Anuj Kumar

List of Publications by Year
in descending order

48 papers	2,448 citations	304743 22 h-index	223800 46 g-index
48 all docs	48 docs citations	48 times ranked	2780 citing authors

#	Article	IF	Citations
1	The Complex Genetic Basis and Multilayered Regulatory Control of Yeast Pseudohyphal Growth. Annual Review of Genetics, 2021, 55, 1-21.	7.6	15
2	Jump around: transposons in and out of the laboratory. F1000Research, 2020, 9, 135.	1.6	10
3	Filamentation Regulatory Pathways Control Adhesion-Dependent Surface Responses in Yeast. Genetics, 2019, 212, 667-690.	2.9	20
4	A Stress-Responsive Signaling Network Regulating Pseudohyphal Growth and Ribonucleoprotein Granule Abundance in *Saccharomyces cerevisiae*. Genetics, 2019, 213, 705-720.	2.9	6
5	Messengers for morphogenesis: inositol polyphosphate signaling and yeast pseudohyphal growth. Current Genetics, 2019, 65, 119-125.	1.7	7
6	Genome-Wide Screen for *Saccharomyces cerevisiae* Genes Contributing to Opportunistic Pathogenicity in an Invertebrate Model Host. G3: Genes, Genomes, Genetics, 2018, 8, 63-78.	1.8	11
7	Inositol polyphosphates regulate and predict yeast pseudohyphal growth phenotypes. PLoS Genetics, 2018, 14, e1007493.	3.5	15
8	Using Yeast Transposon-Insertion Libraries for Phenotypic Screening and Protein Localization. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot085217.	0.3	5
9	Multipurpose Transposon-Insertion Libraries in Yeast. Cold Spring Harbor Protocols, 2016, 2016, pdb.top080259.	0.3	6
10	Using Interactive Data Visualizations for Exploratory Analysis in Undergraduate Genomics Coursework: Field Study Findings and Guidelines. Journal of Science Education and Technology, 2016, 25, 91-110.	3.9	6
11	Mutant power: using mutant allele collections for yeast functional genomics. Briefings in Functional Genomics, 2016, 15, 75-84.	2.7	9
12	Mapping paths: new approaches to dissect eukaryotic signaling circuitry. F1000Research, 2016, 5, 1853.	1.6	0
13	Genome-Wide Synthetic Genetic Screening by Transposon Mutagenesis in Candida albicans. Methods in Molecular Biology, 2015, 1279, 125-135.	0.9	7
14	Large-Scale Analysis of Kinase Signaling in Yeast Pseudohyphal Development Identifies Regulation of Ribonucleoprotein Granules. PLoS Genetics, 2015, 11, e1005564.	3.5	24
15	The Yeast Sks1p Kinase Signaling Network Regulates Pseudohyphal Growth and Glucose Response. PLoS Genetics, 2014, 10, e1004183.	3.5	28
16	Pooled Segregant Sequencing Reveals Genetic Determinants of Yeast Pseudohyphal Growth. PLoS Genetics, 2014, 10, e1004570.	3.5	24
17	Genetic Networks Inducing Invasive Growth in *Saccharomyces cerevisiae* Identified Through Systematic Genome-Wide Overexpression. Genetics, 2013, 193, 1297-1310.	2.9	44
18	TEAK: Topology Enrichment Analysis frameworK for detecting activated biological subpathways. Nucleic Acids Research, 2013, 41, 1425-1437.	14.5	59

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19	An Overview of Autophagy and Yeast Pseudohyphal Growth: Integration of Signaling Pathways during Nitrogen Stress. Cells, 2012, 1, 263-283.	4.1	28
20	Genome-Wide Transposon Mutagenesis in Saccharomyces cerevisiae and Candida albicans. Methods in Molecular Biology, 2011, 765, 207-224.	0.9	15
21	A Large-Scale Complex Haploinsufficiency-Based Genetic Interaction Screen in Candida albicans: Analysis of the RAM Network during Morphogenesis. PLoS Genetics, 2011, 7, e1002058.	3.5	46
22	Conditionally controlling nuclear trafficking in yeast by chemical-induced protein dimerization. Nature Protocols, 2010, 5, 1831-1843.	12.0	25
23	A Profile of Differentially Abundant Proteins at the Yeast Cell Periphery during Pseudohyphal Growth. Journal of Biological Chemistry, 2010, 285, 15476-15488.	3.4	32
24	An Overview of Nested Genes in Eukaryotic Genomes. Eukaryotic Cell, 2009, 8, 1321-1329.	3.4	59
25	Conditional Nuclear Import and Export of Yeast Proteins Using a Chemical Inducer of Dimerization. Cell Biochemistry and Biophysics, 2009, 53, 127-134.	1.8	9
26	A small molecule‒directed approach to control protein localization and function. Yeast, 2008, 25, 577-594.	1.7	31
27	Unconventional Genomic Architecture in the Budding Yeast *Saccharomyces cerevisiae* Masks the Nested Antisense Gene *NAG1*. Eukaryotic Cell, 2008, 7, 1289-1298.	3.4	17
28	Localization of autophagy-related proteins in yeast using a versatile plasmid-based resource of fluorescent protein fusions. Autophagy, 2008, 4, 792-800.	9.1	11
29	Large-Scale Analysis of Yeast Filamentous Growth by Systematic Gene Disruption and Overexpression. Molecular Biology of the Cell, 2008, 19, 284-296.	2.1	118
30	Analysis of the Yeast Kinome Reveals a Network of Regulated Protein Localization during Filamentous Growth. Molecular Biology of the Cell, 2008, 19, 2708-2717.	2.1	50
31	Multipurpose Transposon Insertion Libraries for Large-Scale Analysis of Gene Function in Yeast. Methods in Molecular Biology, 2008, 416, 117-129.	0.9	6
32	Overexpression of Autophagy-Related Genes Inhibits Yeast Filamentous Growth. Autophagy, 2007, 3, 604-609.	9.1	12
33	An Interrelationship Between Autophagy and Filamentous Growth in Budding Yeast. Genetics, 2007, 177, 205-214.	2.9	36
34	Genomic analysis of insertion behavior and target specificity of mini-Tn7 and Tn3 transposons in Saccharomyces cerevisiae. Nucleic Acids Research, 2006, 34, e57-e57.	14.5	17
35	A Systems Biology Approach to Learning Autophagy. Autophagy, 2006, 2, 12-23.	9.1	5
36	Teaching Systems Biology: An Active-learning Approach. CBE: Life Sciences Education, 2005, 4, 323-329.	0.7	19

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37	Large-Scale Mutagenesis of the Yeast Genome Using a Tn7-Derived Multipurpose Transposon. Genome Research, 2004, 14, 1975-1986.	5.5	52
38	Where do all the proteins go?. Targets, 2003, 2, 237-244.	0.3	3
39	A novel mitochondrial protein, Tar1p, is encoded on the antisense strand of the nuclear 25S rDNA. Genes and Development, 2002, 16, 2755-2760.	5.9	67
40	Insertional mutagenesis: Transposon-insertion libraries as mutagens in yeast. Methods in Enzymology, 2002, 350, 219-229.	1.0	22
41	The TRIPLES database: a community resource for yeast molecular biology. Nucleic Acids Research, 2002, 30, 73-75.	14.5	40
42	Subcellular localization of the yeast proteome. Genes and Development, 2002, 16, 707-719.	5.9	667
43	An integrated approach for finding overlooked genes in yeast. Nature Biotechnology, 2002, 20, 58-63.	17.5	112
44	Emerging technologies in yeast genomics. Nature Reviews Genetics, 2001, 2, 302-312.	16.3	96
45	An integrated web interface for large-scale characterization of sequence data. Functional and Integrative Genomics, 2000, 1, 70-75.	3.5	2
46	[33] High-throughput methods for the large-scale analysis of gene function by transposon tagging. Methods in Enzymology, 2000, 328, 550-574.	1.0	34
47	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. Nature, 1999, 402, 413-418.	27.8	521
48	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0