

David L Gibbs

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7717805/publications.pdf>

Version: 2024-02-01

23
papers

5,102
citations

759233

12
h-index

839539

18
g-index

27
all docs

27
docs citations

27
times ranked

9552
citing authors

#	ARTICLE	IF	CITATIONS
1	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
2	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	9.4	422
3	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
4	Combining dependent χ^2 values with an empirical adaptation of Brown's method. <i>Bioinformatics</i> , 2016, 32, i430-i436.	4.1	107
5	Genomic and molecular characterization of preterm birth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5819-5827.	7.1	53
6	The ISB Cancer Genomics Cloud: A Flexible Cloud-Based Platform for Cancer Genomics Research. <i>Cancer Research</i> , 2017, 77, e7-e10.	0.9	41
7	CRI iAtlas: an interactive portal for immuno-oncology research. <i>F1000Research</i> , 2020, 9, 1028.	1.6	39
8	A Pan-Cancer Approach to Predict Responsiveness to Immune Checkpoint Inhibitors by Machine Learning. <i>Cancers</i> , 2019, 11, 1562.	3.7	31
9	Protein co-expression network analysis (ProCoNA). <i>Journal of Clinical Bioinformatics</i> , 2013, 3, 11.	1.2	26
10	Copy Number Variation Analysis in 98 Individuals with PHACE Syndrome. <i>Journal of Investigative Dermatology</i> , 2013, 133, 677-684.	0.7	25
11	Multi-omic network signatures of disease. <i>Frontiers in Genetics</i> , 2014, 4, 309.	2.3	21
12	A generalizable data-driven multicellular model of pancreatic ductal adenocarcinoma. <i>GigaScience</i> , 2020, 9, .	6.4	20
13	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. <i>PLoS ONE</i> , 2019, 14, e0224693.	2.5	19
14	Solving the influence maximization problem reveals regulatory organization of the yeast cell cycle. <i>PLoS Computational Biology</i> , 2017, 13, e1005591.	3.2	12
15	Flexibility of Boolean Network Reservoir Computers in Approximating Arbitrary Recursive and Non-Recursive Binary Filters. <i>Entropy</i> , 2018, 20, 954.	2.2	9
16	Patient-Specific Cell Communication Networks Associate With Disease Progression in Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 667382.	2.3	5
17	Intrinsic Genetic and Transcriptomic Patterns Reflect Tumor Immune Subtypes Facilitating Exploring Possible Combinatory Therapy. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 53.	3.5	1
18	A functional module states framework reveals transcriptional states for drug and target prediction. <i>Cell Reports</i> , 2022, 38, 110269.	6.4	1

#	ARTICLE	IF	CITATIONS
19	PRoBE the cloud toolkit: finding the best biomarkers of drug response within a breast cancer clinical trial. JAMIA Open, 2021, 4, ooab038.	2.0	0
20	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
21	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
22	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
23	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0