

Leopold Parts

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3649594/publications.pdf>

Version: 2024-02-01

50
papers

11,636
citations

136950

32
h-index

197818

49
g-index

61
all docs

61
docs citations

61
times ranked

21015
citing authors

#	ARTICLE	IF	CITATIONS
1	Live-cell microscopy or fluorescence anisotropy with budded baculoviruses— which way to go with measuring ligand binding to M ₄ muscarinic receptors?. <i>Open Biology</i> , 2022, 12, .	3.6	6
2	ArtSeg—Artifact segmentation and removal in brightfield cell microscopy images without manual pixel-level annotations. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
3	Genomic Epidemiology and Evolution of <i>Escherichia coli</i> in Wild Animals in Mexico. <i>MSphere</i> , 2021, 6, .	2.9	19
4	Natural variants suppress mutations in hundreds of essential genes. <i>Molecular Systems Biology</i> , 2021, 17, e10138.	7.2	13
5	Evaluating Very Deep Convolutional Neural Networks for Nucleus Segmentation from Brightfield Cell Microscopy Images. <i>SLAS Discovery</i> , 2021, 26, 1125-1137.	2.7	16
6	Practical segmentation of nuclei in brightfield cell images with neural networks trained on fluorescently labelled samples. <i>Journal of Microscopy</i> , 2021, 284, 12-24.	1.8	6
7	Machine Learning Prediction of Resistance to Subinhibitory Antimicrobial Concentrations from <i>Escherichia coli</i> Genomes. <i>MSystems</i> , 2021, 6, e0034621.	3.8	6
8	Minimal genome-wide human CRISPR-Cas9 library. <i>Genome Biology</i> , 2021, 22, 40.	8.8	40
9	Type II and type IV toxin—antitoxin systems show different evolutionary patterns in the global <i>Klebsiella pneumoniae</i> population. <i>Nucleic Acids Research</i> , 2020, 48, 4357-4370.	14.5	14
10	JACKS: joint analysis of CRISPR/Cas9 knockout screens. <i>Genome Research</i> , 2019, 29, 464-471.	5.5	64
11	Binding of ISRIB reveals a regulatory site in the nucleotide exchange factor eIF2B. <i>Science</i> , 2018, 359, 1533-1536.	12.6	157
12	Prediction of antibiotic resistance in <i>Escherichia coli</i> from large-scale pan-genome data. <i>PLoS Computational Biology</i> , 2018, 14, e1006258.	3.2	127
13	SLING: a tool to search for linked genes in bacterial datasets. <i>Nucleic Acids Research</i> , 2018, 46, e128.	14.5	18
14	The genetic architecture of low-temperature adaptation in the wine yeast <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2017, 18, 159.	2.8	58
15	Accurate Classification of Protein Subcellular Localization from High-Throughput Microscopy Images Using Deep Learning. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1385-1392.	1.8	130
16	Computational biology: deep learning. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 257-274.	2.6	65
17	Predicting quantitative traits from genome and phenome with near perfect accuracy. <i>Nature Communications</i> , 2016, 7, 11512.	12.8	32
18	Deep learning for computational biology. <i>Molecular Systems Biology</i> , 2016, 12, 878.	7.2	1,059

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19	Powerful decomposition of complex traits in a diploid model. <i>Nature Communications</i> , 2016, 7, 13311.	12.8	34
20	Pathway-Based Factor Analysis of Gene Expression Data Produces Highly Heritable Phenotypes That Associate with Age. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 839-847.	1.8	7
21	Genetic Interaction Scoring Procedure for Bacterial Species. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 169-185.	1.6	2
22	Personalized medicine: from genotypes, molecular phenotypes and the quantified self, towards improved medicine. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 342-6.	0.7	12
23	Heritability and genetic basis of protein level variation in an outbred population. <i>Genome Research</i> , 2014, 24, 1363-1370.	5.5	51
24	gitter: A Robust and Accurate Method for Quantification of Colony Sizes From Plate Images. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 547-552.	1.8	109
25	Genome-wide mapping of cellular traits using yeast. <i>Yeast</i> , 2014, 31, 197-205.	1.7	17
26	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 872-888.	8.9	328
27	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	6.2	330
28	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <i>Genetics</i> , 2013, 195, 1141-1155.	2.9	164
29	Gene expression changes with age in skin, adipose tissue, blood and brain. <i>Genome Biology</i> , 2013, 14, R75.	9.6	263
30	SGAtools: one-stop analysis and visualization of array-based genetic interaction screens. <i>Nucleic Acids Research</i> , 2013, 41, W591-W596.	14.5	141
31	Inferring Genome-Wide Recombination Landscapes from Advanced Intercross Lines: Application to Yeast Crosses. <i>PLoS ONE</i> , 2013, 8, e62266.	2.5	29
32	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
33	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. <i>PLoS ONE</i> , 2013, 8, e55272.	2.5	178
34	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	3.5	48
35	Patterns of Cis Regulatory Variation in Diverse Human Populations. <i>PLoS Genetics</i> , 2012, 8, e1002639.	3.5	439
36	Quantifying Selection Acting on a Complex Trait Using Allele Frequency Time Series Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 1187-1197.	8.9	64

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37	Using probabilistic estimation of expression residuals (PEER) to obtain increased power and interpretability of gene expression analyses. <i>Nature Protocols</i> , 2012, 7, 500-507.	12.0	799
38	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	21.4	701
39	Assessing the complex architecture of polygenic traits in diverged yeast populations. <i>Molecular Ecology</i> , 2011, 20, 1401-1413.	3.9	194
40	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	5.5	263
41	Joint Genetic Analysis of Gene Expression Data with Inferred Cellular Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1001276.	3.5	76
42	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. <i>PLoS Genetics</i> , 2011, 7, e1002003.	3.5	392
43	A Bayesian Framework to Account for Complex Non-Genetic Factors in Gene Expression Levels Greatly Increases Power in eQTL Studies. <i>PLoS Computational Biology</i> , 2010, 6, e1000770.	3.2	408
44	No Correlation Between Childhood Maltreatment and Telomere Length. <i>Biological Psychiatry</i> , 2010, 68, e21-e22.	1.3	70
45	Simultaneous assay of every <i>Salmonella</i> Typhi gene using one million transposon mutants. <i>Genome Research</i> , 2009, 19, 2308-2316.	5.5	544
46	Segregating YKU80 and TLC1 Alleles Underlying Natural Variation in Telomere Properties in Wild Yeast. <i>PLoS Genetics</i> , 2009, 5, e1000659.	3.5	46
47	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
48	Systematic discovery and characterization of fly microRNAs using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1865-1879.	5.5	182
49	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	27.8	573
50	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886