Leonid Kruglyak

List of Publications by Year
in descending order

73	18,149	44069 48	88630 70
papers	citations	h-index	g-index

95	95	95	15560
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. Nature Genetics, 1995, 11, 241-247.	21.4	5,020
2	Genetic Dissection of Transcriptional Regulation in Budding Yeast. Science, 2002, 296, 752-755.	12.6	1,261
3	The role of regulatory variation in complex traits and disease. Nature Reviews Genetics, 2015, 16, 197-212.	16.3	864
4	Genetic basis of proteome variation in yeast. Nature Genetics, 2007, 39, 1369-1375.	21.4	767
5	Trans-acting regulatory variation in Saccharomyces cerevisiae and the role of transcription factors. Nature Genetics, 2003, 35, 57-64.	21.4	583
6	Guilt by association. Nature Genetics, 2000, 26, 135-137.	21.4	569
7	The landscape of genetic complexity across 5,700 gene expression traits in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1572-1577.	7.1	544
8	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. Nature Genetics, 2008, 40, 854-861.	21.4	515
9	The use of a genetic map of biallelic markers in linkage studies. Nature Genetics, 1997, 17, 21-24.	21.4	452
10	Comprehensive polymorphism survey elucidates population structure of Saccharomyces cerevisiae. Nature, 2009, 458, 342-345.	27.8	431
11	Finding the sources of missing heritability in a yeast cross. Nature, 2013, 494, 234-237.	27.8	427
12	Recombinational Landscape and Population Genomics of Caenorhabditis elegans. PLoS Genetics, 2009, 5, e1000419.	3.5	381
13	Dissection of genetically complex traits with extremely large pools of yeast segregants. Nature, 2010, 464, 1039-1042.	27.8	380
14	Chromosome-scale selective sweeps shape Caenorhabditis elegans genomic diversity. Nature Genetics, 2012, 44, 285-290.	21.4	366
15	Geneâ€“Environment Interaction in Yeast Gene Expression. PLoS Biology, 2008, 6, e83.	5.6	346
16	Genetic interactions between polymorphisms that affect gene expression in yeast. Nature, 2005, 436, 701-703.	27.8	296
17	Widespread Genetic Incompatibility in C. Elegans Maintained by Balancing Selection. Science, 2008, 319, 589-594.	12.6	276
18	Selection at Linked Sites Shapes Heritable Phenotypic Variation in C. elegans. Science, 2010, 330, 372-376.	12.6	250

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19	Quantitative Mapping of a Digenic Behavioral Trait Implicates Globin Variation in C. elegans Sensory Behaviors. Neuron, 2009, 61, 692-699.	8.1	219
20	Population genomic analysis of outcrossing and recombination in yeast. Nature Genetics, 2006, 38, 1077-1081.	21.4	217
21	A Variant in the Neuropeptide Receptor npr-1 is a Major Determinant of Caenorhabditis elegans Growth and Physiology. PLoS Genetics, 2014, 10, e1004156.	3.5	174
22	Multiple Locus Linkage Analysis of Genomewide Expression in Yeast. PLoS Biology, 2005, 3, e267.	5.6	163
23	Polymorphisms in Multiple Genes Contribute to the Spontaneous Mitochondrial Genome Instability of Saccharomyces cerevisiae S288C Strains. Genetics, 2009, 183, 365-383.	2.9	161
24	Natural Variation in a Chloride Channel Subunit Confers Avermectin Resistance in C. elegans. Science, 2012, 335, 574-578.	12.6	160
25	A Novel Sperm-Delivered Toxin Causes Late-Stage Embryo Lethality and Transmission Ratio Distortion in C. elegans. PLoS Biology, 2011, 9, e1001115.	5.6	158
26	Genetics of trans-regulatory variation in gene expression. ELife, 2018, 7, .	6.0	146
27	Local Regulatory Variation in Saccharomyces cerevisiae. PLoS Genetics, 2005, 1, e25.	3.5	141
28	Accounting for genetic interactions improves modeling of individual quantitative trait phenotypes in yeast. Nature Genetics, 2017, 49, 497-503.	21.4	141
29	Genetic interactions contribute less than additive effects to quantitative trait variation in yeast. Nature Communications, 2015, 6, 8712.	12.8	139
30	Remarkably Divergent Regions Punctuate the Genome Assembly of theCaenorhabditis elegansHawaiian Strain CB4856. Genetics, 2015, 200, 975-989.	2.9	136
31	Genetics of single-cell protein abundance variation in large yeast populations. Nature, 2014, 506, 494-497.	27.8	134
32	Molecular basis of the copulatory plug polymorphism in Caenorhabditis elegans. Nature, 2008, 454, 1019-1022.	27.8	122
33	The Genetic Basis of Natural Variation inCaenorhabditis elegansTelomere Length. Genetics, 2016, 204, 371-383.	2.9	117
34	Simultaneous genotyping, gene-expression measurement, and detection of allele-specific expression with oligonucleotide arrays. Genome Research, 2005, 15, 284-291.	5.5	116
35	A Powerful New Quantitative Genetics Platform, CombiningCaenorhabditis elegansHigh-Throughput Fitness Assays with a Large Collection of Recombinant Strains. G3: Genes, Genomes, Genetics, 2015, 5, 911-920.	1.8	106
36	Genetic Variation Shapes Protein Networks Mainly through Non-transcriptional Mechanisms. PLoS Biology, 2011, 9, e1001144.	5.6	101

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37	Genome-Wide Analysis of Nucleotide-Level Variation in Commonly Used Saccharomyces cerevisiae Strains. PLoS ONE, 2007, 2, e322.	2.5	100
38	Breeding Designs for Recombinant Inbred Advanced Intercross Lines. Genetics, 2008, 179, 1069-1078.	2.9	94
39	A maternal-effect selfish genetic element in Caenorhabditis elegans. Science, 2017, 356, 1051-1055.	12.6	93
40	Full-genome evolutionary histories of selfing, splitting, and selection in Caenorhabditis. Genome Research, 2015, 25, 667-678.	5.5	92
41	CRISPR-directed mitotic recombination enables genetic mapping without crosses. Science, 2016, 352, 1113-1116.	12.6	90
42	Genetic Architecture of Highly Complex Chemical Resistance Traits across Four Yeast Strains. PLoS Genetics, 2012, 8, e1002570.	3.5	85
43	A Wild C. Elegans Strain Has Enhanced Epithelial Immunity to a Natural Microsporidian Parasite. PLoS Pathogens, 2015, 11, e1004583.	4.7	80
44	Genetic Influences on Brain Gene Expression in Rats Selected for Tameness and Aggression. Genetics, 2014, 198, 1277-1290.	2.9	78
45	Screening Human Embryos for Polygenic Traits Has Limited Utility. Cell, 2019, 179, 1424-1435.e8.	28.9	78
46	Genetic Influences on Translation in Yeast. PLoS Genetics, 2014, 10, e1004692.	3.5	77
47	A genetic signature of the evolution of loss of flight in the Galapagos cormorant. Science, 2017, 356, .	12.6	76
48	Highly parallel genome variant engineering with CRISPRâ€“Cas9. Nature Genetics, 2018, 50, 510-514.	21.4	73
49	Rare variants contribute disproportionately to quantitative trait variation in yeast. ELife, 2019, 8, .	6.0	70
50	Identification and Dissection of a Complex DNA Repair Sensitivity Phenotype in Baker's Yeast. PLoS Genetics, 2008, 4, e1000123.	3.5	66
51	Genetic variation in adaptability and pleiotropy in budding yeast. ELife, 2017, 6, .	6.0	62
52	Genetic Basis of Metabolome Variation in Yeast. PLoS Genetics, 2014, 10, e1004142.	3.5	53
53	The genetic basis of natural variation in a phoretic behavior. Nature Communications, 2017, 8, 273.	12.8	48
54	Genetic Mapping of MAPK-Mediated Complex Traits Across S. cerevisiae. PLoS Genetics, 2015, 11, e1004913.	3.5	46

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55	Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples. Nature Biomedical Engineering, 2021, 5, 657-665.	22.5	46
56	Fast genetic mapping of complex traits in C. elegans using millions of individuals in bulk. Nature Communications, 2019, 10, 2680.	12.8	40
57	The Genetic Basis of Mutation Rate Variation in Yeast. Genetics, 2019, 211, 731-740.	2.9	39
58	Toxin-Antidote Elements Across the Tree of Life. Annual Review of Genetics, 2020, 54, 387-415.	7.6	30
59	Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast. Science, 2021, 371, 415-419.	12.6	27
60	Ubiquitous Selfish Toxin-Antidote Elements in Caenorhabditis Species. Current Biology, 2021, 31, 990-1001.e5.	3.9	27
61	Whole-organism eQTL mapping at cellular resolution with single-cell sequencing. ELife, 2021, 10, .	6.0	24
62	Island-specific evolution of a sex-primed autosome in a sexual planarian. Nature, 2022, 606, 329-334.	27.8	19
63	Genetic Basis of Haloperidol Resistance in Saccharomyces cerevisiae Is Complex and Dose Dependent. PLoS Genetics, 2014, 10, e1004894.	3.5	18
64	Systematic identification of cis-regulatory variants that cause gene expression differences in a yeast cross. ELife, 2020, 9, .	6.0	18
65	Genetics of white color and iridophoroma in â€œLemon Frostâ€•leopard geckos. PLoS Genetics, 2021, 17, e1009580.	3.5	13
66	Genetics of Intraspecies Variation in Avoidance Behavior Induced by a Thermal Stimulus in Caenorhabditis elegans. Genetics, 2015, 200, 1327-1339.	2.9	9
67	Lower SARS-CoV-2 viral shedding following COVID-19 vaccination among healthcare workers in Los Angeles, California. Open Forum Infectious Diseases, 2021, 8, ofab526.	0.9	5
68	Retrospective Detection of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Symptomatic Patients Prior to Widespread Diagnostic Testing in Southern California. Clinical Infectious Diseases, 2022, 74, 271-277.	5.8	4
69	How Low Can You Go?. CRISPR Journal, 2018, 1, 312-313.	2.9	1
70	Analysis of the genetic basis of height in large Jewish nuclear families. PLoS Genetics, 2019, 15, e1008082.	3.5	1
71	2015 Curt Stern Award 1. American Journal of Human Genetics, 2016, 98, 428-430.	6.2	0
72	Planarian Ovary Dissection for Ultrastructural Analysis and Antibody Staining. Journal of Visualized Experiments, 2021, , .	0.3	0

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73	Genomic epidemiology of the Los Angeles COVID-19 outbreak and the early history of the B.1.43 strain in the USA. BMC Genomics, 2022, 23, 260.	2.8	0