

Elinor K Karlsson

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

17,991
citations

81839

39
h-index

98753

67
g-index

77
all docs

77
docs citations

77
times ranked

24684
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
2	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
3	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	13.7	1,405
4	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. <i>Cell</i> , 2005, 120, 169-181.	13.5	1,348
5	Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22311-22322.	3.3	517
6	Efficient mapping of mendelian traits in dogs through genome-wide association. <i>Nature Genetics</i> , 2007, 39, 1321-1328.	9.4	474
7	A Composite of Multiple Signals Distinguishes Causal Variants in Regions of Positive Selection. <i>Science</i> , 2010, 327, 883-886.	6.0	457
8	Rethinking dog domestication by integrating genetics, archeology, and biogeography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8878-8883.	3.3	412
9	Genomic Targets of Nuclear Estrogen Receptors. <i>Molecular Endocrinology</i> , 2004, 18, 1859-1875.	3.7	365
10	Natural selection and infectious disease in human populations. <i>Nature Reviews Genetics</i> , 2014, 15, 379-393.	7.7	353
11	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. <i>PLoS Genetics</i> , 2011, 7, e1002316.	1.5	339
12	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	13.5	325
13	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	13.7	256
14	Leader of the pack: gene mapping in dogs and other model organisms. <i>Nature Reviews Genetics</i> , 2008, 9, 713-725.	7.7	228
15	Duplication of FGF3, FGF4, FGF19 and ORAOV1 causes hair ridge and predisposition to dermoid sinus in Ridgeback dogs. <i>Nature Genetics</i> , 2007, 39, 1318-1320.	9.4	176
16	Assembly of polymorphic genomes: Algorithms and application to <i>Ciona savignyi</i> . <i>Genome Research</i> , 2005, 15, 1127-1135.	2.4	170
17	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2566-E2574.	3.3	142
18	A Mutation in Hairless Dogs Implicates <i>FOXI3</i> in Ectodermal Development. <i>Science</i> , 2008, 321, 1462-1462.	6.0	135

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19	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B. <i>Genome Biology</i> , 2013, 14, R132.	13.9	132
20	Jagged 1 Rescues the Duchenne Muscular Dystrophy Phenotype. <i>Cell</i> , 2015, 163, 1204-1213.	13.5	126
21	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
22	A Novel Unstable Duplication Upstream of HAS2 Predisposes to a Breed-Defining Skin Phenotype and a Periodic Fever Syndrome in Chinese Shar-Pei Dogs. <i>PLoS Genetics</i> , 2011, 7, e1001332.	1.5	118
23	A canine chromosome 7 locus confers compulsive disorder susceptibility. <i>Molecular Psychiatry</i> , 2010, 15, 8-10.	4.1	116
24	The History of Farm Foxes Undermines the Animal Domestication Syndrome. <i>Trends in Ecology and Evolution</i> , 2020, 35, 125-136.	4.2	101
25	Genome-wide association mapping identifies multiple loci for a canine SLE-related disease complex. <i>Nature Genetics</i> , 2010, 42, 250-254.	9.4	99
26	LG12 Truncation Causes a Remitting Focal Epilepsy in Dogs. <i>PLoS Genetics</i> , 2011, 7, e1002194.	1.5	88
27	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001383.	1.5	85
28	Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. <i>Genome Biology</i> , 2014, 15, R25.	13.9	78
29	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. <i>Science Translational Medicine</i> , 2013, 5, 192ra86.	5.8	77
30	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	6.0	77
31	Comparative Genomics Reveals Shared Mutational Landscape in Canine Hemangiosarcoma and Human Angiosarcoma. <i>Molecular Cancer Research</i> , 2019, 17, 2410-2421.	1.5	72
32	Genome-wide Association Study Identifies Shared Risk Loci Common to Two Malignancies in Golden Retrievers. <i>PLoS Genetics</i> , 2015, 11, e1004922.	1.5	66
33	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019, 6, 810-824.	4.6	65
34	A genetic basis of variation in eccrine sweat gland and hair follicle density. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9932-9937.	3.3	57
35	Comparative Proteomic Analysis Reveals Activation of Mucosal Innate Immune Signaling Pathways during Cholera. <i>Infection and Immunity</i> , 2015, 83, 1089-1103.	1.0	55
36	Integrating evolutionary and regulatory information with a multispecies approach implicates genes and pathways in obsessive-compulsive disorder. <i>Nature Communications</i> , 2017, 8, 774.	5.8	52

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37	Construction of a 2-Mb resolution BAC microarray for CGH analysis of canine tumors. <i>Genome Research</i> , 2005, 15, 1831-1837.	2.4	51
38	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	51
39	A Simple Repeat Polymorphism in the MITF-M Promoter Is a Key Regulator of White Spotting in Dogs. <i>PLoS ONE</i> , 2014, 9, e104363.	1.1	50
40	Aquatic Adaptation and Depleted Diversity: A Deep Dive into the Genomes of the Sea Otter and Giant Otter. <i>Molecular Biology and Evolution</i> , 2019, 36, 2631-2655.	3.5	48
41	An open science study of ageing in companion dogs. <i>Nature</i> , 2022, 602, 51-57.	13.7	43
42	Solenodon genome reveals convergent evolution of venom in eulipotyphlan mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25745-25755.	3.3	42
43	Reconsidering domestication from a process archaeology perspective. <i>World Archaeology</i> , 2021, 53, 56-77.	0.5	36
44	A genome assembly-integrated dog 1 Mb BAC microarray: a cytogenetic resource for canine cancer studies and comparative genomic analysis. <i>Cytogenetic and Genome Research</i> , 2008, 122, 110-121.	0.6	33
45	A Cytogenetically Characterized, Genome-Anchored 10-Mb BAC Set and CGH Array for the Domestic Dog. <i>Journal of Heredity</i> , 2007, 98, 474-484.	1.0	32
46	Evaluation of the Serotonergic Genes <i>htr1A</i> , <i>htr1B</i> , <i>htr2A</i> , and <i>slc6A4</i> in Aggressive Behavior of Golden Retriever Dogs. <i>Behavior Genetics</i> , 2008, 38, 55-66.	1.4	31
47	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020, 32, 107949.	2.9	26
48	Combining Citizen Science and Genomics to Investigate Tick, Pathogen, and Commensal Microbiome at Single-Tick Resolution. <i>Frontiers in Genetics</i> , 2020, 10, 1322.	1.1	26
49	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	1.0	25
50	Analysis of the Human Mucosal Response to Cholera Reveals Sustained Activation of Innate Immune Signaling Pathways. <i>Infection and Immunity</i> , 2018, 86, .	1.0	21
51	Pet genomics medicine runs wild. <i>Nature</i> , 2018, 559, 470-472.	13.7	20
52	Humanity's Best Friend: A Dog-Centric Approach to Addressing Global Challenges. <i>Animals</i> , 2020, 10, 502.	1.0	20
53	Darwinian genomics and diversity in the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
54	How to Make a Rodent Giant: Genomic Basis and Tradeoffs of Gigantism in the Capybara, the World's Largest Rodent. <i>Molecular Biology and Evolution</i> , 2021, 38, 1715-1730.	3.5	16

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55	Microarray-based cytogenetic profiling reveals recurrent and subtype-associated genomic copy number aberrations in feline sarcomas. <i>Chromosome Research</i> , 2009, 17, 987-1000.	1.0	14
56	Low guanylyl cyclase activity in Weddell seals: implications for peripheral vasoconstriction and perfusion of the brain during diving. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2019, 316, R704-R715.	0.9	12
57	Brain Size Does Not Rescue Domestication Syndrome. <i>Trends in Ecology and Evolution</i> , 2020, 35, 1061-1062.	4.2	12
58	Genomically Complex Human Angiosarcoma and Canine Hemangiosarcoma Establish Convergent Angiogenic Transcriptional Programs Driven by Novel Gene Fusions. <i>Molecular Cancer Research</i> , 2021, 19, 847-861.	1.5	12
59	Nordic OCD & Related Disorders Consortium: Rationale, design, and methods. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 38-50.	1.1	11
60	Age and Physical Activity Levels in Companion Dogs: Results From the Dog Aging Project. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1986-1993.	1.7	10
61	Advancing Genetic Selection and Behavioral Genomics of Working Dogs Through Collaborative Science. <i>Frontiers in Veterinary Science</i> , 2021, 8, 662429.	0.9	9
62	March Mammal Madness and the power of narrative in science outreach. <i>ELife</i> , 2021, 10, .	2.8	5
63	The Antarctic Weddell seal genome reveals evidence of selection on cardiovascular phenotype and lipid handling. <i>Communications Biology</i> , 2022, 5, 140.	2.0	5
64	Reply to Zeder and Trut et al.: An Attractive Hypothesis in Need of Evidence. <i>Trends in Ecology and Evolution</i> , 2020, 35, 651-652.	4.2	4
65	Whole-genome sequences shed light on the demographic history and contemporary genetic erosion of free-ranging jaguar (<i>Panthera onca</i>) populations. <i>Journal of Genetics and Genomics</i> , 2022, 49, 77-80.	1.7	4
66	Examination of Huntington's disease with atypical clinical features in a Bangladeshi family tree. <i>Clinical Case Reports (discontinued)</i> , 2016, 4, 1191-1194.	0.2	2
67	America's lost dogs. <i>Science</i> , 2018, 361, 27-28.	6.0	2
68	Mining data from 1000 genomes to identify the causal variant in regions under positive selection. <i>Genome Biology</i> , 2010, 11, l22.	13.9	0