

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	A functional module states framework reveals transcriptional states for drug and target prediction. Cell Reports, 2022, 38, 110269.	6.4	1
2	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
3	Patient-Specific Cell Communication Networks Associate With Disease Progression in Cancer. Frontiers in Genetics, 2021, 12, 667382.	2.3	5
4	A generalizable data-driven multicellular model of pancreatic ductal adenocarcinoma. GigaScience, 2020, 9, .	6.4	20
5	Intrinsic Genetic and Transcriptomic Patterns Reflect Tumor Immune Subtypes Facilitating Exploring Possible Combinatory Therapy. Frontiers in Molecular Biosciences, 2020, 7, 53.	3.5	1
6	CRI iAtlas: an interactive portal for immuno-oncology research. F1000Research, 2020, 9, 1028.	1.6	39
7	A Pan-Cancer Approach to Predict Responsiveness to Immune Checkpoint Inhibitors by Machine Learning. Cancers, 2019, 11, 1562.	3.7	31
8	Genomic and molecular characterization of preterm birth. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5819-5827.	7.1	53
9	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. PLoS ONE, 2019, 14, e0224693.	2.5	19
10	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
11	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
12	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
13	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
14	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
15	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
16	Flexibility of Boolean Network Reservoir Computers in Approximating Arbitrary Recursive and Non-Recursive Binary Filters. Entropy, 2018, 20, 954.	2.2	9
17	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
18	The ISB Cancer Genomics Cloud: A Flexible Cloud-Based Platform for Cancer Genomics Research. Cancer Research, 2017, 77, e7-e10.	0.9	41

#	ARTICLE	IF	CITATIONS
19	Solving the influence maximization problem reveals regulatory organization of the yeast cell cycle. PLoS Computational Biology, 2017, 13, e1005591.	3.2	12
20	Combining dependent <i>P</i> -values with an empirical adaptation of Brown's method. Bioinformatics, 2016, 32, i430-i436.	4.1	107
21	Multi-omic network signatures of disease. Frontiers in Genetics, 2014, 4, 309.	2.3	21
22	Protein co-expression network analysis (ProCoNA). Journal of Clinical Bioinformatics, 2013, 3, 11.	1.2	26
23	Copy Number Variation Analysis in 98 Individuals with PHACE Syndrome. Journal of Investigative Dermatology, 2013, 133, 677-684.	0.7	25