

Michael Springer

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

3,098
citations

257450

24
h-index

214800

47
g-index

67
all docs

67
docs citations

67
times ranked

4574
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutation effects predicted from sequence co-variation. <i>Nature Biotechnology</i> , 2017, 35, 128-135.	17.5	543
2	Stable isotope-free relative and absolute quantitation of protein phosphorylation stoichiometry by MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3948-3953.	7.1	202
3	Genetic Redundancy: New Tricks for Old Genes. <i>Cell</i> , 2009, 136, 389-392.	28.9	158
4	Natural Variation in Preparation for Nutrient Depletion Reveals a Cost-Benefit Tradeoff. <i>PLoS Biology</i> , 2015, 13, e1002041.	5.6	128
5	Multiplexed CRISPR-based microfluidic platform for clinical testing of respiratory viruses and identification of SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1083-1094.	30.7	127
6	A general lack of compensation for gene dosage in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 368.	7.2	118
7	An enhanced isothermal amplification assay for viral detection. <i>Nature Communications</i> , 2020, 11, 5920.	12.8	117
8	Galactose metabolic genes in yeast respond to a ratio of galactose and glucose. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1636-1641.	7.1	115
9	FLEXIQuant: A Novel Tool for the Absolute Quantification of Proteins, and the Simultaneous Identification and Quantification of Potentially Modified Peptides. <i>Journal of Proteome Research</i> , 2009, 8, 2201-2210.	3.7	109
10	The Signal Sequence Coding Region Promotes Nuclear Export of mRNA. <i>PLoS Biology</i> , 2007, 5, e322.	5.6	103
11	Need-Based Up-Regulation of Protein Levels in Response to Deletion of Their Duplicate Genes. <i>PLoS Biology</i> , 2010, 8, e1000347.	5.6	102
12	A Chromatin-Based Mechanism for Limiting Divergent Noncoding Transcription. <i>Cell</i> , 2014, 157, 1712-1723.	28.9	98
13	Profiling of Ubiquitin-like Modifications Reveals Features of Mitotic Control. <i>Cell</i> , 2013, 152, 1160-1172.	28.9	91
14	Proteotoxicity from aberrant ribosome biogenesis compromises cell fitness. <i>ELife</i> , 2019, 8, .	6.0	88
15	Aneuploidy Causes Non-genetic Individuality. <i>Cell</i> , 2017, 169, 229-242.e21.	28.9	81
16	Accurate concentration control of mitochondria and nucleoids. <i>Science</i> , 2016, 351, 169-172.	12.6	78
17	Different phosphorylation states of the anaphase promoting complex in response to antimetabolic drugs: A quantitative proteomic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6069-6074.	7.1	77
18	Simplified Cas13-based assays for the fast identification of SARS-CoV-2 and its variants. <i>Nature Biomedical Engineering</i> , 2022, 6, 932-943.	22.5	76

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19	Multi-site phosphorylation of pho4 by the cyclin-CDK pho80-pho85 is semi-processive with site preference. <i>Journal of Molecular Biology</i> , 2001, 306, 997-1010.	4.2	73
20	Measurement of the state-specific differential cross section for the $H+D_2^+\rightarrow HD(v=4, j=3)+D$ reaction at a collision energy of 2.2 eV. <i>Journal of Chemical Physics</i> , 1995, 103, 5157-5160.	3.0	60
21	SnapShot-Seq: A Method for Extracting Genome-Wide, In Vivo mRNA Dynamics from a Single Total RNA Sample. <i>PLoS ONE</i> , 2014, 9, e89673.	2.5	53
22	No current evidence for widespread dosage compensation in <i>S. cerevisiae</i> . <i>ELife</i> , 2016, 5, e10996.	6.0	52
23	The relationship between evolutionary and physiological variation in hemoglobin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16998-17003.	7.1	37
24	Harmonies from noise. <i>Nature</i> , 2006, 439, 27-28.	27.8	35
25	Decoupling transcription factor expression and activity enables dimmer switch gene regulation. <i>Science</i> , 2021, 372, 292-295.	12.6	32
26	Barcoded microbial system for high-resolution object provenance. <i>Science</i> , 2020, 368, 1135-1140.	12.6	27
27	Total RNA-seq to identify pharmacological effects on specific stages of mRNA synthesis. <i>Nature Chemical Biology</i> , 2017, 13, 501-507.	8.0	26
28	The Quantitative Methods Boot Camp: Teaching Quantitative Thinking and Computing Skills to Graduate Students in the Life Sciences. <i>PLoS Computational Biology</i> , 2015, 11, e1004208.	3.2	24
29	Probabilistic adaptation in changing microbial environments. <i>PeerJ</i> , 2016, 4, e2716.	2.0	24
30	Abundance-based Classifier for the Prediction of Mass Spectrometric Peptide Detectability Upon Enrichment (PPA). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 430-440.	3.8	23
31	A competitive trade-off limits the selective advantage of increased antibiotic production. <i>Nature Microbiology</i> , 2016, 1, 16175.	13.3	23
32	Early Introduction and Rise of the Omicron Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variant in Highly Vaccinated University Populations. <i>Clinical Infectious Diseases</i> , 2023, 76, e400-e408.	5.8	22
33	Polymorphisms in the yeast galactose sensor underlie a natural continuum of nutrient-decision phenotypes. <i>PLoS Genetics</i> , 2017, 13, e1006766.	3.5	20
34	A Distal, High-affinity Binding Site on the Cyclin-CDK Substrate Pho4 is Important for its Phosphorylation and Regulation. <i>Journal of Molecular Biology</i> , 2004, 335, 57-70.	4.2	15
35	A Semi-Quantitative Isothermal Diagnostic Assay Utilizing Competitive Amplification. <i>Analytical Chemistry</i> , 2021, 93, 9541-9548.	6.5	13
36	Amplicon residues in research laboratories masquerade as COVID-19 in surveillance tests. <i>Cell Reports Methods</i> , 2021, 1, 100005.	2.9	10

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37	Association of COVID-19 Quarantine Duration and Postquarantine Transmission Risk in 4 University Cohorts. <i>JAMA Network Open</i> , 2022, 5, e220088.	5.9	10
38	Achieving global perfect homeostasis through transporter regulation. <i>PLoS Computational Biology</i> , 2017, 13, e1005458.	3.2	9
39	Accessioning and automation compatible anterior nares swab design. <i>Journal of Virological Methods</i> , 2021, 294, 114153.	2.1	9
40	Competitive Inhibition Can Linearize Dose-Response and Generate a Linear Rectifier. <i>Cell Systems</i> , 2015, 1, 238-245.	6.2	7
41	Widespread Cumulative Influence of Small Effect Size Mutations on Yeast Quantitative Traits. <i>Cell Systems</i> , 2018, 7, 590-600.e6.	6.2	7
42	Variation in the modality of a yeast signaling pathway is mediated by a single regulator. <i>ELife</i> , 2021, 10, .	6.0	7
43	Evaluation of Dunphy et al.: Suggestions to Solidify, Clarify, and Focus without Substantial New Work. <i>Cell Systems</i> , 2019, 8, 1-2.	6.2	5
44	Computational study on ratio-sensing in yeast galactose utilization pathway. <i>PLoS Computational Biology</i> , 2020, 16, e1007960.	3.2	5
45	Identifying Metabolic Subpopulations from Population Level Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0151659.	2.5	5
46	Assigning function to natural allelic variation via dynamic modeling of gene network induction. <i>Molecular Systems Biology</i> , 2018, 14, e7803.	7.2	1
47	Computational analysis of GAL pathway pinpoints mechanisms underlying natural variation. <i>PLoS Computational Biology</i> , 2021, 17, e1008691.	3.2	1