

Paul Shannon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10949159/publications.pdf>

Version: 2024-02-01

24
papers

42,967
citations

394421
19
h-index

642732
23
g-index

26
all docs

26
docs citations

26
times ranked

72315
citing authors

#	ARTICLE	IF	CITATIONS
1	Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. <i>Genome Research</i> , 2003, 13, 2498-2504.	5.5	37,062
2	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
3	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. <i>Neuron</i> , 2018, 99, 64-82.e7.	8.1	558
4	The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. <i>Genome Biology</i> , 2006, 7, R36.	9.6	456
5	VariantAnnotation : a Bioconductor package for exploration and annotation of genetic variants. <i>Bioinformatics</i> , 2014, 30, 2076-2078.	4.1	293
6	A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. <i>Cell</i> , 2007, 131, 1354-1365.	28.9	284
7	Genome sequence of <i>Haloarcula marismortui</i> : A halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004, 14, 2221-2234.	5.5	268
8	Coordinate regulation of energy transduction modules in <i>Halobacterium</i> sp. analyzed by a global systems approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14913-14918.	7.1	123
9	Derivation of genetic interaction networks from quantitative phenotype data. <i>Genome Biology</i> , 2005, 6, R38.	9.6	114
10	General transcription factor specified global gene regulation in archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4630-4635.	7.1	105
11	Evidence for the Presence of Disease-Perturbed Networks in Prostate Cancer Cells by Genomic and Proteomic Analyses: A Systems Approach to Disease. <i>Cancer Research</i> , 2005, 65, 3081-3091.	0.9	104
12	Single-Cell Proteomics Reveal that Quantitative Changes in Co-expressed Lineage-Specific Transcription Factors Determine Cell Fate. <i>Cell Stem Cell</i> , 2019, 24, 812-820.e5.	11.1	99
13	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	9.7	83
14	CyREST: Turbocharging Cytoscape Access for External Tools via a RESTful API. <i>F1000Research</i> , 2015, 4, 478.	1.6	81
15	System-based proteomic analysis of the interferon response in human liver cells. <i>Genome Biology</i> , 2004, 5, R54.	9.6	63
16	Comprehensive de novo structure prediction in a systems-biology context for the archaea <i>Halobacterium</i> sp. NRC-1. <i>Genome Biology</i> , 2004, 5, R52.	9.6	45
17	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. <i>Cell Systems</i> , 2019, 8, 122-135.e7.	6.2	45
18	Reproducible big data science: A case study in continuous FAIRness. <i>PLoS ONE</i> , 2019, 14, e0213013.	2.5	29

#	ARTICLE	IF	CITATIONS
19	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. Cell Reports, 2020, 32, 108029.	6.4	28
20	Wrangling Phosphoproteomic Data to Elucidate Cancer Signaling Pathways. PLoS ONE, 2013, 8, e52884.	2.5	22
21	Differential Plasma Glycoproteome of p19ARF Skin Cancer Mouse Model Using the Corra Label-Free LC-MS Proteomics Platform. Clinical Proteomics, 2008, 4, 105-116.	2.1	11
22	Analysis and visualization of linked molecular and clinical cancer data by using Oncoscape. Nature Genetics, 2018, 50, 1203-1204.	21.4	10
23	The Protein Information and Property Explorer 2: Gaggles-like exploration of biological proteomic data within one webpage. Proteomics, 2011, 11, 154-158.	2.2	9
24	MECHANISTIC AND DIRECTIONAL TRANSCRIPTIONAL REGULATORY NETWORKS IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P1014.	0.8	0