Kirk E Lohmueller

List of Publications by Year
in descending order

79	11,018	81900 39	74163 75
papers	citations	h-index	g-index

107	107	107	14068
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease. Nature Genetics, 2003, 33, 177-182.	21.4	1,818
2	A comprehensive review of genetic association studies. Genetics in Medicine, 2002, 4, 45-61.	2.4	1,518
3	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	12.6	675
4	Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. Nature, 2010, 464, 898-902.	27.8	635
5	Assessing the Evolutionary Impact of Amino Acid Mutations in the Human Genome. PLoS Genetics, 2008, 4, e1000083.	3.5	586
6	Methods for High-Density Admixture Mapping of Disease Genes. American Journal of Human Genetics, 2004, 74, 979-1000.	6.2	437
7	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. PLoS Biology, 2010, 8, e1000451.	5.6	429
8	Proportionally more deleterious genetic variation in European than in African populations. Nature, 2008, 451, 994-997.	27.8	365
9	Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 152-157.	7.1	265
10	Genomic Flatlining in the Endangered Island Fox. Current Biology, 2016, 26, 1183-1189.	3.9	201
11	Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. Science Advances, 2019, 5, eaau0757.	10.3	173
12	Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231.	2.6	170
13	Inference of the Distribution of Selection Coefficients for New Nonsynonymous Mutations Using Large Samples. Genetics, 2017, 206, 345-361.	2.9	170
14	A Model-Based Approach for Identifying Signatures of Ancient Balancing Selection in Genetic Data. PLoS Genetics, 2014, 10, e1004561.	3.5	159
15	Global distribution of genomic diversity underscores rich complex history of continental human populations. Genome Research, 2009, 19, 795-803.	5.5	155
16	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326.	3.5	146
17	The Impact of Population Demography and Selection on the Genetic Architecture of Complex Traits. PLoS Genetics, 2014, 10, e1004379.	3.5	146
18	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.	8.3	143

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19	Purging of Strongly Deleterious Mutations Explains Long-Term Persistence and Absence of Inbreeding Depression in Island Foxes. Current Biology, 2018, 28, 3487-3494.e4.	3.9	140
20	Strongly deleterious mutations are a primary determinant of extinction risk due to inbreeding depression. Evolution Letters, 2021, 5, 33-47.	3.3	127
21	The distribution of deleterious genetic variation in human populations. Current Opinion in Genetics and Development, 2014, 29, 139-146.	3.3	126
22	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. American Journal of Human Genetics, 2013, 93, 1072-1086.	6.2	124
23	Patterns of de novo tandem repeat mutations and their role in autism. Nature, 2021, 589, 246-250.	27.8	114
24	Detecting Ancient Admixture and Estimating Demographic Parameters in Multiple Human Populations. Molecular Biology and Evolution, 2009, 26, 1823-1827.	8.9	113
25	Determining the factors driving selective effects of new nonsynonymous mutations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4465-4470.	7.1	113
26	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	6.0	112
27	Gene expression drives the evolution of dominance. Nature Communications, 2018, 9, 2750.	12.8	97
28	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	21.4	96
29	Deleterious variation shapes the genomic landscape of introgression. PLoS Genetics, 2018, 14, e1007741.	3.5	95
30	Natural Selection Reduced Diversity on Human Y Chromosomes. PLoS Genetics, 2014, 10, e1004064.	3.5	91
31	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	12.8	81
32	Selection and Reduced Population Size Cannot Explain Higher Amounts of Neandertal Ancestry in East Asian than in European Human Populations. American Journal of Human Genetics, 2015, 96, 454-461.	6.2	80
33	Genomic history of the Sardinian population. Nature Genetics, 2018, 50, 1426-1434.	21.4	71
34	Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. G3: Genes, Genomes, Genetics, 2017, 7, 3605-3620.	1.8	70
35	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	9.5	65
36	Population genetic models of GERP scores suggest pervasive turnover of constrained sites across mammalian evolution. PLoS Genetics, 2020, 16, e1008827.	3.5	65

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37	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. Genetics, 2017, 205, 787-801.	2.9	54
38	Methods for Human Demographic Inference Using Haplotype Patterns From Genomewide Single-Nucleotide Polymorphism Data. Genetics, 2009, 182, 217-231.	2.9	53
39	Variants Associated with Common Disease Are Not Unusually Differentiated in Frequency across Populations. American Journal of Human Genetics, 2006, 78, 130-136.	6.2	52
40	Determining the Effect of Natural Selection on Linked Neutral Divergence across Species. PLoS Genetics, 2016, 12, e1006199.	3.5	49
41	The critically endangered vaquita is not doomed to extinction by inbreeding depression. Science, 2022, 376, 635-639.	12.6	49
42	Understanding the Hidden Complexity of Latin American Population Isolates. American Journal of Human Genetics, 2018, 103, 707-726.	6.2	48
43	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
44	Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. Molecular Biology and Evolution, 2018, 35, 1190-1209.	8.9	45
45	Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles. BMC Bioinformatics, 2015, 16, 298.	2.6	40
46	Evolutionary History, Selective Sweeps, and Deleterious Variation in the Dog. Annual Review of Ecology, Evolution, and Systematics, 2016, 47, 73-96.	8.3	37
47	Genomic divergence across ecological gradients in the Central African rainforest songbird (<scp>A</scp>ndropadus virens). Molecular Ecology, 2017, 26, 4966-4977.	3.9	35
48	RADseq data reveal ancient, but not pervasive, introgression between Californian tree and scrub oak species (Quercus sect. Quercus: Fagaceae). Molecular Ecology, 2018, 27, 4556-4571.	3.9	33
49	Detecting Directional Selection in the Presence of Recent Admixture in African-Americans. Genetics, 2011, 187, 823-835.	2.9	32
50	The Impact of Recessive Deleterious Variation on Signals of Adaptive Introgression in Human Populations. Genetics, 2020, 215, 799-812.	2.9	30
51	Negative selection on complex traits limits phenotype prediction accuracy between populations. American Journal of Human Genetics, 2021, 108, 620-631.	6.2	30
52	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. Nature Communications, 2022, 13, 2047.	12.8	30
53	The Effect of Recent Admixture on Inference of Ancient Human Population History. Genetics, 2010, 185, 611-622.	2.9	29
54	On the prospect of achieving accurate joint estimation of selection with population history. Genome Biology and Evolution, 2022, 14, .	2.5	28

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55	Calculating the Weight of Evidence in Lowâ€Template Forensic <scp>DNA</scp> Casework. Journal of Forensic Sciences, 2013, 58, S243-9.	1.6	27
56	Growth factor gene IGF1 is associated with bill size in the black-bellied seedcracker Pyrenestes ostrinus. Nature Communications, 2018, 9, 4855.	12.8	24
57	Validation of probabilistic genotyping software for use in forensic DNA casework: Definitions and illustrations. Science and Justice - Journal of the Forensic Science Society, 2016, 56, 104-108.	2.1	23
58	Sex-Averaged Recombination and Mutation Rates on the X Chromosome: A Comment on Labuda etÂal.. American Journal of Human Genetics, 2010, 86, 978-980.	6.2	22
59	Analysis of allelic drop-out using the IdentifilerÂ® and PowerPlexÂ® 16 forensic STR typing systems. Forensic Science International: Genetics, 2014, 12, 1-11.	3.1	19
60	Greater strength of selection and higher proportion of beneficial amino acid changing mutations in humans compared with mice and Drosophila melanogaster. Genome Research, 2021, 31, 110-120.	5.5	17
61	The impact of identity by descent on fitness and disease in dogs. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	17
62	Negative linkage disequilibrium between amino acid changing variants reveals interference among deleterious mutations in the human genome. PLoS Genetics, 2021, 17, e1009676.	3.5	15
63	Genomic analyses reveal rangeâ€wide devastation of sea otter populations. Molecular Ecology, 2023, 32, 281-298.	3.9	12
64	PReFerSim: fast simulation of demography and selection under the Poisson Random Field model. Bioinformatics, 2016, 32, 3516-3518.	4.1	11
65	An assessment of the information content of likelihood ratios derived from complex mixtures. Forensic Science International: Genetics, 2016, 22, 64-72.	3.1	7
66	Testing whether stutter and low-level DNA peaks are additive. Forensic Science International: Genetics, 2019, 43, 102166.	3.1	7
67	Complex patterns of sex-biased demography in canines. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20181976.	2.6	6
68	Ten simple rules for giving an effective academic job talk. PLoS Computational Biology, 2019, 15, e1007163.	3.2	5
69	A signature of Neanderthal introgression on molecular mechanisms of environmental responses. PLoS Genetics, 2021, 17, e1009493.	3.5	5
70	Graydon et al. provide no new evidence that forensic STR loci are functional. Forensic Science International: Genetics, 2010, 4, 273-274.	3.1	4
71	Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders. European Journal of Human Genetics, 2016, 24, 113-119.	2.8	3
72	On the origin of Peter Rabbit. Science, 2014, 345, 1000-1001.	12.6	2

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73	Fitting the Baldingâ€“Nichols model to forensic databases. Forensic Science International: Genetics, 2015, 19, 86-91.	3.1	2
74	Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. Nature Communications, 2020, 11, 6168.	12.8	1
75	Haplotype-based inference of the distribution of fitness effects. Genetics, 2022, 220, .	2.9	1
76	Title is missing!. , 2020, 16, e1008827.		0
77	Title is missing!. , 2020, 16, e1008827.		0
78	Title is missing!. , 2020, 16, e1008827.		0
79	Title is missing!. , 2020, 16, e1008827.		0