

# Janet Kelso

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4128175/publications.pdf>

Version: 2024-02-01

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	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	24
2	The earliest Denisovans and their cultural adaptation. <i>Nature Ecology and Evolution</i> , 2022, 6, 28-35.	7.8	19
3	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. <i>Science Advances</i> , 2022, 8, eabl6496.	10.3	9
4	Reduced lipolysis in lipoma phenocopies lipid accumulation in obesity. <i>International Journal of Obesity</i> , 2021, 45, 565-576.	3.4	14
5	A novel compound heterozygous leptin receptor mutation causes more severe obesity than in <i>Lepr</i> mice. <i>Journal of Lipid Research</i> , 2021, 62, 100105.	4.2	5
6	Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. <i>Science</i> , 2021, 372, .	12.6	86
7	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. <i>Nature</i> , 2021, 592, 253-257.	27.8	119
8	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. <i>Nature</i> , 2021, 595, 399-403.	27.8	67
9	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021, 599, 41-46.	27.8	49
10	A Neanderthal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. <i>Current Biology</i> , 2020, 30, 3465-3469.e4.	3.9	33
11	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. <i>Stem Cell Reports</i> , 2020, 15, 214-225.	4.8	18
12	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. <i>Science</i> , 2020, 370, 584-587.	12.6	129
13	Denisovan ancestry and population history of early East Asians. <i>Science</i> , 2020, 370, 579-583.	12.6	57
14	The evolutionary history of Neanderthal and Denisovan Y chromosomes. <i>Science</i> , 2020, 369, 1653-1656.	12.6	90
15	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.	7.1	176
16	The Neandertal Progesterone Receptor. <i>Molecular Biology and Evolution</i> , 2020, 37, 2655-2660.	8.9	38
17	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.	7.1	30
18	Reviewer-coerced citation: case report, update on journal policy and suggestions for future prevention. <i>Bioinformatics</i> , 2019, 35, 3217-3218.	4.1	24

#	ARTICLE	IF	CITATIONS
19	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. <i>Nature</i> , 2019, 565, 640-644.	27.8	137
20	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , 2019, 5, eaaw5873.	10.3	52
21	<i>admixr</i> R package for reproducible analyses using ADMIXTOOLS. <i>Bioinformatics</i> , 2019, 35, 3194-3195.	4.1	111
22	Immune Gene Diversity in Archaic and Present-day Humans. <i>Genome Biology and Evolution</i> , 2019, 11, 232-241.	2.5	5
23	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.	7.1	151
24	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , 2019, 29, 120-127.e5.	3.9	86
25	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	27.8	197
26	Expression signatures of early-stage and advanced medaka melanomas. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2018, 208, 20-28.	2.6	11
27	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018, 9, 5018.	12.8	86
28	RNA-seq analysis identifies different transcriptomic types and developmental trajectories of primary melanomas. <i>Oncogene</i> , 2018, 37, 6136-6151.	5.9	91
29	The genome of the offspring of a Neanderthal mother and a Denisovan father. <i>Nature</i> , 2018, 561, 113-116.	27.8	323
30	Functional implications of Neandertal introgression in modern humans. <i>Genome Biology</i> , 2017, 18, 61.	8.8	81
31	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , 2017, 356, 605-608.	12.6	329
32	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	12.6	501
33	The Contribution of Neanderthals to Phenotypic Variation in Modern Humans. <i>American Journal of Human Genetics</i> , 2017, 101, 578-589.	6.2	140
34	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , 2017, 27, 3202-3208.e9.	3.9	191
35	A fourth Denisovan individual. <i>Science Advances</i> , 2017, 3, e1700186.	10.3	74
36	ABAEEnrichment: an R package to test for gene set expression enrichment in the adult and developing human brain. <i>Bioinformatics</i> , 2016, 32, 3201-3203.	4.1	43

#	ARTICLE	IF	CITATIONS
37	What we have learned from Neanderthals about genes involved in energy metabolism and adiposity. <i>Neuropeptides</i> , 2016, 55, 9.	2.2	0
38	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	27.8	729
39	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.	7.1	251
40	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	27.8	1,216
41	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , 2016, 167, 643-656.e17.	28.9	373
42	Genetic Evidence of Human Adaptation to a Cooked Diet. <i>Genome Biology and Evolution</i> , 2016, 8, 1091-1103.	2.5	29
43	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , 2016, 352, 235-239.	12.6	391
44	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. <i>Nature</i> , 2016, 531, 504-507.	27.8	436
45	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.	6.2	226
46	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.	7.1	154
47	Human-specific gene <i>ARHGAP11B</i> promotes basal progenitor amplification and neocortex expansion. <i>Science</i> , 2015, 347, 1465-1470.	12.6	487
48	Kiwi genome provides insights into evolution of a nocturnal lifestyle. <i>Genome Biology</i> , 2015, 16, 147.	8.8	68
49	An early modern human from Romania with a recent Neandertal ancestor. <i>Nature</i> , 2015, 524, 216-219.	27.8	633
50	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. <i>Genome Biology</i> , 2015, 16, 224.	8.8	307
51	deML: robust demultiplexing of Illumina sequences using a likelihood-based approach. <i>Bioinformatics</i> , 2015, 31, 770-772.	4.1	184
52	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , 2015, 10, e0134548.	2.5	7
53	leeHom: adaptor trimming and merging for Illumina sequencing reads. <i>Nucleic Acids Research</i> , 2014, 42, e141-e141.	14.5	200
54	The Earliest Transcribed Zygotic Genes Are Short, Newly Evolved, and Different across Species. <i>Cell Reports</i> , 2014, 6, 285-292.	6.4	179

#	ARTICLE	IF	CITATIONS
55	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. <i>Science</i> , 2014, 344, 523-527.	12.6	188
56	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.	7.1	223
57	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , 2014, 5, 3584.	12.8	70
58	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	27.8	1,830
59	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. <i>Nature</i> , 2014, 506, 97-101.	27.8	439
60	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	27.8	877
61	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	27.8	856
62	Ancient humans and the origin of modern humans. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 133-138.	3.3	26
63	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
64	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.	7.1	484
65	A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene. <i>Molecular Biology and Evolution</i> , 2013, 30, 844-852.	8.9	205
66	High-throughput sequencing of the melanoma genome. <i>Experimental Dermatology</i> , 2013, 22, 10-17.	2.9	33
67	freebisc: an efficient basecaller with calibrated quality scores for Illumina sequencers. <i>Bioinformatics</i> , 2013, 29, 1208-1209.	4.1	71
68	ISCB Computational Biology Wikipedia Competition. <i>PLoS Computational Biology</i> , 2013, 9, e1003242.	3.2	8
69	Sequencing ancient genomes. <i>EMBnet Journal</i> , 2013, 19, 10.	0.6	0
70	Impact of ontology evolution on functional analyses. <i>Bioinformatics</i> , 2012, 28, 2671-2677.	4.1	33
71	Analysis of Human Accelerated DNA Regions Using Archaic Hominin Genomes. <i>PLoS ONE</i> , 2012, 7, e32877.	2.5	38
72	Transcription Factors Are Targeted by Differentially Expressed miRNAs in Primates. <i>Genome Biology and Evolution</i> , 2012, 4, 552-564.	2.5	30

#	ARTICLE	IF	CITATIONS
73	Paving the future: finding suitable ISMB venues. <i>Bioinformatics</i> , 2012, 28, 2556-2559.	4.1	2
74	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	12.6	1,695
75	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012, 486, 527-531.	27.8	445
76	Annotation of primate miRNAs by high throughput sequencing of small RNA libraries. <i>BMC Genomics</i> , 2012, 13, 116.	2.8	16
77	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011, 7, 548.	7.2	878
78	OBML – Ontologies in Biomedicine and Life Sciences. <i>Journal of Biomedical Semantics</i> , 2011, 2, 11.	1.6	2
79	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, S1.	2.6	20
80	Addressing challenges in the production and analysis of illumina sequencing data. <i>BMC Genomics</i> , 2011, 12, 382.	2.8	126
81	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
82	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32
83	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
84	Relations as patterns: bridging the gap between OBO and OWL. <i>BMC Bioinformatics</i> , 2010, 11, 441.	2.6	44
85	Applying the functional abnormality ontology pattern to anatomical functions. <i>Journal of Biomedical Semantics</i> , 2010, 1, 4.	1.6	12
86	High-throughput DNA sequencing – concepts and limitations. <i>BioEssays</i> , 2010, 32, 524-536.	2.5	490
87	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	27.8	1,537
88	Statistical Tests for Associations between Two Directed Acyclic Graphs. <i>PLoS ONE</i> , 2010, 5, e10996.	2.5	3
89	DATABASE: A new forum for biological databases and curation. Database: the Journal of Biological Databases and Curation, 2010, 2009, bap002-bap002.	3.0	10
90	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010, 11, R47.	9.6	135

#	ARTICLE	IF	CITATIONS
91	Ontologies in Biology. , 2010, , 347-371.		3
92	A Formal Ontology of Sequences. Nature Precedings, 2009, , .	0.1	0
93	The ontology of biological sequences. BMC Bioinformatics, 2009, 10, 377.	2.6	11
94	BOWiki: an ontology-based wiki for annotation of data and integration of knowledge in biology. BMC Bioinformatics, 2009, 10, S5.	2.6	13
95	Improved base calling for the Illumina Genome Analyzer using machine learning strategies. Genome Biology, 2009, 10, R83.	9.6	212
96	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
97	Identification and Analysis of Genomic Regions with Large Between-Population Differentiation in Humans. Annals of Human Genetics, 2008, 72, 99-110.	0.8	62
98	Population transcriptomics of life-history variation in the genus <i>Salmo</i> . Molecular Ecology, 2008, 17, 3095-3108.	3.9	41
99	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. Cell, 2008, 134, 416-426.	28.9	503
100	GFO-Bio: A biological core ontology. Applied Ontology, 2008, 3, 219-227.	2.0	20
101	PatMaN: rapid alignment of short sequences to large databases. Bioinformatics, 2008, 24, 1530-1531.	4.1	193
102	A Splice Variant of the Human CCA-adding Enzyme with Modified Activity. Journal of Molecular Biology, 2007, 366, 1258-1265.	4.2	13
103	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
104	Comparison of Protein and mRNA Expression Evolution in Humans and Chimpanzees. PLoS ONE, 2007, 2, e216.	2.5	67
105	Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. BMC Bioinformatics, 2007, 8, 377.	2.6	38
106	Identifying genes underlying skin pigmentation differences among human populations. Human Genetics, 2006, 120, 613-621.	3.8	128
107	Positive selection on gene expression in the human brain. Current Biology, 2006, 16, R356-R358.	3.9	50
108	A top-level ontology of functions and its application in the Open Biomedical Ontologies. Bioinformatics, 2006, 22, e66-e73.	4.1	40

#	ARTICLE	IF	CITATIONS
109	Functionality of Intergenic Transcription: An Evolutionary Comparison. PLoS Genetics, 2006, 2, e171.	3.5	73
110	A Proposal for a Gene Functions Wiki. Lecture Notes in Computer Science, 2006, , 669-678.	1.3	8
111	Integration of text- and data-mining using ontologies successfully selects disease gene candidates. Nucleic Acids Research, 2005, 33, 1544-1552.	14.5	167
112	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
113	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
114	Allele-specific transcript isoforms in human. FEBS Letters, 2004, 577, 233-238.	2.8	31
115	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
116	Application of eVOC: controlled vocabularies for unifying gene expression data. Comptes Rendus - Biologies, 2003, 326, 1089-1096.	0.2	8
117	eVOC: A Controlled Vocabulary for Unifying Gene Expression Data. Genome Research, 2003, 13, 1222-1230.	5.5	144
118	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
119	Transcriptome Analysis of Mouse Stem Cells and Early Embryos. PLoS Biology, 2003, 1, e74.	5.6	156
120	Assembly, Verification, and Initial Annotation of the NIA Mouse 7.4K cDNA Clone Set. Genome Research, 2002, 12, 1999-2003.	5.5	49
121	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
122	The Contribution of Exon-Skipping Events on Chromosome 22 to Protein Coding Diversity. Genome Research, 2001, 11, 1848-1853.	5.5	46
123	The evolutionary history of human spindle genes includes back-and-forth gene flow with Neandertals. ELife, 0, 11, .	6.0	12