Kirk E Lohmueller

List of Publications by Year
in descending order

79	11,018	93792 39	84171 75
papers	citations	h-index	g-index

107	107	107	15750
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic analyses reveal rangeâ€wide devastation of sea otter populations. Molecular Ecology, 2023, 32, 281-298.	2.0	12
2	Haplotype-based inference of the distribution of fitness effects. Genetics, 2022, 220, .	1.2	1
3	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. Nature Communications, 2022, 13, 2047.	5.8	30
4	The critically endangered vaquita is not doomed to extinction by inbreeding depression. Science, 2022, 376, 635-639.	6.0	49
5	On the prospect of achieving accurate joint estimation of selection with population history. Genome Biology and Evolution, 2022, 14, .	1.1	28
6	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.	2.4	17
7	Patterns of de novo tandem repeat mutations and their role in autism. Nature, 2021, 589, 246-250.	13.7	114
8	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, .	3.3	17
9	Negative selection on complex traits limits phenotype prediction accuracy between populations. American Journal of Human Genetics, 2021, 108, 620-631.	2.6	30
10	Negative linkage disequilibrium between amino acid changing variants reveals interference among deleterious mutations in the human genome. PLoS Genetics, 2021, 17, e1009676.	1.5	15
11	A signature of Neanderthal introgression on molecular mechanisms of environmental responses. PLoS Genetics, 2021, 17, e1009493.	1.5	5
12	Strongly deleterious mutations are a primary determinant of extinction risk due to inbreeding depression. Evolution Letters, 2021, 5, 33-47.	1.6	127
13	Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. Nature Communications, 2020, 11, 6168.	5.8	1
14	Population genetic models of GERP scores suggest pervasive turnover of constrained sites across mammalian evolution. PLoS Genetics, 2020, 16, e1008827.	1.5	65
15	The Impact of Recessive Deleterious Variation on Signals of Adaptive Introgression in Human Populations. Genetics, 2020, 215, 799-812.	1.2	30
16	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	2.8	112
17	Title is missing!. , 2020, 16, e1008827.		0
18	Title is missing!. , 2020, 16, e1008827.		0

#	Article	IF	Citations
19	Title is missing!. , 2020, 16, e1008827.		0
20	Title is missing!. , 2020, 16, e1008827.		0
21	Ten simple rules for giving an effective academic job talk. PLoS Computational Biology, 2019, 15, e1007163.	1.5	5
22	Testing whether stutter and low-level DNA peaks are additive. Forensic Science International: Genetics, 2019, 43, 102166.	1.6	7
23	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.	3.5	48
24	Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. Science Advances, 2019, 5, eaau0757.	4.7	173
25	Complex patterns of sex-biased demography in canines. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20181976.	1.2	6
26	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	4.6	65
27	Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. Molecular Biology and Evolution, 2018, 35, 1190-1209.	3.5	45
28	Growth factor gene IGF1 is associated with bill size in the black-bellied seedcracker Pyrenestes ostrinus. Nature Communications, 2018, 9, 4855.	5.8	24
29	Deleterious variation shapes the genomic landscape of introgression. PLoS Genetics, 2018, 14, e1007741.	1.5	95
30	Understanding the Hidden Complexity of Latin American Population Isolates. American Journal of Human Genetics, 2018, 103, 707-726.	2.6	48
31	Purging of Strongly Deleterious Mutations Explains Long-Term Persistence and Absence of Inbreeding Depression in Island Foxes. Current Biology, 2018, 28, 3487-3494.e4.	1.8	140
32	Genomic history of the Sardinian population. Nature Genetics, 2018, 50, 1426-1434.	9.4	71
33	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.	2.0	33
34	Gene expression drives the evolution of dominance. Nature Communications, 2018, 9, 2750.	5.8	97
35	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.	3.8	143
36	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.	3.3	113

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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.	1.2	54
38	Genomic divergence across ecological gradients in the Central African rainforest songbird (<scp>A</scp>ndropadus virens). Molecular Ecology, 2017, 26, 4966-4977.	2.0	35
39	Inference of the Distribution of Selection Coefficients for New Nonsynonymous Mutations Using Large Samples. Genetics, 2017, 206, 345-361.	1.2	170
40	Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. G3: Genes, Genomes, Genetics, 2017, 7, 3605-3620.	0.8	70
41	Genomic Flatlining in the Endangered Island Fox. Current Biology, 2016, 26, 1183-1189.	1.8	201
42	PReFerSim: fast simulation of demography and selection under the Poisson Random Field model. Bioinformatics, 2016, 32, 3516-3518.	1.8	11
43	Evolutionary History, Selective Sweeps, and Deleterious Variation in the Dog. Annual Review of Ecology, Evolution, and Systematics, 2016, 47, 73-96.	3.8	37
44	An assessment of the information content of likelihood ratios derived from complex mixtures. Forensic Science International: Genetics, 2016, 22, 64-72.	1.6	7
45	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.	1.3	23
46	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.	3.3	265
47	Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders. European Journal of Human Genetics, 2016, 24, 113-119.	1.4	3
48	Determining the Effect of Natural Selection on Linked Neutral Divergence across Species. PLoS Genetics, 2016, 12, e1006199.	1.5	49
49	Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles. BMC Bioinformatics, 2015, 16, 298.	1.2	40
50	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.	2.6	80
51	Fitting the Baldingâ€“Nichols model to forensic databases. Forensic Science International: Genetics, 2015, 19, 86-91.	1.6	2
52	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	9.4	96
53	Natural Selection Reduced Diversity on Human Y Chromosomes. PLoS Genetics, 2014, 10, e1004064.	1.5	91
54	A Model-Based Approach for Identifying Signatures of Ancient Balancing Selection in Genetic Data. PLoS Genetics, 2014, 10, e1004561.	1.5	159

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55	The Impact of Population Demography and Selection on the Genetic Architecture of Complex Traits. PLoS Genetics, 2014, 10, e1004379.	1.5	146
56	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	5.8	81
57	Analysis of allelic drop-out using the IdentifilerÂ® and PowerPlexÂ® 16 forensic STR typing systems. Forensic Science International: Genetics, 2014, 12, 1-11.	1.6	19
58	On the origin of Peter Rabbit. Science, 2014, 345, 1000-1001.	6.0	2
59	The distribution of deleterious genetic variation in human populations. Current Opinion in Genetics and Development, 2014, 29, 139-146.	1.5	126
60	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.	2.6	124
61	Calculating the Weight of Evidence in Lowâ€Template Forensic <scp>DNA</scp> Casework. Journal of Forensic Sciences, 2013, 58, S243-9.	0.9	27
62	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	6.0	675
63	Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231.	1.2	170
64	Detecting Directional Selection in the Presence of Recent Admixture in African-Americans. Genetics, 2011, 187, 823-835.	1.2	32
65	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326.	1.5	146
66	Sex-Averaged Recombination and Mutation Rates on the X Chromosome: A Comment on Labuda etÂal.. American Journal of Human Genetics, 2010, 86, 978-980.	2.6	22
67	Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. Nature, 2010, 464, 898-902.	13.7	635
68	The Effect of Recent Admixture on Inference of Ancient Human Population History. Genetics, 2010, 185, 611-622.	1.2	29
69	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. PLoS Biology, 2010, 8, e1000451.	2.6	429
70	Graydon et al. provide no new evidence that forensic STR loci are functional. Forensic Science International: Genetics, 2010, 4, 273-274.	1.6	4
71	Global distribution of genomic diversity underscores rich complex history of continental human populations. Genome Research, 2009, 19, 795-803.	2.4	155
72	Detecting Ancient Admixture and Estimating Demographic Parameters in Multiple Human Populations. Molecular Biology and Evolution, 2009, 26, 1823-1827.	3.5	113

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73	Methods for Human Demographic Inference Using Haplotype Patterns From Genomewide Single-Nucleotide Polymorphism Data. Genetics, 2009, 182, 217-231.	1.2	53
74	Proportionally more deleterious genetic variation in European than in African populations. Nature, 2008, 451, 994-997.	13.7	365
75	Assessing the Evolutionary Impact of Amino Acid Mutations in the Human Genome. PLoS Genetics, 2008, 4, e1000083.	1.5	586
76	Variants Associated with Common Disease Are Not Unusually Differentiated in Frequency across Populations. American Journal of Human Genetics, 2006, 78, 130-136.	2.6	52
77	Methods for High-Density Admixture Mapping of Disease Genes. American Journal of Human Genetics, 2004, 74, 979-1000.	2.6	437
78	Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease. Nature Genetics, 2003, 33, 177-182.	9.4	1,818
79	A comprehensive review of genetic association studies. Genetics in Medicine, 2002, 4, 45-61.	1.1	1,518