

# 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	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
2	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	27.8	2,215
3	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.	27.8	1,600
4	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
5	The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 2014, 513, 375-381.	27.8	874
6	The genomic signature of dog domestication reveals adaptation to a starch-rich diet. <i>Nature</i> , 2013, 495, 360-364.	27.8	805
7	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661
8	The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 2013, 496, 311-316.	27.8	612
9	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
10	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
11	The mosaic structure of variation in the laboratory mouse genome. <i>Nature</i> , 2002, 420, 574-578.	27.8	448
12	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.	7.1	412
13	Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. <i>Science</i> , 2014, 345, 1074-1079.	12.6	343
14	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	27.8	256
15	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. <i>PLoS ONE</i> , 2014, 9, e91172.	2.5	206
16	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near <i>CDKN2A/B</i> . <i>Genome Biology</i> , 2013, 14, R132.	9.6	132
17	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
18	Three Periods of Regulatory Innovation During Vertebrate Evolution. <i>Science</i> , 2011, 333, 1019-1024.	12.6	127

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19	Jagged 1 Rescues the Duchenne Muscular Dystrophy Phenotype. <i>Cell</i> , 2015, 163, 1204-1213.	28.9	126
20	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
21	Death of <i>PRDM9</i> coincides with stabilization of the recombination landscape in the dog genome. <i>Genome Research</i> , 2012, 22, 51-63.	5.5	116
22	The draft genome sequence of the ferret ( <i>Mustela putorius furo</i> ) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , 2014, 32, 1250-1255.	17.5	110
23	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
24	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. <i>Genome Research</i> , 2015, 25, 1634-1645.	5.5	96
25	Origins of Shared Genetic Variation in African Cichlids. <i>Molecular Biology and Evolution</i> , 2013, 30, 906-917.	8.9	86
26	Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. <i>Genome Biology</i> , 2014, 15, R25.	9.6	78
27	<i>SETD2</i> Is Recurrently Mutated in Whole-Exome Sequenced Canine Osteosarcoma. <i>Cancer Research</i> , 2018, 78, 3421-3431.	0.9	76
28	The Naked Mole Rat Genome Resource: facilitating analyses of cancer and longevity-related adaptations. <i>Bioinformatics</i> , 2014, 30, 3558-3560.	4.1	71
29	Identification of Three Molecular and Functional Subtypes in Canine Hemangiosarcoma through Gene Expression Profiling and Progenitor Cell Characterization. <i>American Journal of Pathology</i> , 2014, 184, 985-995.	3.8	68
30	Genome-wide Association Study Identifies Shared Risk Loci Common to Two Malignancies in Golden Retrievers. <i>PLoS Genetics</i> , 2015, 11, e1004922.	3.5	66
31	Regulatory mutations in <i>TBX3</i> disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. <i>Nature Genetics</i> , 2016, 48, 152-158.	21.4	59
32	A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. <i>Communications Biology</i> , 2021, 4, 185.	4.4	59
33	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. <i>PLoS Genetics</i> , 2016, 12, e1006000.	3.5	54
34	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
35	Genome-Wide Analysis in German Shepherd Dogs Reveals Association of a Locus on CFA 27 with Atopic Dermatitis. <i>PLoS Genetics</i> , 2013, 9, e1003475.	3.5	51
36	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	51

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37	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
38	Aquatic Adaptation and Depleted Diversity: A Deep Dive into the Genomes of the Sea Otter and Giant Otter. Molecular Biology and Evolution, 2019, 36, 2631-2655.	8.9	48
39	Dissecting evolution and disease using comparative vertebrate genomics. Nature Reviews Genetics, 2017, 18, 624-636.	16.3	46
40	Whole-genome sequencing of glioblastoma reveals enrichment of non-coding constraint mutations in known and novel genes. Genome Biology, 2020, 21, 127.	8.8	43
41	Solenodon genome reveals convergent evolution of venom in eulipotyphlan mammals. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25745-25755.	7.1	42
42	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
43	Molecular pathways in patients with systemic lupus erythematosus revealed by gene-centred DNA sequencing. Annals of the Rheumatic Diseases, 2021, 80, 109-117.	0.9	35
44	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
45	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
46	Linked genetic variants on chromosome 10 control ear morphology and body mass among dog breeds. BMC Genomics, 2015, 16, 474.	2.8	32
47	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
48	Lack of Evidence for a Role of Islet Autoimmunity in the Aetiology of Canine Diabetes Mellitus. PLoS ONE, 2014, 9, e105473.	2.5	31
49	Improved canine exome designs, featuring ncRNAs and increased coverage of protein coding genes. Scientific Reports, 2015, 5, 12810.	3.3	31
50	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
51	BarkBase: Epigenomic Annotation of Canine Genomes. Genes, 2019, 10, 433.	2.4	25
52	Common genetic variation in the autoimmune regulator (AIRE) locus is associated with autoimmune Addison's disease in Sweden. Scientific Reports, 2018, 8, 8395.	3.3	22
53	Genome-Wide Analysis Identifies Germ-Line Risk Factors Associated with Canine Mammary Tumours. PLoS Genetics, 2016, 12, e1006029.	3.5	22
54	Multiple Changes of Gene Expression and Function Reveal Genomic and Phenotypic Complexity in SLE-like Disease. PLoS Genetics, 2015, 11, e1005248.	3.5	21

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55	An Improved microRNA Annotation of the Canine Genome. PLoS ONE, 2016, 11, e0153453.	2.5	20
56	Complement <i>C4</i> Copy Number Variation is Linked to SSA/Ro and SSB/La Autoantibodies in Systemic Inflammatory Autoimmune Diseases. Arthritis and Rheumatology, 2022, 74, 1440-1450.	5.6	17
57	Cytokine Autoantibody Screening in the Swedish Addison Registry Identifies Patients With Undiagnosed APS1. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 179-186.	3.6	16
58	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
59	OUP accepted manuscript. Rheumatology, 2021, 60, 837-848.	1.9	15
60	cgmisc: enhanced genome-wide association analyses and visualization. Bioinformatics, 2015, 31, 3830-3831.	4.1	14
61	Genome-Wide Analyses Suggest Mechanisms Involving Early B-Cell Development in Canine IgA Deficiency. PLoS ONE, 2015, 10, e0133844.	2.5	14
62	A rare regulatory variant in the MEF2D gene affects gene regulation and splicing and is associated with a SLE sub-phenotype in Swedish cohorts. European Journal of Human Genetics, 2019, 27, 432-441.	2.8	12
63	What animals can teach us about evolution, the human genome, and human disease. Upsala Journal of Medical Sciences, 2020, 125, 1-9.	0.9	12
64	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. PLoS Genetics, 2021, 17, e1009726.	3.5	12
65	SweHLA: the high confidence HLA typing bio-resource drawn from 1000 Swedish genomes. European Journal of Human Genetics, 2020, 28, 627-635.	2.8	11
66	Targeted sequencing reveals the somatic mutation landscape in a Swedish breast cancer cohort. Scientific Reports, 2020, 10, 19304.	3.3	10
67	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. PLoS Genetics, 2019, 15, e1007967.	3.5	9
68	Thoracolumbar meningeal fibrosis in pugs. Journal of Veterinary Internal Medicine, 2020, 34, 797-807.	1.6	9
69	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
70	Whole-genome genotyping and resequencing reveal the association of a deletion in the complex interferon alpha gene cluster with hypothyroidism in dogs. BMC Genomics, 2020, 21, 307.	2.8	8
71	The Shepherds™ 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
72	Identification and functional characterization of a novel susceptibility locus for small vessel vasculitis with MPO-ANCA. Rheumatology, 2022, 61, 3461-3470.	1.9	8

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73	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
74	High prevalence of gait abnormalities in pugs. <i>Veterinary Record</i> , 2018, 182, 167-167.	0.3	7
75	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
76	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
77	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
78	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
79	The ABCC4 gene is associated with pyometra in golden retriever dogs. <i>Scientific Reports</i> , 2021, 11, 16647.	3.3	5
80	Association of Protective HLA-A With HLA-B*27 Positive Ankylosing Spondylitis. <i>Frontiers in Genetics</i> , 2021, 12, 659042.	2.3	2