

Denis Larkin

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

8,595
citations

87888

38
h-index

49909

87
g-index

103
all docs

103
docs citations

103
times ranked

10222
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
2	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
3	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
4	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949.	21.4	708
5	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. <i>Science</i> , 2005, 309, 613-617.	12.6	542
6	Identification of a missense mutation in the bovine <i>ABCG2</i> gene with a major effect on the QTL on chromosome 6 affecting milk yield and composition in Holstein cattle. <i>Genome Research</i> , 2005, 15, 936-944.	5.5	335
7	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
8	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	12.8	229
9	Breakpoint regions and homologous syntenic blocks in chromosomes have different evolutionary histories. <i>Genome Research</i> , 2009, 19, 770-777.	5.5	163
10	Every genome sequence needs a good map. <i>Genome Research</i> , 2009, 19, 1925-1928.	5.5	148
11	A near-chromosome-scale genome assembly of the gemsbok (<i>Oryx gazella</i>): an iconic antelope of the Kalahari desert. <i>GigaScience</i> , 2019, 8, .	6.4	138
12	A 1463 Gene Cattle-Human Comparative Map With Anchor Points Defined by Human Genome Sequence Coordinates. <i>Genome Research</i> , 2004, 14, 1424-1437.	5.5	133
13	A Cattle-Human Comparative Map Built with Cattle BAC-Ends and Human Genome Sequence. <i>Genome Research</i> , 2003, 13, 1966-1972.	5.5	126
14	Reference-assisted chromosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1785-1790.	7.1	124
15	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	12.8	124
16	A high-resolution whole-genome cattle-human comparative map reveals details of mammalian chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18526-18531.	7.1	115
17	Piggy-BACing the human genome. <i>Genomics</i> , 2005, 86, 739-752.	2.9	103
18	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97

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19	Upgrading short-read animal genome assemblies to chromosome level using comparative genomics and a universal probe set. <i>Genome Research</i> , 2017, 27, 875-884.	5.5	97
20	Reconstruction and evolutionary history of eutherian chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5379-E5388.	7.1	94
21	Chromosome Segregation Is Biased by Kinetochores Size. <i>Current Biology</i> , 2018, 28, 1344-1356.e5.	3.9	94
22	Inferring Demography from Runs of Homozygosity in Whole-Genome Sequence, with Correction for Sequence Errors. <i>Molecular Biology and Evolution</i> , 2013, 30, 2209-2223.	8.9	91
23	Scans for signatures of selection in Russian cattle breed genomes reveal new candidate genes for environmental adaptation and acclimation. <i>Scientific Reports</i> , 2018, 8, 12984.	3.3	85
24	Extreme heterogeneity in sex chromosome differentiation and dosage compensation in livebearers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19031-19036.	7.1	79
25	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
26	Reconstruction of gross avian genome structure, organization and evolution suggests that the chicken lineage most closely resembles the dinosaur avian ancestor. <i>BMC Genomics</i> , 2014, 15, 1060.	2.8	71
27	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	8.8	71
28	Population structure and history of the Welsh sheep breeds determined by whole genome genotyping. <i>BMC Genetics</i> , 2015, 16, 65.	2.7	69
29	Germline-restricted chromosome (GRC) is widespread among songbirds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11845-11850.	7.1	68
30	Whole-genome resequencing of two elite sires for the detection of haplotypes under selection in dairy cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7693-7698.	7.1	67
31	Patterns of microchromosome organization remain highly conserved throughout avian evolution. <i>Chromosoma</i> , 2019, 128, 21-29.	2.2	67
32	Novel Insights into Chromosome Evolution in Birds, Archosaurs, and Reptiles. <i>Genome Biology and Evolution</i> , 2016, 8, 2442-2451.	2.5	66
33	Identification of a nonsense mutation in <i>APAF1</i> that is likely causal for a decrease in reproductive efficiency in Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 6693-6701.	3.4	66
34	Chromosome-level assembly reveals extensive rearrangement in saker falcon and budgerigar, but not ostrich, genomes. <i>Genome Biology</i> , 2018, 19, 171.	8.8	65
35	Genome-wide genotyping uncovers genetic profiles and history of the Russian cattle breeds. <i>Heredity</i> , 2018, 120, 125-137.	2.6	61
36	Reconstruction of the diapsid ancestral genome permits chromosome evolution tracing in avian and non-avian dinosaurs. <i>Nature Communications</i> , 2018, 9, 1883.	12.8	60

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37	Transcription of a protein-coding gene on B chromosomes of the Siberian roe deer (<i>Capreolus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	3.8	58
38	High-density genotyping reveals signatures of selection related to acclimation and economically important traits in 15 local sheep breeds from Russia. <i>BMC Genomics</i> , 2019, 20, 294.	2.8	57
39	Contrasting origin of B chromosomes in two cervids (Siberian roe deer and grey brocket deer) unravelled by chromosome-specific DNA sequencing. <i>BMC Genomics</i> , 2016, 17, 618.	2.8	47
40	Reconstruction of avian ancestral karyotypes reveals differences in the evolutionary history of macro- and microchromosomes. <i>Genome Biology</i> , 2018, 19, 155.	8.8	44
41	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019, 29, 576-589.	5.5	39
42	A compendium and functional characterization of mammalian genes involved in adaptation to Arctic or Antarctic environments. <i>BMC Genetics</i> , 2017, 18, 111.	2.7	37
43	<i>Schistosoma</i> comparative genomics: integrating genome structure, parasite biology and anthelmintic discovery. <i>Trends in Parasitology</i> , 2011, 27, 555-564.	3.3	31
44	Chromosome Level Genome Assembly and Comparative Genomics between Three Falcon Species Reveals an Unusual Pattern of Genome Organisation. <i>Diversity</i> , 2018, 10, 113.	1.7	31
45	SytenyTracker: a tool for defining homologous synteny blocks using radiation hybrid maps and whole-genome sequence. <i>BMC Research Notes</i> , 2009, 2, 148.	1.4	28
46	Demographic History, Adaptation, and NRAP Convergent Evolution at Amino Acid Residue 100 in the World Northernmost Cattle from Siberia. <i>Molecular Biology and Evolution</i> , 2021, 38, 3093-3110.	8.9	27
47	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5' UTRs and identification of species-specific transcripts. <i>BMC Genomics</i> , 2009, 10, 189.	2.8	25
48	Genome-wide association study and scan for signatures of selection point to candidate genes for body temperature maintenance under the cold stress in Siberian cattle populations. <i>BMC Genetics</i> , 2019, 20, 26.	2.7	25
49	X Chromosome Evolution in Cetartiodactyla. <i>Genes</i> , 2017, 8, 216.	2.4	24
50	Mammalian comparative genomics reveals genetic and epigenetic features associated with genome reshuffling in Rodentia. <i>Genome Biology and Evolution</i> , 2016, 8, evw276.	2.5	21
51	Construction of two whole genome radiation hybrid panels for dromedary (<i>Camelus dromedarius</i>): 5000RAD and 15000RAD. <i>Scientific Reports</i> , 2018, 8, 1982.	3.3	20
52	Genome-wide association study for body weight in cattle populations from Siberia. <i>Animal Genetics</i> , 2019, 50, 250-253.	1.7	16
53	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018, 9, 308.	2.4	14
54	Augmin-dependent microtubule self-organization drives kinetochore fiber maturation in mammals. <i>Cell Reports</i> , 2022, 39, 110610.	6.4	14

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55	An integrated chromosome-scale genome assembly of the Masai giraffe (<i>Giraffa camelopardalis</i>) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	6.4	13
56	Comparative Mapping of the Macrochromosomes of Eight Avian Species Provides Further Insight into Their Phylogenetic Relationships and Avian Karyotype Evolution. <i>Cells</i> , 2021, 10, 362.	4.1	13
57	Multisite haplotype on cattle chromosome 3 is associated with quantitative trait locus effects on lactation traits. <i>Physiological Genomics</i> , 2011, 43, 1185-1197.	2.3	12
58	Cattle genomics and its implications for future nutritional strategies for dairy cattle. <i>Animal</i> , 2013, 7, 172-183.	3.3	12
59	The genomes and history of domestic animals. <i>Molecular Genetics, Microbiology and Virology</i> , 2016, 31, 197-202.	0.3	11
60	Multi-species comparative mapping in silico using the COMPASS strategy. <i>Bioinformatics</i> , 2004, 20, 148-154.	4.1	9
61	Comparative mapping of mink chromosome 8p: in situ hybridization of seven cattle BAC clones. <i>Animal Genetics</i> , 2006, 37, 429-430.	1.7	9
62	Chromosomal Localization of Korean Cattle (Hanwoo) BAC Clones via BAC end Sequence Analysis. <i>Asian-Australasian Journal of Animal Sciences</i> , 2007, 20, 316-327.	2.4	9
63	Comparative Chromosome Mapping of Musk Ox and the X Chromosome among Some Bovidae Species. <i>Genes</i> , 2019, 10, 857.	2.4	8
64	Genotyping and Whole-Genome Resequencing of Welsh Sheep Breeds Reveal Candidate Genes and Variants for Adaptation to Local Environment and Socioeconomic Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612492.	2.3	8
65	Whole-Genome Resequencing Points to Candidate DNA Loci Affecting Body Temperature under Cold Stress in Siberian Cattle Populations. <i>Life</i> , 2021, 11, 959.	2.4	8
66	Whole genome studies of origin, selection and adaptation of the Russian cattle breeds. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2019, 23, 559-568.	1.1	8
67	Copy number variants in genomes of local sheep breeds from Russia. <i>Animal Genetics</i> , 2022, 53, 119-132.	1.7	8
68	Piggy-BACing the Human Genome I: Constructing a Porcine BAC Physical Map Through Comparative Genomics. <i>Animal Biotechnology</i> , 2008, 19, 28-42.	1.5	7
69	Synteny Explorer: An Interactive Visualization Application for Teaching Genome Evolution. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2017, 23, 711-720.	4.4	7
70	A Near Chromosome Assembly of the Dromedary Camel Genome. <i>Frontiers in Genetics</i> , 2019, 10, 32.	2.3	7
71	Resequencing and signatures of selection scan in two Siberian native sheep breeds point to candidate genetic variants for adaptation and economically important traits. <i>Animal Genetics</i> , 2021, 52, 126-131.	1.7	6
72	Shared Signatures of Selection Related to Adaptation and Acclimation in Local Cattle and Sheep Breeds from Russia. <i>Russian Journal of Genetics</i> , 2019, 55, 1008-1014.	0.6	5

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73	Identification and chromosomal localization of repeat sequences through BAC end sequence analysis in Korean cattle. <i>Journal of Genetics</i> , 2005, 84, 329-335.	0.7	4
74	Synthesis and Practical Use of 1Hâ€1,2,3â€Benzotriazoleâ€5â€carboxaldehyde for Reductive Amination. <i>Synthetic Communications</i> , 2005, 35, 2587-2595.	2.1	4
75	Role of chromosomal rearrangements and conserved chromosome regions in amniote evolution. <i>Molecular Genetics, Microbiology and Virology</i> , 2010, 25, 1-7.	0.3	4
76	Avian Chromosomal Evolution. , 2019, , 69-92.		4
77	Time lapse: A glimpse into prehistoric genomics. <i>European Journal of Medical Genetics</i> , 2020, 63, 103640.	1.3	4
78	Resequencing the Yaroslavl cattle genomes reveals signatures of selection and a rare haplotype on <scp>BTA28</scp> likely to be related to breed phenotypes. <i>Animal Genetics</i> , 2022, 53, 680-684.	1.7	4
79	Comparative mapping of cattle chromosome 19: cytogenetic localization of 19 BAC clones. <i>Cytogenetic and Genome Research</i> , 2006, 112, 235-240.	1.1	3
80	G-Anchor: a novel approach for whole-genome comparative mapping utilizing evolutionary conserved DNA sequences. <i>GigaScience</i> , 2018, 7, .	6.4	3
81	Genes related to the white face colour pattern in eight Russian cattle breeds. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2018, 22, 217-223.	1.1	3
82	Comparative genome mapping in mammals: the shrew map. <i>Acta Theriologica</i> , 2000, 45, 131-141.	1.1	3
83	Fate of parental mitochondria in embryonic stem hybrid cells. <i>Cell and Tissue Biology</i> , 2008, 2, 393-399.	0.4	2
84	Status of the Cattle Genome Map. <i>Cytogenetic and Genome Research</i> , 2011, 134, 1-8.	1.1	2
85	Cytogenetics and chromosome maps.. , 0, , 103-129.		2
86	Using PCR Markers for Mapping Pig Chromosome 12. <i>Russian Journal of Genetics</i> , 2001, 37, 276-282.	0.6	1
87	The Structure of a Conserved Region of Porcine Genome, Represented in Human Genome by Chromosome 17. <i>Russian Journal of Genetics</i> , 2004, 40, 782-788.	0.6	1
88	Construction of High-Resolution Comparative Maps in Mammals Using BAC-End Sequences. <i>Methods in Molecular Biology</i> , 2008, 422, 79-90.	0.9	1
89	Importance of genomic research in studying the history of development of domestic animals. <i>Molekuliarnaia Genetika, Mikrobiologiya I Virusologiya</i> , 2016, 34, 123.	0.4	1
90	Mapping of five genes from human chromosome 17 to chromosome hn of the common shrew <i>Sorex araneus</i> . <i>Acta Theriologica</i> , 2000, 45, 143-146.	1.1	1

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91	Comparative analysis of allele frequencies for DNA polymorphisms associated with disease and economically important traits in the genomes of Russian and foreign cattle breeds. Vavilovskii Zhurnal Genetiki i Seleksii, 2022, 26, 298-307.	1.1	1
92	Discovery, validation and characterization of 1039 cattle single nucleotide polymorphisms. Animal Genetics, 2010, 41, 421-423.	1.7	0
93	Jurassic Park: What Did the Genomes of Dinosaurs Look Like?. , 2019, , 331-348.		0