

Denis Larkin

List of Publications by Year in descending order

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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	Augmin-dependent microtubule self-organization drives kinetochore fiber maturation in mammals. <i>Cell Reports</i> , 2022, 39, 110610.	6.4	14
2	Copy number variants in genomes of local sheep breeds from Russia. <i>Animal Genetics</i> , 2022, 53, 119-132.	1.7	8
3	Comparative analysis of allele frequencies for DNA polymorphisms associated with disease and economically important traits in the genomes of Russian and foreign cattle breeds. <i>Vavilovskii Zhurnal Genetiki i Selekcii</i> , 2022, 26, 298-307.	1.1	1
4	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
5	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
6	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
7	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
8	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
9	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
10	Time lapse: A glimpse into prehistoric genomics. <i>European Journal of Medical Genetics</i> , 2020, 63, 103640.	1.3	4
11	Avian Chromosomal Evolution. , 2019, , 69-92.		4
12	Jurassic Park: What Did the Genomes of Dinosaurs Look Like?. , 2019, , 331-348.		0
13	An integrated chromosome-scale genome assembly of the Masai giraffe (<i>Giraffa camelopardalis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	6.4	13
14	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
15	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	8.8	71
16	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
17	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
18	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

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19	Genome-wide association study for body weight in cattle populations from Siberia. <i>Animal Genetics</i> , 2019, 50, 250-253.	1.7	16
20	A Near Chromosome Assembly of the Dromedary Camel Genome. <i>Frontiers in Genetics</i> , 2019, 10, 32.	2.3	7
21	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
22	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
23	Comparative Chromosome Mapping of Musk Ox and the X Chromosome among Some Bovidae Species. <i>Genes</i> , 2019, 10, 857.	2.4	8
24	Patterns of microchromosome organization remain highly conserved throughout avian evolution. <i>Chromosoma</i> , 2019, 128, 21-29.	2.2	67
25	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
26	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
27	G-Anchor: a novel approach for whole-genome comparative mapping utilizing evolutionary conserved DNA sequences. <i>GigaScience</i> , 2018, 7, .	6.4	3
28	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
29	Chromosome Segregation Is Biased by Kinetochore Size. <i>Current Biology</i> , 2018, 28, 1344-1356.e5.	3.9	94
30	Genome-wide genotyping uncovers genetic profiles and history of the Russian cattle breeds. <i>Heredity</i> , 2018, 120, 125-137.	2.6	61
31	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
32	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
33	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
34	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
35	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
36	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018, 9, 308.	2.4	14

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37	Genes related to the white face colour pattern in eight Russian cattle breeds. Vavilovskii Zhurnal Genetiki i Seleksii, 2018, 22, 217-223.	1.1	3
38	Upgrading short-read animal genome assemblies to chromosome level using comparative genomics and a universal probe set. Genome Research, 2017, 27, 875-884.	5.5	97
39	Reconstruction and evolutionary history of eutherian chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5379-E5388.	7.1	94
40	Synteny Explorer: An Interactive Visualization Application for Teaching Genome Evolution. IEEE Transactions on Visualization and Computer Graphics, 2017, 23, 711-720.	4.4	7
41	A compendium and functional characterization of mammalian genes involved in adaptation to Arctic or Antarctic environments. BMC Genetics, 2017, 18, 111.	2.7	37
42	X Chromosome Evolution in Cetartiodactyla. Genes, 2017, 8, 216.	2.4	24
43	Contrasting origin of B chromosomes in two cervids (Siberian roe deer and grey brocket deer) unravelled by chromosome-specific DNA sequencing. BMC Genomics, 2016, 17, 618.	2.8	47
44	The genomes and history of domestic animals. Molecular Genetics, Microbiology and Virology, 2016, 31, 197-202.	0.3	11
45	Novel Insights into Chromosome Evolution in Birds, Archosaurs, and Reptiles. Genome Biology and Evolution, 2016, 8, 2442-2451.	2.5	66
46	Mammalian comparative genomics reveals genetic and epigenetic features associated with genome reshuffling in Rodentia. Genome Biology and Evolution, 2016, 8, evw276.	2.5	21
47	Identification of a nonsense mutation in APAF1 that is likely causal for a decrease in reproductive efficiency in Holstein dairy cattle. Journal of Dairy Science, 2016, 99, 6693-6701.	3.4	66
48	Importance of genomic research in studying the history of development of domestic animals. Molekuliarnaia Genetika, Mikrobiologiia i Virusologiia, 2016, 34, 123.	0.4	1
49	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
50	Population structure and history of the Welsh sheep breeds determined by whole genome genotyping. BMC Genetics, 2015, 16, 65.	2.7	69
51	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	12.6	895
52	Reconstruction of gross avian genome structure, organization and evolution suggests that the chicken lineage most closely resembles the dinosaur avian ancestor. BMC Genomics, 2014, 15, 1060.	2.8	71
53	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
54	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	12.8	124

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55	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
56	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
57	Cattle genomics and its implications for future nutritional strategies for dairy cattle. <i>Animal</i> , 2013, 7, 172-183.	3.3	12
58	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	12.8	229
59	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
60	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
61	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
62	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949.	21.4	708
63	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
64	Schistosoma comparative genomics: integrating genome structure, parasite biology and anthelmintic discovery. <i>Trends in Parasitology</i> , 2011, 27, 555-564.	3.3	31
65	Status of the Cattle Genome Map. <i>Cytogenetic and Genome Research</i> , 2011, 134, 1-8.	1.1	2
66	Discovery, validation and characterization of 1039 cattle single nucleotide polymorphisms. <i>Animal Genetics</i> , 2010, 41, 421-423.	1.7	0
67	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
68	Every genome sequence needs a good map. <i>Genome Research</i> , 2009, 19, 1925-1928.	5.5	148
69	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
70	SytenyTracker: a tool for defining homologous syteny blocks using radiation hybrid maps and whole-genome sequence. <i>BMC Research Notes</i> , 2009, 2, 148.	1.4	28
71	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
72	Breakpoint regions and homologous syteny blocks in chromosomes have different evolutionary histories. <i>Genome Research</i> , 2009, 19, 770-777.	5.5	163

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73	Fate of parental mitochondria in embryonic stem hybrid cells. <i>Cell and Tissue Biology</i> , 2008, 2, 393-399.	0.4	2
74	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
75	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
76	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
77	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
78	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
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	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
81	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
82	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
83	Synthesis and Practical Use of 1H-1,2,3-Benzotriazole-5-carboxaldehyde for Reductive Amination. <i>Synthetic Communications</i> , 2005, 35, 2587-2595.	2.1	4
84	Piggy-BACing the human genome. <i>Genomics</i> , 2005, 86, 739-752.	2.9	103
85	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. <i>Science</i> , 2005, 309, 613-617.	12.6	542
86	Multi-species comparative mapping in silico using the COMPASS strategy. <i>Bioinformatics</i> , 2004, 20, 148-154.	4.1	9
87	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
88	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
89	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
90	Using PCR Markers for Mapping Pig Chromosome 12. <i>Russian Journal of Genetics</i> , 2001, 37, 276-282.	0.6	1

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91	Comparative genome mapping in mammals: the shrew map. Acta Theriologica, 2000, 45, 131-141.	1.1	3
92	Mapping of five genes from human chromosome 17 to chromosome hn of the common shrew Sorex araneus. Acta Theriologica, 2000, 45, 143-146.	1.1	1
93	Cytogenetics and chromosome maps., 0, , 103-129.		2