

Kerstin Lindblad-Toh

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

19,629
citations

87888

38
h-index

62596

80
g-index

85
all docs

85
docs citations

85
times ranked

26058
citing authors

#	ARTICLE	IF	CITATIONS
1	Contribution of Rare Genetic Variation to Disease Susceptibility in a Large Scandinavian Myositis Cohort. <i>Arthritis and Rheumatology</i> , 2022, 74, 342-352.	5.6	7
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	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
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	Complement <i>C4</i> Copy Number Variation is Linked to SSA/Ro and SSB/La Autoantibodies in Systemic Inflammatory Autoimmune Diseases. <i>Arthritis and Rheumatology</i> , 2022, 74, 1440-1450.	5.6	17
6	Identification and functional characterization of a novel susceptibility locus for small vessel vasculitis with MPO-ANCA. <i>Rheumatology</i> , 2022, 61, 3461-3470.	1.9	8
7	Toll-like receptors revisited; a possible role for TLR1 in lupus nephritis. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 404-406.	0.9	7
8	Molecular pathways in patients with systemic lupus erythematosus revealed by gene-centred DNA sequencing. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 109-117.	0.9	35
9	A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. <i>Communications Biology</i> , 2021, 4, 185.	4.4	59
10	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	12.6	132
11	Association of Protective HLA-A With HLA-B*27 Positive Ankylosing Spondylitis. <i>Frontiers in Genetics</i> , 2021, 12, 659042.	2.3	2
12	The ABCC4 gene is associated with pyometra in golden retriever dogs. <i>Scientific Reports</i> , 2021, 11, 16647.	3.3	5
13	The genetic consequences of dog breed formation—Accumulation of deleterious genetic variation and fixation of mutations associated with myxomatous mitral valve disease in cavalier King Charles spaniels. <i>PLoS Genetics</i> , 2021, 17, e1009726.	3.5	12
14	OUP accepted manuscript. <i>Rheumatology</i> , 2021, 60, 837-848.	1.9	15
15	Genome-Wide Analyses for Osteosarcoma in Leonberger Dogs Reveal the CDKN2A/B Gene Locus as a Major Risk Locus. <i>Genes</i> , 2021, 12, 1964.	2.4	8
16	SweHLA: the high confidence HLA typing bio-resource drawn from 1000 Swedish genomes. <i>European Journal of Human Genetics</i> , 2020, 28, 627-635.	2.8	11
17	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	27.8	256
18	Targeted sequencing reveals the somatic mutation landscape in a Swedish breast cancer cohort. <i>Scientific Reports</i> , 2020, 10, 19304.	3.3	10

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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	Whole-genome sequencing of glioblastoma reveals enrichment of non-coding constraint mutations in known and novel genes. <i>Genome Biology</i> , 2020, 21, 127.	8.8	43
21	Transcriptomes from German shepherd dogs reveal differences in immune activity between atopic dermatitis affected and control skin. <i>Immunogenetics</i> , 2020, 72, 315-323.	2.4	6
22	What animals can teach us about evolution, the human genome, and human disease. <i>Upsala Journal of Medical Sciences</i> , 2020, 125, 1-9.	0.9	12
23	Whole-genome genotyping and resequencing reveal the association of a deletion in the complex interferon alpha gene cluster with hypothyroidism in dogs. <i>BMC Genomics</i> , 2020, 21, 307.	2.8	8
24	Thoracolumbar meningeal fibrosis in pugs. <i>Journal of Veterinary Internal Medicine</i> , 2020, 34, 797-807.	1.6	9
25	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
26	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	2.4	25
27	A synonymous germline variant in a gene encoding a cell adhesion molecule is associated with cutaneous mast cell tumour development in Labrador and Golden Retrievers. <i>PLoS Genetics</i> , 2019, 15, e1007967.	3.5	9
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 rare regulatory variant in the MEF2D gene affects gene regulation and splicing and is associated with a SLE sub-phenotype in Swedish cohorts. <i>European Journal of Human Genetics</i> , 2019, 27, 432-441.	2.8	12
30	Cytokine Autoantibody Screening in the Swedish Addison Registry Identifies Patients With Undiagnosed APS1. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 179-186.	3.6	16
31	High prevalence of gait abnormalities in pugs. <i>Veterinary Record</i> , 2018, 182, 167-167.	0.3	7
32	Common genetic variation in the autoimmune regulator (AIRE) locus is associated with autoimmune Addison's disease in Sweden. <i>Scientific Reports</i> , 2018, 8, 8395.	3.3	22
33	<i>SETD2</i> Is Recurrently Mutated in Whole-Exome Sequenced Canine Osteosarcoma. <i>Cancer Research</i> , 2018, 78, 3421-3431.	0.9	76
34	Comparison of cellular location and expression of Plakophilin-2 in epidermal cells from nonlesional atopic skin and healthy skin in German shepherd dogs. <i>Veterinary Dermatology</i> , 2017, 28, 377.	1.2	5
35	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
36	Dissecting evolution and disease using comparative vertebrate genomics. <i>Nature Reviews Genetics</i> , 2017, 18, 624-636.	16.3	46

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37	An Improved microRNA Annotation of the Canine Genome. PLoS ONE, 2016, 11, e0153453.	2.5	20
38	Multiple regulatory variants located in cell type-specific enhancers within the PKP2 locus form major risk and protective haplotypes for canine atopic dermatitis in German shepherd dogs. BMC Genetics, 2016, 17, 97.	2.7	8
39	Variants within the SP110 nuclear body protein modify risk of canine degenerative myelopathy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3091-100.	7.1	32
40	Regulatory mutations in TBX3 disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. Nature Genetics, 2016, 48, 152-158.	21.4	59
41	Utilizing the Dog Genome in the Search for Novel Candidate Genes Involved in Glioma Developmentâ€”Genome Wide Association Mapping followed by Targeted Massive Parallel Sequencing Identifies a Strongly Associated Locus. PLoS Genetics, 2016, 12, e1006000.	3.5	54
42	Genome-Wide Analysis Identifies Germ-Line Risk Factors Associated with Canine Mammary Tumours. PLoS Genetics, 2016, 12, e1006029.	3.5	22
43	Improved canine exome designs, featuring ncRNAs and increased coverage of protein coding genes. Scientific Reports, 2015, 5, 12810.	3.3	31
44	Multiple Changes of Gene Expression and Function Reveal Genomic and Phenotypic Complexity in SLE-like Disease. PLoS Genetics, 2015, 11, e1005248.	3.5	21
45	Jagged 1 Rescues the Duchenne Muscular Dystrophy Phenotype. Cell, 2015, 163, 1204-1213.	28.9	126
46	Genome-wide Association Study Identifies Shared Risk Loci Common to Two Malignancies in Golden Retrievers. PLoS Genetics, 2015, 11, e1004922.	3.5	66
47	Linked genetic variants on chromosome 10 control ear morphology and body mass among dog breeds. BMC Genomics, 2015, 16, 474.	2.8	32
48	cgmisc: enhanced genome-wide association analyses and visualization. Bioinformatics, 2015, 31, 3830-3831.	4.1	14
49	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome Research, 2015, 25, 1634-1645.	5.5	96
50	Genome-Wide Association Study of Golden Retrievers Identifies Germ-Line Risk Factors Predisposing to Mast Cell Tumours. PLoS Genetics, 2015, 11, e1005647.	3.5	41
51	The Shepherdsâ€™ Tale: A Genome-Wide Study across 9 Dog Breeds Implicates Two Loci in the Regulation of Fructosamine Serum Concentration in Belgian Shepherds. PLoS ONE, 2015, 10, e0123173.	2.5	8
52	Genome-Wide Analyses Suggest Mechanisms Involving Early B-Cell Development in Canine IgA Deficiency. PLoS ONE, 2015, 10, e0133844.	2.5	14
53	A Multi-Breed Genome-Wide Association Analysis for Canine Hypothyroidism Identifies a Shared Major Risk Locus on CFA12. PLoS ONE, 2015, 10, e0134720.	2.5	16
54	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

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55	Lack of Evidence for a Role of Islet Autoimmunity in the Aetiology of Canine Diabetes Mellitus. PLoS ONE, 2014, 9, e105473.	2.5	31
56	Canine Hereditary Ataxia in Old English Sheepdogs and Gordon Setters Is Associated with a Defect in the Autophagy Gene Encoding RAB24. PLoS Genetics, 2014, 10, e1003991.	3.5	33
57	The draft genome sequence of the ferret (<i>Mustela putorius furo</i>) facilitates study of human respiratory disease. Nature Biotechnology, 2014, 32, 1250-1255.	17.5	110
58	The Naked Mole Rat Genome Resource: facilitating analyses of cancer and longevity-related adaptations. Bioinformatics, 2014, 30, 3558-3560.	4.1	71
59	Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. Science, 2014, 345, 1074-1079.	12.6	343
60	The genomic substrate for adaptive radiation in African cichlid fish. Nature, 2014, 513, 375-381.	27.8	874
61	Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. Genome Biology, 2014, 15, R25.	9.6	78
62	Identification of Three Molecular and Functional Subtypes in Canine Hemangiosarcoma through Gene Expression Profiling and Progenitor Cell Characterization. American Journal of Pathology, 2014, 184, 985-995.	3.8	68
63	The dog as a genetic model for immunoglobulin A (IgA) deficiency: Identification of several breeds with low serum IgA concentrations. Veterinary Immunology and Immunopathology, 2014, 160, 255-259.	1.2	27
64	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. PLoS ONE, 2014, 9, e91172.	2.5	206
65	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B. Genome Biology, 2013, 14, R132.	9.6	132
66	The genomic signature of dog domestication reveals adaptation to a starch-rich diet. Nature, 2013, 495, 360-364.	27.8	805
67	The African coelacanth genome provides insights into tetrapod evolution. Nature, 2013, 496, 311-316.	27.8	612
68	Origins of Shared Genetic Variation in African Cichlids. Molecular Biology and Evolution, 2013, 30, 906-917.	8.9	86
69	Genome-Wide Analysis in German Shepherd Dogs Reveals Association of a Locus on CFA 27 with Atopic Dermatitis. PLoS Genetics, 2013, 9, e1003475.	3.5	51
70	Death of <i>PRDM9</i> coincides with stabilization of the recombination landscape in the dog genome. Genome Research, 2012, 22, 51-63.	5.5	116
71	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
72	The genomic basis of adaptive evolution in threespine sticklebacks. Nature, 2012, 484, 55-61.	27.8	1,600

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73	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	27.8	575
74	Three Periods of Regulatory Innovation During Vertebrate Evolution. <i>Science</i> , 2011, 333, 1019-1024.	12.6	127
75	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
76	Genome-wide association mapping identifies multiple loci for a canine SLE-related disease complex. <i>Nature Genetics</i> , 2010, 42, 250-254.	21.4	99
77	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661
78	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	27.8	2,215
79	The mosaic structure of variation in the laboratory mouse genome. <i>Nature</i> , 2002, 420, 574-578.	27.8	448
80	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319