

# Michael Knop

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

5,801  
citations

236833

25  
h-index

214721

47  
g-index

60  
all docs

60  
docs citations

60  
times ranked

7707  
citing authors

#	ARTICLE	IF	CITATIONS
1	A versatile toolbox for PCR-based tagging of yeast genes: new fluorescent proteins, more markers and promoter substitution cassettes. <i>Yeast</i> , 2004, 21, 947-962.	0.8	1,837
2	Epitope tagging of yeast genes using a PCR-based strategy: more tags and improved practical routines. <i>Yeast</i> , 1999, 15, 963-972.	0.8	946
3	A colorimetric RT-LAMP assay and LAMP-sequencing for detecting SARS-CoV-2 RNA in clinical samples. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	516
4	Directional tissue migration through a self-generated chemokine gradient. <i>Nature</i> , 2013, 503, 285-289.	13.7	320
5	Tandem fluorescent protein timers for in vivo analysis of protein dynamics. <i>Nature Biotechnology</i> , 2012, 30, 708-714.	9.4	239
6	Protein quality control at the inner nuclear membrane. <i>Nature</i> , 2014, 516, 410-413.	13.7	188
7	System of centromeric, episomal, and integrative vectors based on drug resistance markers for <i>Saccharomyces cerevisiae</i> . <i>BioTechniques</i> , 2006, 40, 73-78.	0.8	174
8	One library to make them all: streamlining the creation of yeast libraries via a SWAp-Tag strategy. <i>Nature Methods</i> , 2016, 13, 371-378.	9.0	171
9	Evolution of the hemiascomycete yeasts: on life styles and the importance of inbreeding. <i>BioEssays</i> , 2006, 28, 696-708.	1.2	91
10	Mapping Degradation Signals and Pathways in a Eukaryotic N-terminome. <i>Molecular Cell</i> , 2018, 70, 488-501.e5.	4.5	80
11	SARS-CoV-2 RNA Extraction Using Magnetic Beads for Rapid Large-Scale Testing by RT-qPCR and RT-LAMP. <i>Viruses</i> , 2020, 12, 863.	1.5	79
12	Exploring whole-genome duplicate gene retention with complex genetic interaction analysis. <i>Science</i> , 2020, 368, .	6.0	79
13	ESCRT machinery mediates selective microautophagy of endoplasmic reticulum in yeast. <i>EMBO Journal</i> , 2020, 39, e102586.	3.5	77
14	Spore number control and breeding in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 2005, 171, 627-640.	2.3	73
15	Incomplete proteasomal degradation of green fluorescent proteins in the context of tandem fluorescent protein timers. <i>Molecular Biology of the Cell</i> , 2016, 27, 360-370.	0.9	72
16	Cooperation of mitochondrial and ER factors in quality control of tail-anchored proteins. <i>ELife</i> , 2019, 8, .	2.8	68
17	CDK1 couples proliferation with protein synthesis. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	58
18	Genome-wide C-SWAT library for high-throughput yeast genome tagging. <i>Nature Methods</i> , 2018, 15, 598-600.	9.0	57

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19	Seamless Gene Tagging by Endonuclease-Driven Homologous Recombination. <i>PLoS ONE</i> , 2011, 6, e23794.	1.1	56
20	Protein Abundance Control by Non-coding Antisense Transcription. <i>Cell Reports</i> , 2016, 15, 2625-2636.	2.9	51
21	A Memory System of Negative Polarity Cues Prevents Replicative Aging. <i>Cell</i> , 2014, 159, 1056-1069.	13.5	50
22	Bicoid gradient formation mechanism and dynamics revealed by protein lifetime analysis. <i>Molecular Systems Biology</i> , 2018, 14, e8355.	3.2	46
23	CRISPR-Cas12a-assisted PCR tagging of mammalian genes. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	42
24	YeastRGB: comparing the abundance and localization of yeast proteins across cells and libraries. <i>Nucleic Acids Research</i> , 2019, 47, D1245-D1249.	6.5	39
25	Timer-based proteomic profiling of the ubiquitin-proteasome system reveals a substrate receptor of the GID ubiquitin ligase. <i>Molecular Cell</i> , 2021, 81, 2460-2476.e11.	4.5	39
26	Analysis of Protein Dynamics with Tandem Fluorescent Protein Timers. <i>Methods in Molecular Biology</i> , 2014, 1174, 195-210.	0.4	36
27	Characterization of spindle pole body duplication reveals a regulatory role for nuclear pore complexes. <i>Journal of Cell Biology</i> , 2017, 216, 2425-2442.	2.3	30
28	Extensive 5' surveillance guards against non-canonical NAD-caps of nuclear mRNAs in yeast. <i>Nature Communications</i> , 2020, 11, 5508.	5.8	28
29	Evolution of Mutational Robustness in the Yeast Genome: A Link to Essential Genes and Meiotic Recombination Hotspots. <i>PLoS Genetics</i> , 2009, 5, e1000533.	1.5	27
30	N <sup>1</sup> -terminal acetylation of proteins by NatA and NatB serves distinct physiological roles in <i>Saccharomyces cerevisiae</i> . <i>Cell Reports</i> , 2021, 34, 108711.	2.9	26
31	Effectiveness and cost-effectiveness of four different strategies for SARS-CoV-2 surveillance in the general population (CoV-Surv Study): a structured summary of a study protocol for a cluster-randomised, two-factorial controlled trial. <i>Trials</i> , 2021, 22, 39.	0.7	23
32	Cells Escape an Operational Mitotic Checkpoint through a Stochastic Process. <i>Current Biology</i> , 2018, 28, 28-37.e7.	1.8	17
33	PCR Duplication: A One-Step Cloning-Free Method to Generate Duplicated Chromosomal Loci and Interference-Free Expression Reporters in Yeast. <i>PLoS ONE</i> , 2014, 9, e114590.	1.1	16
34	CRISPR/Cas12a-mediated labeling of MET receptor enables quantitative single-molecule imaging of endogenous protein organization and dynamics. <i>IScience</i> , 2021, 24, 101895.	1.9	14
35	Pooled clone collections by multiplexed CRISPR-Cas12a-assisted gene tagging in yeast. <i>Nature Communications</i> , 2019, 10, 2960.	5.8	12
36	Establishment of conidial fusion in the asexual fungus <i>Verticillium dahliae</i> as a useful system for the study of non-sexual genetic interactions. <i>Current Genetics</i> , 2021, 67, 471-485.	0.8	11

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37	Up-regulation of ubiquitinâ€“proteasome activity upon loss of NatA-dependent N-terminal acetylation. <i>Life Science Alliance</i> , 2022, 5, e202000730.	1.3	11
38	Monitoring Protein Dynamics in Protein O-Mannosyltransferase Mutants In Vivo by Tandem Fluorescent Protein Timers. <i>Molecules</i> , 2018, 23, 2622.	1.7	10
39	Hex1, the Major Component of Woronin Bodies, Is Required for Normal Development, Pathogenicity, and Stress Response in the Plant Pathogenic Fungus <i>Verticillium dahliae</i> . <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.7843.54 rgBT /Overlock	1.7	10
40	Starvation-induced cell fusion and heterokaryosis frequently escape imperfect allorecognition systems in an asexual fungal pathogen. <i>BMC Biology</i> , 2021, 19, 169.	1.7	8
41	Rapid comparative evaluation of SARS-CoV-2 rapid point-of-care antigen tests. <i>Infection</i> , 2022, 50, 1281-1293.	2.3	8
42	Effectiveness and cost-effectiveness of four different strategies for SARS-CoV-2 surveillance in the general population (CoV-Surv Study): study protocol for a two-factorial randomized controlled multi-armÄtrialÄwith cluster sampling. <i>Trials</i> , 2021, 22, 656.	0.7	6
43	Upregulation of SPS100 gene expression by an antisense RNA via a switch of mRNA isoforms with different stabilities. <i>Nucleic Acids Research</i> , 2017, 45, 11144-11158.	6.5	5
44	Î±-Synuclein Decreases the Abundance of Proteasome Subunits and Alters Ubiquitin Conjugates in Yeast. <i>Cells</i> , 2021, 10, 2229.	1.8	5
45	The NADPH Oxidase A of <i>Verticillium dahliae</i> Is Essential for Pathogenicity, Normal Development, and Stress Tolerance, and It Interacts with Yap1 to Regulate Redox Homeostasis. <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 rgBT /Overlock	1.7	10
46	Colorimetric RT-LAMP and LAMP-sequencing for Detecting SARS-CoV-2 RNA in Clinical Samples. <i>Bio-protocol</i> , 2021, 11, e3964.	0.2	4
47	Sex without crossing over in the yeast <i>Saccharomyces ludwigii</i> . <i>Genome Biology</i> , 2021, 22, 303.	3.8	3