8, 377.	2.6	38
82	Analysis of Human Accelerated DNA Regions Using Archaic Hominin Genomes. PLoS ONE, 2012, 7, e32877.	2.5	38
83	The Neandertal Progesterone Receptor. Molecular Biology and Evolution, 2020, 37, 2655-2660.	8.9	38
84	Impact of ontology evolution on functional analyses. Bioinformatics, 2012, 28, 2671-2677.	4.1	33
85	High‐throughput sequencing of the melanoma genome. Experimental Dermatology, 2013, 22, 10-17.	2.9	33
86	A Neanderthal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. Current Biology, 2020, 30, 3465-3469.e4.	3.9	33
87	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
88	Allele-specific transcript isoforms in human. FEBS Letters, 2004, 577, 233-238.	2.8	31
89	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
90	Transcription Factors Are Targeted by Differentially Expressed miRNAs in Primates. Genome Biology and Evolution, 2012, 4, 552-564.	2.5	30

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91	A genetic analysis of the Gibraltar Neanderthals. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15610-15615.	7.1	30
92	Genetic Evidence of Human Adaptation to a Cooked Diet. Genome Biology and Evolution, 2016, 8, 1091-1103.	2.5	29
93	Ancient humans and the origin of modern humans. Current Opinion in Genetics and Development, 2014, 29, 133-138.	3.3	26
94	Reviewer-coerced citation: case report, update on journal policy and suggestions for future prevention. Bioinformatics, 2019, 35, 3217-3218.	4.1	24
95	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. Molecular Biology and Evolution, 2022, 39, .	8.9	24
96	GFO-Bio: A biological core ontology. Applied Ontology, 2008, 3, 219-227.	2.0	20
97	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. BMC Bioinformatics, 2011, 12, S1.	2.6	20
98	The earliest Denisovans and their cultural adaptation. Nature Ecology and Evolution, 2022, 6, 28-35.	7.8	19
99	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. Stem Cell Reports, 2020, 15, 214-225.	4.8	18
100	The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate technologies and platforms. Nucleic Acids Research, 2004, 33, D567-D572.	14.5	16
101	Annotation of primate miRNAs by high throughput sequencing of small RNA libraries. BMC Genomics, 2012, 13, 116.	2.8	16
102	Reduced lipolysis in lipoma phenocopies lipid accumulation in obesity. International Journal of Obesity, 2021, 45, 565-576.	3.4	14
103	A Splice Variant of the Human CCA-adding Enzyme with Modified Activity. Journal of Molecular Biology, 2007, 366, 1258-1265.	4.2	13
104	BOWiki: an ontology-based wiki for annotation of data and integration of knowledge in biology. BMC Bioinformatics, 2009, 10, S5.	2.6	13
105	Applying the functional abnormality ontology pattern to anatomical functions. Journal of Biomedical Semantics, 2010, 1, 4.	1.6	12
106	The evolutionary history of human spindle genes includes back-and-forth gene flow with Neandertals. ELife, 0, 11, .	6.0	12
107	The ontology of biological sequences. BMC Bioinformatics, 2009, 10, 377.	2.6	11
108	Expression signatures of early-stage and advanced medaka melanomas. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2018, 208, 20-28.	2.6	11

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109	DATABASE: A new forum for biological databases and curation. Database: the Journal of Biological Databases and Curation, 2010, 2009, bap002-bap002.	3.0	10
110	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. Science Advances, 2022, 8, eabl6496.	10.3	9
111	Application of eVOC: controlled vocabularies for unifying gene expression data. Comptes Rendus - Biologies, 2003, 326, 1089-1096.	0.2	8
112	ISCB Computational Biology Wikipedia Competition. PLoS Computational Biology, 2013, 9, e1003242.	3.2	8
113	A Proposal for a Gene Functions Wiki. Lecture Notes in Computer Science, 2006, , 669-678.	1.3	8
114	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. PLoS ONE, 2015, 10, e0134548.	2.5	7
115	Immune Gene Diversity in Archaic and Present-day Humans. Genome Biology and Evolution, 2019, 11, 232-241.	2.5	5
116	A novel compound heterozygous leptin receptor mutation causes more severe obesity than in Lepr mice. Journal of Lipid Research, 2021, 62, 100105.	4.2	5
117	Statistical Tests for Associations between Two Directed Acyclic Graphs. PLoS ONE, 2010, 5, e10996.	2.5	3
118	Ontologies in Biology. , 2010, , 347-371.		3
119	OBML – Ontologies in Biomedicine and Life Sciences. Journal of Biomedical Semantics, 2011, 2, I1.	1.6	2
120	Paving the future: finding suitable ISMB venues. Bioinformatics, 2012, 28, 2556-2559.	4.1	2
121	A Formal Ontology of Sequences. Nature Precedings, 2009, , .	0.1	0
122	What we have learned from Neanderthals about genes involved in energy metabolism and adiposity. Neuropeptides, 2016, 55, 9.	2.2	0
123	Sequencing ancient genomes. EMBnet Journal, 2013, 19, 10.	0.6	0