

Elinor K Karlsson

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

17,991
citations

81900

39
h-index

98798

67
g-index

77
all docs

77
docs citations

77
times ranked

24684
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.9	4
2	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, .	7.1	124
3	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, .	7.1	19
4	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	51
5	An open science study of ageing in companion dogs. <i>Nature</i> , 2022, 602, 51-57.	27.8	43
6	The Antarctic Weddell seal genome reveals evidence of selection on cardiovascular phenotype and lipid handling. <i>Communications Biology</i> , 2022, 5, 140.	4.4	5
7	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.	3.6	10
8	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	12.6	77
9	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.	8.9	16
10	March Mammal Madness and the power of narrative in science outreach. <i>ELife</i> , 2021, 10, .	6.0	5
11	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.	3.4	12
12	Reconsidering domestication from a process archaeology perspective. <i>World Archaeology</i> , 2021, 53, 56-77.	1.1	36
13	Advancing Genetic Selection and Behavioral Genomics of Working Dogs Through Collaborative Science. <i>Frontiers in Veterinary Science</i> , 2021, 8, 662429.	2.2	9
14	Nordic OCD & Related Disorders Consortium: Rationale, design, and methods. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 38-50.	1.7	11
15	The History of Farm Foxes Undermines the Animal Domestication Syndrome. <i>Trends in Ecology and Evolution</i> , 2020, 35, 125-136.	8.7	101
16	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	27.8	256
17	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020, 32, 107949.	6.4	26
18	Brain Size Does Not Rescue Domestication Syndrome. <i>Trends in Ecology and Evolution</i> , 2020, 35, 1061-1062.	8.7	12

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19	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.	7.1	517
20	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.	8.7	4
21	Humanity's Best Friend: A Dog-Centric Approach to Addressing Global Challenges. <i>Animals</i> , 2020, 10, 502.	2.3	20
22	Combining Citizen Science and Genomics to Investigate Tick, Pathogen, and Commensal Microbiome at Single-Tick Resolution. <i>Frontiers in Genetics</i> , 2020, 10, 1322.	2.3	26
23	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.	8.9	48
24	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	2.4	25
25	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.	1.8	12
26	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019, 6, 810-824.	9.5	65
27	Comparative Genomics Reveals Shared Mutational Landscape in Canine Hemangiosarcoma and Human Angiosarcoma. <i>Molecular Cancer Research</i> , 2019, 17, 2410-2421.	3.4	72
28	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.	7.1	42
29	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.	7.1	142
30	Analysis of the Human Mucosal Response to Cholera Reveals Sustained Activation of Innate Immune Signaling Pathways. <i>Infection and Immunity</i> , 2018, 86, .	2.2	21
31	America's lost dogs. <i>Science</i> , 2018, 361, 27-28.	12.6	2
32	Pet genomics medicine runs wild. <i>Nature</i> , 2018, 559, 470-472.	27.8	20
33	Integrating evolutionary and regulatory information with a multispecies approach implicates genes and pathways in obsessive-compulsive disorder. <i>Nature Communications</i> , 2017, 8, 774.	12.8	52
34	Examination of Huntington's disease with atypical clinical features in a Bangladeshi family tree. <i>Clinical Case Reports (discontinued)</i> , 2016, 4, 1191-1194.	0.5	2
35	Jagged 1 Rescues the Duchenne Muscular Dystrophy Phenotype. <i>Cell</i> , 2015, 163, 1204-1213.	28.9	126
36	Comparative Proteomic Analysis Reveals Activation of Mucosal Innate Immune Signaling Pathways during Cholera. <i>Infection and Immunity</i> , 2015, 83, 1089-1103.	2.2	55

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37	A genetic basis of variation in eccrine sweat gland and hair follicle density. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9932-9937.	7.1	57
38	Genome-wide Association Study Identifies Shared Risk Loci Common to Two Malignancies in Golden Retrievers. PLoS Genetics, 2015, 11, e1004922.	3.5	66
39	A Simple Repeat Polymorphism in the MITF-M Promoter Is a Key Regulator of White Spotting in Dogs. PLoS ONE, 2014, 9, e104363.	2.5	50
40	Natural selection and infectious disease in human populations. Nature Reviews Genetics, 2014, 15, 379-393.	16.8	353
41	Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. Genome Biology, 2014, 15, R25.	9.6	78
42	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B. Genome Biology, 2013, 14, R132.	9.6	132
43	Identifying Recent Adaptations in Large-Scale Genomic Data. Cell, 2013, 152, 703-713.	28.9	325
44	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. Science Translational Medicine, 2013, 5, 192ra86.	12.4	77
45	Rethinking dog domestication by integrating genetics, archeology, and biogeography. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8878-8883.	7.1	412
46	A Novel Unstable Duplication Upstream of HAS2 Predisposes to a Breed-Defining Skin Phenotype and a Periodic Fever Syndrome in Chinese Shar-Pei Dogs. PLoS Genetics, 2011, 7, e1001332.	3.5	118
47	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	3.5	85
48	LGI2 Truncation Causes a Remitting Focal Epilepsy in Dogs. PLoS Genetics, 2011, 7, e1002194.	3.5	88
49	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. PLoS Genetics, 2011, 7, e1002316.	3.5	339
50	A canine chromosome 7 locus confers compulsive disorder susceptibility. Molecular Psychiatry, 2010, 15, 8-10.	7.9	116
51	Genome-wide association mapping identifies multiple loci for a canine SLE-related disease complex. Nature Genetics, 2010, 42, 250-254.	21.4	99
52	A Composite of Multiple Signals Distinguishes Causal Variants in Regions of Positive Selection. Science, 2010, 327, 883-886.	12.6	457
53	Mining data from 1000 genomes to identify the causal variant in regions under positive selection. Genome Biology, 2010, 11, l22.	9.6	0
54	Microarray-based cytogenetic profiling reveals recurrent and subtype-associated genomic copy number aberrations in feline sarcomas. Chromosome Research, 2009, 17, 987-1000.	2.2	14

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55	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
56	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.	2.1	31
57	Leader of the pack: gene mapping in dogs and other model organisms. <i>Nature Reviews Genetics</i> , 2008, 9, 713-725.	16.3	228
58	A Mutation in Hairless Dogs Implicates <i>FOXI3</i> in Ectodermal Development. <i>Science</i> , 2008, 321, 1462-1462.	12.6	135
59	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.	1.1	33
60	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.	2.4	32
61	Efficient mapping of mendelian traits in dogs through genome-wide association. <i>Nature Genetics</i> , 2007, 39, 1321-1328.	21.4	474
62	Duplication of <i>FGF3</i> , <i>FGF4</i> , <i>FGF19</i> and <i>ORAOV1</i> causes hair ridge and predisposition to dermoid sinus in Ridgeback dogs. <i>Nature Genetics</i> , 2007, 39, 1318-1320.	21.4	176
63	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	27.8	2,215
64	Assembly of polymorphic genomes: Algorithms and application to <i>Ciona savignyi</i> . <i>Genome Research</i> , 2005, 15, 1127-1135.	5.5	170
65	Construction of a 2-Mb resolution BAC microarray for CGH analysis of canine tumors. <i>Genome Research</i> , 2005, 15, 1831-1837.	5.5	51
66	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. <i>Cell</i> , 2005, 120, 169-181.	28.9	1,348
67	Genomic Targets of Nuclear Estrogen Receptors. <i>Molecular Endocrinology</i> , 2004, 18, 1859-1875.	3.7	365
68	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319