

# Patrick Kemmeren

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8252492/publications.pdf>

Version: 2024-02-01

23  
papers

2,394  
citations

567281

15  
h-index

677142

22  
g-index

29  
all docs

29  
docs citations

29  
times ranked

3848  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Toward a Comprehensive Atlas of the Physical Interactome of <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 439-450.                                  | 3.8  | 692       |
| 2  | Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors. <i>Cell</i> , 2014, 157, 740-752.  | 28.9 | 248       |
| 3  | Functional Organization of the <i>S. cerevisiae</i> Phosphorylation Network. <i>Cell</i> , 2009, 136, 952-963.  | 28.9 | 235       |
| 4  | Protein Interaction Verification and Functional Annotation by Integrated Analysis of Genome-Scale Data. <i>Molecular Cell</i> , 2002, 9, 1133-1143.   | 9.7  | 221       |
| 5  | An organoid biobank for childhood kidney cancers that captures disease and tissue heterogeneity. <i>Nature Communications</i> , 2020, 11, 1310.   | 12.8 | 183       |
| 6  | The Genomic Landscape of Compensatory Evolution. <i>PLoS Biology</i> , 2014, 12, e1001935.  | 5.6  | 150       |
| 7  | Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. <i>Cell</i> , 2010, 143, 991-1004.   | 28.9 | 123       |
| 8  | Cell cycle population effects in perturbation studies. <i>Molecular Systems Biology</i> , 2014, 10, 732.  | 7.2  | 118       |
| 9  | A Consensus of Core Protein Complex Compositions for <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2010, 38, 916-928.   | 9.7  | 91        |
| 10 | Proteome-wide Changes in Protein Turnover Rates in <i>C.Âelegans</i> Models of Longevity and Age-Related Disease. <i>Cell Reports</i> , 2016, 16, 3041-3051.                                | 6.4  | 54        |
| 11 | Molecular mechanisms that distinguish TFIID housekeeping from regulatable SAGA promoters. <i>EMBO Journal</i> , 2017, 36, 274-290.  | 7.8  | 53        |
| 12 | Epistatic relationships reveal the functional organization of yeast transcription factors. <i>Molecular Systems Biology</i> , 2010, 6, 420.   | 7.2  | 50        |
| 13 | DNA Methylation Profiling Identifies Distinct Clusters in Angiosarcomas. <i>Clinical Cancer Research</i> , 2020, 26, 93-100.  | 7.0  | 34        |
| 14 | Structural variant detection in cancer genomes: computational challenges and perspectives for precision oncology. <i>Npj Precision Oncology</i> , 2021, 5, 15.                              | 5.4  | 30        |
| 15 | Predicting gene function through systematic analysis and quality assessment of high-throughput data. <i>Bioinformatics</i> , 2005, 21, 1644-1652.   | 4.1  | 24        |
| 16 | A high-resolution gene expression atlas of epistasis between gene-specific transcription factors exposes potential mechanisms for genetic interactions. <i>BMC Biology</i> , 2015, 13, 112. | 3.8  | 21        |
| 17 | An Optimized Chromatin Immunoprecipitation Protocol for Quantification of Protein-DNA Interactions. <i>STAR Protocols</i> , 2020, 1, 100020.  | 1.2  | 15        |
| 18 | Genome-wide off-rates reveal how DNA binding dynamics shape transcription factor function. <i>Molecular Systems Biology</i> , 2020, 16, e9885.  | 7.2  | 14        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 19 | Improved Gene Fusion Detection in Childhood Cancer Diagnostics Using RNA Sequencing. JCO Precision Oncology, 2022, 6, e2000504.  | 3.0 | 9         |
| 20 | The ability of transcription factors to differentially regulate gene expression is a crucial component of the mechanism underlying inversion, a frequently observed genetic interaction pattern. PLoS Computational Biology, 2019, 15, e1007061. | 3.2 | 4         |
| 21 | Growth condition dependency is the major cause of non-responsiveness upon genetic perturbation. PLoS ONE, 2017, 12, e0173432.  | 2.5 | 3         |
| 22 | A framework for exhaustive modelling of genetic interaction patterns using Petri nets. Bioinformatics, 2020, 36, 2142-2149.  | 4.1 | 3         |
| 23 | A systematic analysis of genetic interactions and their underlying biology in childhood cancer. Communications Biology, 2021, 4, 1139.   | 4.4 | 2         |