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List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

7,460
citations

567281

15
h-index

610901

24
g-index

26
all docs

26
docs citations

26
times ranked

14634
citing authors

#	ARTICLE	IF	CITATIONS
1	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
2	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518
3	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
4	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482
5	Fewer permutations, more accurate P -values. <i>Bioinformatics</i> , 2009, 25, i161-i168.	4.1	183
6	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	16.8	151
7	Combining dependent P -values with an empirical adaptation of Brown's method. <i>Bioinformatics</i> , 2016, 32, i430-i436.	4.1	107
8	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	6.2	103
9	Epigenetic profiling for the molecular classification of metastatic brain tumors. <i>Nature Communications</i> , 2018, 9, 4627.	12.8	79
10	Extracting Intercellular Signaling Network of Cancer Tissues using Ligand-Receptor Expression Patterns from Whole-tumor and Single-cell Transcriptomes. <i>Scientific Reports</i> , 2017, 7, 8815.	3.3	74
11	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
12	Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. <i>Scientific Reports</i> , 2016, 6, 36812.	3.3	43
13	A multilevel pan-cancer map links gene mutations to cancer hallmarks. <i>Chinese Journal of Cancer</i> , 2015, 34, 439-49.	4.9	38
14	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	19.0	31
15	A regression model approach to enable cell morphology correction in high-throughput flow cytometry. <i>Molecular Systems Biology</i> , 2011, 7, 531.	7.2	22
16	A deep generative model of 3D single-cell organization. <i>PLoS Computational Biology</i> , 2022, 18, e1009155.	3.2	18
17	Multiscale mutation clustering algorithm identifies pan-cancer mutational clusters associated with pathway-level changes in gene expression. <i>PLoS Computational Biology</i> , 2017, 13, e1005347.	3.2	14
18	Increased levels of RECQ5 shift DNA repair from canonical to alternative pathways. <i>Nucleic Acids Research</i> , 2018, 46, 9496-9509.	14.5	13

#	ARTICLE	IF	CITATIONS
19	Identifying Personalized Metabolic Signatures in Breast Cancer. <i>Metabolites</i> , 2021, 11, 20.	2.9	7
20	EPEPT: A web service for enhanced P-value estimation in permutation tests. <i>BMC Bioinformatics</i> , 2011, 12, 411.	2.6	6
21	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. <i>STAR Protocols</i> , 2021, 2, 100483.	1.2	2
22	CloudForest: A Scalable and Efficient Random Forest Implementation for Biological Data. <i>PLoS ONE</i> , 2015, 10, e0144820.	2.5	2
23	Identifying novel transcription factors involved in the inflammatory response by using binding site motif scanning in genomic regions defined by histone acetylation. <i>PLoS ONE</i> , 2017, 12, e0184850.	2.5	2
24	A functional module states framework reveals transcriptional states for drug and target prediction. <i>Cell Reports</i> , 2022, 38, 110269.	6.4	1