## Anuj Kumar

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6665464/publications.pdf

Version: 2024-02-01

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  | Subcellular localization of the yeast proteome. Genes and Development, 2002, 16, 707-719.   | 5.9          | 667       |
| 2  | Large-scale analysis of the yeast genome by transposon tagging and gene disruption. Nature, 1999, 402, 413-418.   | 27.8         | 521       |
| 3  | Large-Scale Analysis of Yeast Filamentous Growth by Systematic Gene Disruption and Overexpression.<br>Molecular Biology of the Cell, 2008, 19, 284-296.                               | 2.1          | 118       |
| 4  | An integrated approach for finding overlooked genes in yeast. Nature Biotechnology, 2002, 20, 58-63.  | <b>17.</b> 5 | 112       |
| 5  | Emerging technologies in yeast genomics. Nature Reviews Genetics, 2001, 2, 302-312.   | 16.3         | 96        |
| 6  | 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        |
| 7  | An Overview of Nested Genes in Eukaryotic Genomes. Eukaryotic Cell, 2009, 8, 1321-1329.   | 3.4          | 59        |
| 8  | TEAK: Topology Enrichment Analysis framework for detecting activated biological subpathways. Nucleic Acids Research, 2013, 41, 1425-1437.   | 14.5         | 59        |
| 9  | Large-Scale Mutagenesis of the Yeast Genome Using a Tn7-Derived Multipurpose Transposon. Genome<br>Research, 2004, 14, 1975-1986.   | 5.5          | 52        |
| 10 | 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        |
| 11 | A Large-Scale Complex Haploinsufficiency-Based Genetic Interaction Screen in Candida albicans:<br>Analysis of the RAM Network during Morphogenesis. PLoS Genetics, 2011, 7, e1002058. | 3.5          | 46        |
| 12 | Genetic Networks Inducing Invasive Growth in <i>Saccharomyces cerevisiae</i> Identified Through Systematic Genome-Wide Overexpression. Genetics, 2013, 193, 1297-1310.                | 2.9          | 44        |
| 13 | The TRIPLES database: a community resource for yeast molecular biology. Nucleic Acids Research, 2002, 30, 73-75.  | 14.5         | 40        |
| 14 | An Interrelationship Between Autophagy and Filamentous Growth in Budding Yeast. Genetics, 2007, 177, 205-214.   | 2.9          | 36        |
| 15 | [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        |
| 16 | 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        |
| 17 | A small moleculeâ€directed approach to control protein localization and function. Yeast, 2008, 25, 577-594.   | 1.7          | 31        |
| 18 | An Overview of Autophagy and Yeast Pseudohyphal Growth: Integration of Signaling Pathways during Nitrogen Stress. Cells, 2012, 1, 263-283.  | 4.1          | 28        |

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|----|---|------|-----------|
| 19 | The Yeast Sks1p Kinase Signaling Network Regulates Pseudohyphal Growth and Glucose Response. PLoS Genetics, 2014, 10, e1004183.   | 3.5  | 28        |
| 20 | Conditionally controlling nuclear trafficking in yeast by chemical-induced protein dimerization. Nature Protocols, 2010, 5, 1831-1843.  | 12.0 | 25        |
| 21 | Pooled Segregant Sequencing Reveals Genetic Determinants of Yeast Pseudohyphal Growth. PLoS Genetics, 2014, 10, e1004570.   | 3.5  | 24        |
| 22 | Large-Scale Analysis of Kinase Signaling in Yeast Pseudohyphal Development Identifies Regulation of Ribonucleoprotein Granules. PLoS Genetics, 2015, 11, e1005564.                      | 3.5  | 24        |
| 23 | Insertional mutagenesis: Transposon-insertion libraries as mutagens in yeast. Methods in Enzymology, 2002, 350, 219-229.  | 1.0  | 22        |
| 24 | Filamentation Regulatory Pathways Control Adhesion-Dependent Surface Responses in Yeast. Genetics, 2019, 212, 667-690.  | 2.9  | 20        |
| 25 | Teaching Systems Biology: An Active-learning Approach. CBE: Life Sciences Education, 2005, 4, 323-329.  | 0.7  | 19        |
| 26 | 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        |
| 27 | Unconventional Genomic Architecture in the Budding Yeast <i>Saccharomyces cerevisiae</i> Masks the Nested Antisense Gene <i>NAG1</i> Eukaryotic Cell, 2008, 7, 1289-1298.               | 3.4  | 17        |
| 28 | Genome-Wide Transposon Mutagenesis in Saccharomyces cerevisiae and Candida albicans. Methods in Molecular Biology, 2011, 765, 207-224.  | 0.9  | 15        |
| 29 | Inositol polyphosphates regulate and predict yeast pseudohyphal growth phenotypes. PLoS Genetics, 2018, 14, e1007493.   | 3.5  | 15        |
| 30 | The Complex Genetic Basis and Multilayered Regulatory Control of Yeast Pseudohyphal Growth. Annual Review of Genetics, 2021, 55, 1-21.  | 7.6  | 15        |
| 31 | Overexpression of Autophagy-Related Genes Inhibits Yeast Filamentous Growth. Autophagy, 2007, 3, 604-609.   | 9.1  | 12        |
| 32 | 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        |
| 33 | Genome-Wide Screen for <i> Saccharomyces cerevisiae </i> Genes Contributing to Opportunistic Pathogenicity in an Invertebrate Model Host. G3: Genes, Genomes, Genetics, 2018, 8, 63-78. | 1.8  | 11        |
| 34 | Jump around: transposons in and out of the laboratory. F1000Research, 2020, 9, 135.   | 1.6  | 10        |
| 35 | 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         |
| 36 | Mutant power: using mutant allele collections for yeast functional genomics. Briefings in Functional Genomics, 2016, 15, 75-84.   | 2.7  | 9         |

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|----|--|-----|-----------|
| 37 | Messengers for morphogenesis: inositol polyphosphate signaling and yeast pseudohyphal growth. Current Genetics, 2019, 65, 119-125.   | 1.7 | 7         |
| 38 | Genome-Wide Synthetic Genetic Screening by Transposon Mutagenesis in Candida albicans. Methods in Molecular Biology, 2015, 1279, 125-135.  | 0.9 | 7         |
| 39 | Multipurpose Transposon-Insertion Libraries in Yeast. Cold Spring Harbor Protocols, 2016, 2016, pdb.top080259.   | 0.3 | 6         |
| 40 | Using Interactive Data Visualizations for Exploratory Analysis in Undergraduate Genomics<br>Coursework: Field Study Findings and Guidelines. Journal of Science Education and Technology, 2016,<br>25, 91-110. | 3.9 | 6         |
| 41 | A Stress-Responsive Signaling Network Regulating Pseudohyphal Growth and Ribonucleoprotein Granule Abundance in <i>Saccharomyces cerevisiae</i> . Genetics, 2019, 213, 705-720.                                | 2.9 | 6         |
| 42 | Multipurpose Transposon Insertion Libraries for Large-Scale Analysis of Gene Function in Yeast. Methods in Molecular Biology, 2008, 416, 117-129.  | 0.9 | 6         |
| 43 | A Systems Biology Approach to Learning Autophagy. Autophagy, 2006, 2, 12-23.   | 9.1 | 5         |
| 44 | Using Yeast Transposon-Insertion Libraries for Phenotypic Screening and Protein Localization. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot085217.  | 0.3 | 5         |
| 45 | Where do all the proteins go?. Targets, 2003, 2, 237-244.  | 0.3 | 3         |
| 46 | An integrated web interface for large-scale characterization of sequence data. Functional and Integrative Genomics, 2000, 1, 70-75.  | 3.5 | 2         |
| 47 | Computational Methods and Bioinformatic Tools. , 0, , 769-904.   |     | 0         |
| 48 | Mapping paths: new approaches to dissect eukaryotic signaling circuitry. F1000Research, 2016, 5, 1853.   | 1.6 | 0         |