

# Patrick J Flaherty

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/525232/publications.pdf>

Version: 2024-02-01

20  
papers

4,982  
citations

840776

11  
h-index

752698

20  
g-index

23  
all docs

23  
docs citations

23  
times ranked

6557  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Model-based identification of conditionally-essential genes from transposon-insertion sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009273.                         | 3.2  | 3         |
| 2  | A Bayesian nonparametric model for inferring subclonal populations from structured DNA sequencing data. <i>Annals of Applied Statistics</i> , 2021, 15, 925-951.                       | 1.1  | 0         |
| 3  | Multi-Biomarker Prediction Models for Multiple Infection Episodes Following Blunt Trauma. <i>IScience</i> , 2020, 23, 101659.  | 4.1  | 7         |
| 4  | SCSIM: Jointly simulating correlated single-cell and bulk next-generation DNA sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 215.  | 2.6  | 6         |
| 5  | Recovering all generalized order-preserving submatrices: new exact formulations and algorithms. <i>Annals of Operations Research</i> , 2018, 263, 385-404.                             | 4.1  | 2         |
| 6  | Conditional genetic screen in <i>Physcomitrella patens</i> reveals a novel microtubule depolymerizing-end-tracking protein. <i>PLoS Genetics</i> , 2018, 14, e1007221.                 | 3.5  | 17        |
| 7  | Comparative functional genomic screens of three yeast deletion collections reveal unexpected effects of genotype in response to diverse stress. <i>Open Biology</i> , 2017, 7, 160330. | 3.6  | 12        |
| 8  | Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 45.                                     | 2.6  | 3         |
| 9  | GEMINI: a computationally-efficient search engine for large gene expression datasets. <i>BMC Bioinformatics</i> , 2016, 17, 102.   | 2.6  | 13        |
| 10 | Reverse Chemical Genetics: Comprehensive Fitness Profiling Reveals the Spectrum of Drug Target Interactions. <i>PLoS Genetics</i> , 2016, 12, e1006275.                                | 3.5  | 13        |
| 11 | RVD2: an ultra-sensitive variant detection model for low-depth heterogeneous next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 2785-2793.                             | 4.1  | 7         |
| 12 | Robust Optimization of Biological Protocols. <i>Technometrics</i> , 2015, 57, 234-244.   | 1.9  | 5         |
| 13 | Identification of a New Class of Antifungals Targeting the Synthesis of Fungal Sphingolipids. <i>MBio</i> , 2015, 6, e00647.   | 4.1  | 124       |
| 14 | GLAD: a mixed-membership model for heterogeneous tumor subtype classification. <i>Bioinformatics</i> , 2015, 31, 225-232.  | 4.1  | 13        |
| 15 | Ultrasensitive detection of rare mutations using next-generation targeted resequencing. <i>Nucleic Acids Research</i> , 2012, 40, e2-e2.   | 14.5 | 117       |
| 16 | A Dual Receptor Crosstalk Model of G-Protein-Coupled Signal Transduction. <i>PLoS Computational Biology</i> , 2008, 4, e1000185.   | 3.2  | 38        |
| 17 | A latent variable model for chemogenomic profiling. <i>Bioinformatics</i> , 2005, 21, 3286-3293.   | 4.1  | 53        |
| 18 | Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.   | 3.5  | 144       |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 793-798. | 7.1  | 460       |
| 20 | Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. Nature, 2002, 418, 387-391.   | 27.8 | 3,938     |