

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	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	27.8	3,938
2	Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 793-798.	7.1	460
3	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	3.5	144
4	Identification of a New Class of Antifungals Targeting the Synthesis of Fungal Sphingolipids. <i>MBio</i> , 2015, 6, e00647.	4.1	124
5	Ultrasensitive detection of rare mutations using next-generation targeted resequencing. <i>Nucleic Acids Research</i> , 2012, 40, e2-e2.	14.5	117
6	A latent variable model for chemogenomic profiling. <i>Bioinformatics</i> , 2005, 21, 3286-3293.	4.1	53
7	A Dual Receptor Crosstalk Model of G-Protein-Coupled Signal Transduction. <i>PLoS Computational Biology</i> , 2008, 4, e1000185.	3.2	38
8	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
9	GLAD: a mixed-membership model for heterogeneous tumor subtype classification. <i>Bioinformatics</i> , 2015, 31, 225-232.	4.1	13
10	GEMINI: a computationally-efficient search engine for large gene expression datasets. <i>BMC Bioinformatics</i> , 2016, 17, 102.	2.6	13
11	Reverse Chemical Genetics: Comprehensive Fitness Profiling Reveals the Spectrum of Drug Target Interactions. <i>PLoS Genetics</i> , 2016, 12, e1006275.	3.5	13
12	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
13	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
14	Multi-Biomarker Prediction Models for Multiple Infection Episodes Following Blunt Trauma. <i>IScience</i> , 2020, 23, 101659.	4.1	7
15	SCSIM: Jointly simulating correlated single-cell and bulk next-generation DNA sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 215.	2.6	6
16	Robust Optimization of Biological Protocols. <i>Technometrics</i> , 2015, 57, 234-244.	1.9	5
17	Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 45.	2.6	3
18	Model-based identification of conditionally-essential genes from transposon-insertion sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009273.	3.2	3

#	ARTICLE	IF	CITATIONS
19	Recovering all generalized order-preserving submatrices: new exact formulations and algorithms. <i>Annals of Operations Research</i> , 2018, 263, 385-404.	4.1	2
20	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