

Kirk E Lohmueller

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

11,018
citations

93792

39
h-index

84171

75
g-index

107
all docs

107
docs citations

107
times ranked

15750
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease. <i>Nature Genetics</i> , 2003, 33, 177-182. | 9.4 | 1,818 |
| 2 | A comprehensive review of genetic association studies. <i>Genetics in Medicine</i> , 2002, 4, 45-61. | 1.1 | 1,518 |
| 3 | An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98. | 6.0 | 675 |
| 4 | Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. <i>Nature</i> , 2010, 464, 898-902. | 13.7 | 635 |
| 5 | Assessing the Evolutionary Impact of Amino Acid Mutations in the Human Genome. <i>PLoS Genetics</i> , 2008, 4, e1000083. | 1.5 | 586 |
| 6 | Methods for High-Density Admixture Mapping of Disease Genes. <i>American Journal of Human Genetics</i> , 2004, 74, 979-1000. | 2.6 | 437 |
| 7 | A Simple Genetic Architecture Underlies Morphological Variation in Dogs. <i>PLoS Biology</i> , 2010, 8, e1000451. | 2.6 | 429 |
| 8 | Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008, 451, 994-997. | 13.7 | 365 |
| 9 | Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 152-157. | 3.3 | 265 |
| 10 | Genomic Flatlining in the Endangered Island Fox. <i>Current Biology</i> , 2016, 26, 1183-1189. | 1.8 | 201 |
| 11 | Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. <i>Science Advances</i> , 2019, 5, eaau0757. | 4.7 | 173 |
| 12 | Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011, 12, 231. | 1.2 | 170 |
| 13 | Inference of the Distribution of Selection Coefficients for New Nonsynonymous Mutations Using Large Samples. <i>Genetics</i> , 2017, 206, 345-361. | 1.2 | 170 |
| 14 | A Model-Based Approach for Identifying Signatures of Ancient Balancing Selection in Genetic Data. <i>PLoS Genetics</i> , 2014, 10, e1004561. | 1.5 | 159 |
| 15 | Global distribution of genomic diversity underscores rich complex history of continental human populations. <i>Genome Research</i> , 2009, 19, 795-803. | 2.4 | 155 |
| 16 | Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002326. | 1.5 | 146 |
| 17 | The Impact of Population Demography and Selection on the Genetic Architecture of Complex Traits. <i>PLoS Genetics</i> , 2014, 10, e1004379. | 1.5 | 146 |
| 18 | Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 433-456. | 3.8 | 143 |

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|----|---|------|-----------|
| 19 | Purging of Strongly Deleterious Mutations Explains Long-Term Persistence and Absence of Inbreeding Depression in Island Foxes. <i>Current Biology</i> , 2018, 28, 3487-3494.e4. | 1.8 | 140 |
| 20 | Strongly deleterious mutations are a primary determinant of extinction risk due to inbreeding depression. <i>Evolution Letters</i> , 2021, 5, 33-47. | 1.6 | 127 |
| 21 | The distribution of deleterious genetic variation in human populations. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 139-146. | 1.5 | 126 |
| 22 | Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2013, 93, 1072-1086. | 2.6 | 124 |
| 23 | Patterns of de novo tandem repeat mutations and their role in autism. <i>Nature</i> , 2021, 589, 246-250. | 13.7 | 114 |
| 24 | Detecting Ancient Admixture and Estimating Demographic Parameters in Multiple Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 1823-1827. | 3.5 | 113 |
| 25 | Determining the factors driving selective effects of new nonsynonymous mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4465-4470. | 3.3 | 113 |
| 26 | A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, . | 2.8 | 112 |
| 27 | Gene expression drives the evolution of dominance. <i>Nature Communications</i> , 2018, 9, 2750. | 5.8 | 97 |
| 28 | Height-reducing variants and selection for short stature in Sardinia. <i>Nature Genetics</i> , 2015, 47, 1352-1356. | 9.4 | 96 |
| 29 | Deleterious variation shapes the genomic landscape of introgression. <i>PLoS Genetics</i> , 2018, 14, e1007741. | 1.5 | 95 |
| 30 | Natural Selection Reduced Diversity on Human Y Chromosomes. <i>PLoS Genetics</i> , 2014, 10, e1004064. | 1.5 | 91 |
| 31 | Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. <i>Nature Communications</i> , 2014, 5, 3983. | 5.8 | 81 |
| 32 | Selection and Reduced Population Size Cannot Explain Higher Amounts of Neandertal Ancestry in East Asian than in European Human Populations. <i>American Journal of Human Genetics</i> , 2015, 96, 454-461. | 2.6 | 80 |
| 33 | Genomic history of the Sardinian population. <i>Nature Genetics</i> , 2018, 50, 1426-1434. | 9.4 | 71 |
| 34 | Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3605-3620. | 0.8 | 70 |
| 35 | Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019, 6, 810-824. | 4.6 | 65 |
| 36 | Population genetic models of GERP scores suggest pervasive turnover of constrained sites across mammalian evolution. <i>PLoS Genetics</i> , 2020, 16, e1008827. | 1.5 | 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. <i>Genetics</i> , 2017, 205, 787-801. | 1.2 | 54 |
| 38 | Methods for Human Demographic Inference Using Haplotype Patterns From Genomewide Single-Nucleotide Polymorphism Data. <i>Genetics</i> , 2009, 182, 217-231. | 1.2 | 53 |
| 39 | Variants Associated with Common Disease Are Not Unusually Differentiated in Frequency across Populations. <i>American Journal of Human Genetics</i> , 2006, 78, 130-136. | 2.6 | 52 |
| 40 | Determining the Effect of Natural Selection on Linked Neutral Divergence across Species. <i>PLoS Genetics</i> , 2016, 12, e1006199. | 1.5 | 49 |
| 41 | The critically endangered vaquita is not doomed to extinction by inbreeding depression. <i>Science</i> , 2022, 376, 635-639. | 6.0 | 49 |
| 42 | Understanding the Hidden Complexity of Latin American Population Isolates. <i>American Journal of Human Genetics</i> , 2018, 103, 707-726. | 2.6 | 48 |
| 43 | 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. | 3.5 | 48 |
| 44 | Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. <i>Molecular Biology and Evolution</i> , 2018, 35, 1190-1209. | 3.5 | 45 |
| 45 | Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles. <i>BMC Bioinformatics</i> , 2015, 16, 298. | 1.2 | 40 |
| 46 | Evolutionary History, Selective Sweeps, and Deleterious Variation in the Dog. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2016, 47, 73-96. | 3.8 | 37 |
| 47 | Genomic divergence across ecological gradients in the Central African rainforest songbird (<i>Ampelis gularis</i>). <i>Molecular Ecology</i> , 2017, 26, 4966-4977. | 2.0 | 35 |
| 48 | RADseq data reveal ancient, but not pervasive, introgression between Californian tree and scrub oak species (<i>Quercus</i> sect. <i>Quercus</i> : Fagaceae). <i>Molecular Ecology</i> , 2018, 27, 4556-4571. | 2.0 | 33 |
| 49 | Detecting Directional Selection in the Presence of Recent Admixture in African-Americans. <i>Genetics</i> , 2011, 187, 823-835. | 1.2 | 32 |
| 50 | The Impact of Recessive Deleterious Variation on Signals of Adaptive Introgression in Human Populations. <i>Genetics</i> , 2020, 215, 799-812. | 1.2 | 30 |
| 51 | Negative selection on complex traits limits phenotype prediction accuracy between populations. <i>American Journal of Human Genetics</i> , 2021, 108, 620-631. | 2.6 | 30 |
| 52 | High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. <i>Nature Communications</i> , 2022, 13, 2047. | 5.8 | 30 |
| 53 | The Effect of Recent Admixture on Inference of Ancient Human Population History. <i>Genetics</i> , 2010, 185, 611-622. | 1.2 | 29 |
| 54 | On the prospect of achieving accurate joint estimation of selection with population history. <i>Genome Biology and Evolution</i> , 2022, 14, . | 1.1 | 28 |

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|----|---|-----|-----------|
| 55 | Calculating the Weight of Evidence in Low-Template Forensic DNA Casework. <i>Journal of Forensic Sciences</i> , 2013, 58, S243-9. | 0.9 | 27 |
| 56 | Growth factor gene IGF1 is associated with bill size in the black-bellied seedcracker <i>Pyrenestes ostrinus</i> . <i>Nature Communications</i> , 2018, 9, 4855. | 5.8 | 24 |
| 57 | Validation of probabilistic genotyping software for use in forensic DNA casework: Definitions and illustrations. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2016, 56, 104-108. | 1.3 | 23 |
| 58 | Sex-Averaged Recombination and Mutation Rates on the X Chromosome: A Comment on Labuda et al.. <i>American Journal of Human Genetics</i> , 2010, 86, 978-980. | 2.6 | 22 |
| 59 | Analysis of allelic drop-out using the Identifiler® and PowerPlex® 16 forensic STR typing systems. <i>Forensic Science International: Genetics</i> , 2014, 12, 1-11. | 1.6 | 19 |
| 60 | Greater strength of selection and higher proportion of beneficial amino acid changing mutations in humans compared with mice and <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2021, 31, 110-120. | 2.4 | 17 |
| 61 | The impact of identity by descent on fitness and disease in dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 17 |
| 62 | Negative linkage disequilibrium between amino acid changing variants reveals interference among deleterious mutations in the human genome. <i>PLoS Genetics</i> , 2021, 17, e1009676. | 1.5 | 15 |
| 63 | Genomic analyses reveal range-wide devastation of sea otter populations. <i>Molecular Ecology</i> , 2023, 32, 281-298. | 2.0 | 12 |
| 64 | PReFerSim: fast simulation of demography and selection under the Poisson Random Field model. <i>Bioinformatics</i> , 2016, 32, 3516-3518. | 1.8 | 11 |
| 65 | An assessment of the information content of likelihood ratios derived from complex mixtures. <i>Forensic Science International: Genetics</i> , 2016, 22, 64-72. | 1.6 | 7 |
| 66 | Testing whether stutter and low-level DNA peaks are additive. <i>Forensic Science International: Genetics</i> , 2019, 43, 102166. | 1.6 | 7 |
| 67 | Complex patterns of sex-biased demography in canines. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20181976. | 1.2 | 6 |
| 68 | Ten simple rules for giving an effective academic job talk. <i>PLoS Computational Biology</i> , 2019, 15, e1007163. | 1.5 | 5 |
| 69 | A signature of Neanderthal introgression on molecular mechanisms of environmental responses. <i>PLoS Genetics</i> , 2021, 17, e1009493. | 1.5 | 5 |
| 70 | Graydon et al. provide no new evidence that forensic STR loci are functional. <i>Forensic Science International: Genetics</i> , 2010, 4, 273-274. | 1.6 | 4 |
| 71 | Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders. <i>European Journal of Human Genetics</i> , 2016, 24, 113-119. | 1.4 | 3 |
| 72 | On the origin of Peter Rabbit. <i>Science</i> , 2014, 345, 1000-1001. | 6.0 | 2 |

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|----|--|-----|-----------|
| 73 | Fitting the Balding-Nichols model to forensic databases. <i>Forensic Science International: Genetics</i> , 2015, 19, 86-91. | 1.6 | 2 |
| 74 | Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. <i>Nature Communications</i> , 2020, 11, 6168. | 5.8 | 1 |
| 75 | Haplotype-based inference of the distribution of fitness effects. <i>Genetics</i> , 2022, 220, . | 1.2 | 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 |