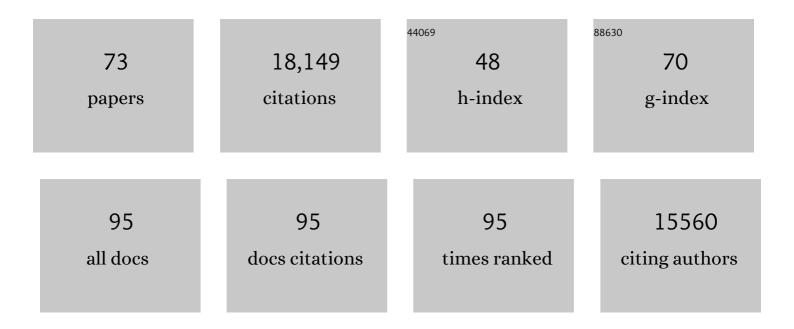
Leonid Kruglyak

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	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
3	Island-specific evolution of a sex-primed autosome in a sexual planarian. Nature, 2022, 606, 329-334.	27.8	19
4	Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast. Science, 2021, 371, 415-419.	12.6	27
5	Ubiquitous Selfish Toxin-Antidote Elements in Caenorhabditis Species. Current Biology, 2021, 31, 990-1001.e5.	3.9	27
6	Whole-organism eQTL mapping at cellular resolution with single-cell sequencing. ELife, 2021, 10, .	6.0	24
7	Genetics of white color and iridophoroma in "Lemon Frost―leopard geckos. PLoS Genetics, 2021, 17, e1009580.	3.5	13
8	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
9	Planarian Ovary Dissection for Ultrastructural Analysis and Antibody Staining. Journal of Visualized Experiments, 2021, , .	0.3	0
10	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
11	Toxin-Antidote Elements Across the Tree of Life. Annual Review of Genetics, 2020, 54, 387-415.	7.6	30
12	Systematic identification of cis-regulatory variants that cause gene expression differences in a yeast cross. ELife, 2020, 9, .	6.0	18
13	Analysis of the genetic basis of height in large Jewish nuclear families. PLoS Genetics, 2019, 15, e1008082.	3.5	1
14	Fast genetic mapping of complex traits in C. elegans using millions of individuals in bulk. Nature Communications, 2019, 10, 2680.	12.8	40
15	Screening Human Embryos for Polygenic Traits Has Limited Utility. Cell, 2019, 179, 1424-1435.e8.	28.9	78
16	The Genetic Basis of Mutation Rate Variation in Yeast. Genetics, 2019, 211, 731-740.	2.9	39
17	Rare variants contribute disproportionately to quantitative trait variation in yeast. ELife, 2019, 8, .	6.0	70
18	Highly parallel genome variant engineering with CRISPR–Cas9. Nature Genetics, 2018, 50, 510-514.	21.4	73

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19	How Low Can You Go?. CRISPR Journal, 2018, 1, 312-313.	2.9	1
20	Genetics of trans-regulatory variation in gene expression. ELife, 2018, 7, .	6.0	146
21	Accounting for genetic interactions improves modeling of individual quantitative trait phenotypes in yeast. Nature Genetics, 2017, 49, 497-503.	21.4	141
22	A maternal-effect selfish genetic element in <i>Caenorhabditis elegans</i> . Science, 2017, 356, 1051-1055.	12.6	93
23	A genetic signature of the evolution of loss of flight in the Galapagos cormorant. Science, 2017, 356, .	12.6	76
24	The genetic basis of natural variation in a phoretic behavior. Nature Communications, 2017, 8, 273.	12.8	48
25	Genetic variation in adaptability and pleiotropy in budding yeast. ELife, 2017, 6, .	6.0	62
26	The Genetic Basis of Natural Variation in <i>Caenorhabditis elegans</i> Telomere Length. Genetics, 2016, 204, 371-383.	2.9	117
27	2015 Curt Stern Award 1. American Journal of Human Genetics, 2016, 98, 428-430.	6.2	0
28	CRISPR-directed mitotic recombination enables genetic mapping without crosses. Science, 2016, 352, 1113-1116.	12.6	90
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 the <i>Caenorhabditis elegans</i> Hawaiian Strain CB4856. Genetics, 2015, 200, 975-989.	2.9	136
31	Genetics of Intraspecies Variation in Avoidance Behavior Induced by a Thermal Stimulus in <i>Caenorhabditis elegans</i> . Genetics, 2015, 200, 1327-1339.	2.9	9
32	Full-genome evolutionary histories of selfing, splitting, and selection in <i>Caenorhabditis</i> . Genome Research, 2015, 25, 667-678.	5.5	92
33	A Powerful New Quantitative Genetics Platform, Combining <i>Caenorhabditis elegans</i> High-Throughput Fitness Assays with a Large Collection of Recombinant Strains. G3: Genes, Genomes, Genetics, 2015, 5, 911-920.	1.8	106
34	The role of regulatory variation in complex traits and disease. Nature Reviews Genetics, 2015, 16, 197-212.	16.3	864
35	A Wild C. Elegans Strain Has Enhanced Epithelial Immunity to a Natural Microsporidian Parasite. PLoS Pathogens, 2015, 11, e1004583.	4.7	80
36	Genetic Mapping of MAPK-Mediated Complex Traits Across S. cerevisiae. PLoS Genetics, 2015, 11, e1004913.	3.5	46

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37	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
38	Genetic Influences on Translation in Yeast. PLoS Genetics, 2014, 10, e1004692.	3.5	77
39	Genetic Basis of Haloperidol Resistance in Saccharomyces cerevisiae Is Complex and Dose Dependent. PLoS Genetics, 2014, 10, e1004894.	3.5	18
40	Genetic Basis of Metabolome Variation in Yeast. PLoS Genetics, 2014, 10, e1004142.	3.5	53
41	Genetic Influences on Brain Gene Expression in Rats Selected for Tameness and Aggression. Genetics, 2014, 198, 1277-1290.	2.9	78
42	Genetics of single-cell protein abundance variation in large yeast populations. Nature, 2014, 506, 494-497.	27.8	134
43	Finding the sources of missing heritability in a yeast cross. Nature, 2013, 494, 234-237.	27.8	427
44	Genetic Architecture of Highly Complex Chemical Resistance Traits across Four Yeast Strains. PLoS Genetics, 2012, 8, e1002570.	3.5	85
45	Chromosome-scale selective sweeps shape Caenorhabditis elegans genomic diversity. Nature Genetics, 2012, 44, 285-290.	21.4	366
46	Natural Variation in a Chloride Channel Subunit Confers Avermectin Resistance in <i>C. elegans</i> . Science, 2012, 335, 574-578.	12.6	160
47	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
48	Genetic Variation Shapes Protein Networks Mainly through Non-transcriptional Mechanisms. PLoS Biology, 2011, 9, e1001144.	5.6	101
49	Dissection of genetically complex traits with extremely large pools of yeast segregants. Nature, 2010, 464, 1039-1042.	27.8	380
50	Selection at Linked Sites Shapes Heritable Phenotypic Variation in <i>C. elegans</i> . Science, 2010, 330, 372-376.	12.6	250
51	Polymorphisms in Multiple Genes Contribute to the Spontaneous Mitochondrial Genome Instability of <i>Saccharomyces cerevisiae</i> S288C Strains. Genetics, 2009, 183, 365-383.	2.9	161
52	Recombinational Landscape and Population Genomics of Caenorhabditis elegans. PLoS Genetics, 2009, 5, e1000419.	3.5	381
53	Comprehensive polymorphism survey elucidates population structure of Saccharomyces cerevisiae. Nature, 2009, 458, 342-345.	27.8	431
54	Quantitative Mapping of a Digenic Behavioral Trait Implicates Globin Variation in C. elegans Sensory Behaviors. Neuron, 2009, 61, 692-699.	8.1	219

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#	Article	IF	CITATIONS
55	Molecular basis of the copulatory plug polymorphism in Caenorhabditis elegans. Nature, 2008, 454, 1019-1022.	27.8	122
56	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. Nature Genetics, 2008, 40, 854-861.	21.4	515
57	Widespread Genetic Incompatibility in <i>C. Elegans</i> Maintained by Balancing Selection. Science, 2008, 319, 589-594.	12.6	276
58	Identification and Dissection of a Complex DNA Repair Sensitivity Phenotype in Baker's Yeast. PLoS Genetics, 2008, 4, e1000123.	3.5	66
59	Gene–Environment Interaction in Yeast Gene Expression. PLoS Biology, 2008, 6, e83.	5.6	346
60	Breeding Designs for Recombinant Inbred Advanced Intercross Lines. Genetics, 2008, 179, 1069-1078.	2.9	94
61	Genetic basis of proteome variation in yeast. Nature Genetics, 2007, 39, 1369-1375.	21.4	767
62	Genome-Wide Analysis of Nucleotide-Level Variation in Commonly Used Saccharomyces cerevisiae Strains. PLoS ONE, 2007, 2, e322.	2.5	100
63	Population genomic analysis of outcrossing and recombination in yeast. Nature Genetics, 2006, 38, 1077-1081.	21.4	217
64	Genetic interactions between polymorphisms that affect gene expression in yeast. Nature, 2005, 436, 701-703.	27.8	296
65	Multiple Locus Linkage Analysis of Genomewide Expression in Yeast. PLoS Biology, 2005, 3, e267.	5.6	163
66	Local Regulatory Variation in Saccharomyces cerevisiae. PLoS Genetics, 2005, 1, e25.	3.5	141
67	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
68	Simultaneous genotyping, gene-expression measurement, and detection of allele-specific expression with oligonucleotide arrays. Genome Research, 2005, 15, 284-291.	5.5	116
69	Trans-acting regulatory variation in Saccharomyces cerevisiae and the role of transcription factors. Nature Genetics, 2003, 35, 57-64.	21.4	583
70	Genetic Dissection of Transcriptional Regulation in Budding Yeast. Science, 2002, 296, 752-755.	12.6	1,261
71	Guilt by association. Nature Genetics, 2000, 26, 135-137.	21.4	569
72	The use of a genetic map of biallelic markers in linkage studies. Nature Genetics, 1997, 17, 21-24.	21.4	452

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73	Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. Nature Genetics, 1995, 11, 241-247.	21.4	5,020