Michael Springer

List of Publications by Year
in descending order

47	3,098	257450	214800
papers	citations	24	47
		h-index	g-index

67	67	67	4574
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Early Introduction and Rise of the Omicron Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variant in Highly Vaccinated University Populations. Clinical Infectious Diseases, 2023, 76, e400-e408.	5.8	22
2	Multiplexed CRISPR-based microfluidic platform for clinical testing of respiratory viruses and identification of SARS-CoV-2 variants. Nature Medicine, 2022, 28, 1083-1094.	30.7	127
3	Association of COVID-19 Quarantine Duration and Postquarantine Transmission Risk in 4 University Cohorts. JAMA Network Open, 2022, 5, e220088.	5.9	10
4	Simplified Cas13-based assays for the fast identification of SARS-CoV-2 and its variants. Nature Biomedical Engineering, 2022, 6, 932-943.	22.5	76
5	Decoupling transcription factor expression and activity enables dimmer switch gene regulation. Science, 2021, 372, 292-295.	12.6	32
6	Amplicon residues in research laboratories masquerade as COVID-19 in surveillance tests. Cell Reports Methods, 2021, 1, 100005.	2.9	10
7	A Semi-Quantitative Isothermal Diagnostic Assay Utilizing Competitive Amplification. Analytical Chemistry, 2021, 93, 9541-9548.	6.5	13
8	Variation in the modality of a yeast signaling pathway is mediated by a single regulator. ELife, 2021, 10, .	6.0	7
9	Accessioning and automation compatible anterior nares swab design. Journal of Virological Methods, 2021, 294, 114153.	2.1	9
10	Computational analysis of GAL pathway pinpoints mechanisms underlying natural variation. PLoS Computational Biology, 2021, 17, e1008691.	3.2	1
11	An enhanced isothermal amplification assay for viral detection. Nature Communications, 2020, 11, 5920.	12.8	117
12	Barcoded microbial system for high-resolution object provenance. Science, 2020, 368, 1135-1140.	12.6	27
13	Computational study on ratio-sensing in yeast galactose utilization pathway. PLoS Computational Biology, 2020, 16, e1007960.	3.2	5
14	Evaluation of Dunphy etÂal.: Suggestions to Solidify, Clarify, and Focus without Substantial New Work. Cell Systems, 2019, 8, 1-2.	6.2	5
15	Proteotoxicity from aberrant ribosome biogenesis compromises cell fitness. ELife, 2019, 8, .	6.0	88
16	Assigning function to natural allelic variation via dynamic modeling of gene network induction. Molecular Systems Biology, 2018, 14, e7803.	7.2	1
17	Widespread Cumulative Influence of Small Effect Size Mutations on Yeast Quantitative Traits. Cell Systems, 2018, 7, 590-600.e6.	6.2	7
18	Mutation effects predicted from sequence co-variation. Nature Biotechnology, 2017, 35, 128-135.	17.5	543

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19	Total RNA-seq to identify pharmacological effects on specific stages of mRNA synthesis. Nature Chemical Biology, 2017, 13, 501-507.	8.0	26
20	Aneuploidy Causes Non-genetic Individuality. Cell, 2017, 169, 229-242.e21.	28.9	81
21	Achieving global perfect homeostasis through transporter regulation. PLoS Computational Biology, 2017, 13, e1005458.	3.2	9
22	Polymorphisms in the yeast galactose sensor underlie a natural continuum of nutrient-decision phenotypes. PLoS Genetics, 2017, 13, e1006766.	3.5	20
23	A competitive trade-off limits the selective advantage of increased antibiotic production. Nature Microbiology, 2016, 1, 16175.	13.3	23
24	Accurate concentration control of mitochondria and nucleoids. Science, 2016, 351, 169-172.	12.6	78
25	Identifying Metabolic Subpopulations from Population Level Mass Spectrometry. PLoS ONE, 2016, 11, e0151659.	2.5	5
26	No current evidence for widespread dosage compensation in S. cerevisiae. ELife, 2016, 5, e10996.	6.0	52
27	Probabilistic adaptation in changing microbial environments. PeerJ, 2016, 4, e2716.	2.0	24
28	Competitive Inhibition Can Linearize Dose-Response and Generate a Linear Rectifier. Cell Systems, 2015, 1, 238-245.	6.2	7
29	Galactose metabolic genes in yeast respond to a ratio of galactose and glucose. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1636-1641.	7.1	115
30	Abundance-based Classifier for the Prediction of Mass Spectrometric Peptide Detectability Upon Enrichment (PPA). Molecular and Cellular Proteomics, 2015, 14, 430-440.	3.8	23
31	The Quantitative Methods Boot Camp: Teaching Quantitative Thinking and Computing Skills to Graduate Students in the Life Sciences. PLoS Computational Biology, 2015, 11, e1004208.	3.2	24
32	Natural Variation in Preparation for Nutrient Depletion Reveals a Cost–Benefit Tradeoff. PLoS Biology, 2015, 13, e1002041.	5.6	128
33	SnapShot-Seq: A Method for Extracting Genome-Wide, In Vivo mRNA Dynamics from a Single Total RNA Sample. PLoS ONE, 2014, 9, e89673.	2.5	53
34	A Chromatin-Based Mechanism for Limiting Divergent Noncoding Transcription. Cell, 2014, 157, 1712-1723.	28.9	98
35	Profiling of Ubiquitin-like Modifications Reveals Features of Mitotic Control. Cell, 2013, 152, 1160-1172.	28.9	91
36	A general lack of compensation for gene dosage in yeast. Molecular Systems Biology, 2010, 6, 368.	7.2	118

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37	Need-Based Up-Regulation of Protein Levels in Response to Deletion of Their Duplicate Genes. PLoS Biology, 2010, 8, e1000347.	5.6	102
38	FLEXIQuant: A Novel Tool for the Absolute Quantification of Proteins, and the Simultaneous Identification and Quantification of Potentially Modified Peptides. Journal of Proteome Research, 2009, 8, 2201-2210.	3.7	109
39	Genetic Redundancy: New Tricks for Old Genes. Cell, 2009, 136, 389-392.	28.9	158
40	Different phosphorylation states of the anaphase promoting complex in response to antimitotic drugs: A quantitative proteomic analysis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6069-6074.	7.1	77
41	The Signal Sequence Coding Region Promotes Nuclear Export of mRNA. PLoS Biology, 2007, 5, e322.	5.6	103
42	The relationship between evolutionary and physiological variation in hemoglobin. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16998-17003.	7.1	37
43	Harmonies from noise. Nature, 2006, 439, 27-28.	27.8	35
44	Stable isotope-free relative and absolute quantitation of protein phosphorylation stoichiometry by MS. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3948-3953.	7.1	202
45	A Distal, High-affinity Binding Site on the Cyclin-CDK Substrate Pho4 is Important for its Phosphorylation and Regulation. Journal of Molecular Biology, 2004, 335, 57-70.	4.2	15
46	Multi-site phosphorylation of pho4 by the cyclin-CDK pho80-pho85 is semi-processive with site preference. Journal of Molecular Biology, 2001, 306, 997-1010.	4.2	73
47	Measurement of the state‐specific differential cross section for the H+D2â†'HD(vâ€²=4, Jâ€²=3)+D reaction at a collision energy of 2.2 eV. Journal of Chemical Physics, 1995, 103, 5157-5160.	3.0	60