Theo A Knijnenburg

List of Publications by Year
in descending order

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	A functional module states framework reveals transcriptional states for drug and target prediction. Cell Reports, 2022, 38, 110269.	6.4	1
2	A deep generative model of 3D single-cell organization. PLoS Computational Biology, 2022, 18, e1009155.	3.2	18
3	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. STAR Protocols, 2021, 2, 100483.	1.2	2
4	Identifying Personalized Metabolic Signatures in Breast Cancer. Metabolites, 2021, 11, 20.	2.9	7
5	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
6	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons' Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
7	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
8	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
9	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
10	Epigenetic profiling for the molecular classification of metastatic brain tumors. Nature Communications, 2018, 9, 4627.	12.8	79
11	Increased levels of RECQ5 shift DNA repair from canonical to alternative pathways. Nucleic Acids Research, 2018, 46, 9496-9509.	14.5	13
12	Extracting Intercellular Signaling Network of Cancer Tissues using Ligand-Receptor Expression Patterns from Whole-tumor and Single-cell Transcriptomes. Scientific Reports, 2017, 7, 8815.	3.3	74
13	Multiscale mutation clustering algorithm identifies pan-cancer mutational clusters associated with pathway-level changes in gene expression. PLoS Computational Biology, 2017, 13, e1005347.	3.2	14
14	Identifying novel transcription factors involved in the inflammatory response by using binding site motif scanning in genomic regions defined by histone acetylation. PLoS ONE, 2017, 12, e0184850.	2.5	2
15	A Landscape of Pharmacogenomic Interactions in Cancer. Cell, 2016, 166, 740-754.	28.9	1,518
16	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
17	Combining dependent *P-*values with an empirical adaptation of Brown's method. Bioinformatics, 2016, 32, i430-i436.	4.1	107
18	Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. Scientific Reports, 2016, 6, 36812.	3.3	43

#	Article	IF	Citations
19	A multilevel pan-cancer map links gene mutations to cancer hallmarks. Chinese Journal of Cancer, 2015, 34, 439-49.	4.9	38
20	CloudForest: A Scalable and Efficient Random Forest Implementation for Biological Data. PLoS ONE, 2015, 10, e0144820.	2.5	2
21	Multiscale representation of genomic signals. Nature Methods, 2014, 11, 689-694.	19.0	31
22	EPEPT: A web service for enhanced P-value estimation in permutation tests. BMC Bioinformatics, 2011, 12, 411.	2.6	6
23	A regression model approach to enable cell morphology correction in high‐throughput flow cytometry. Molecular Systems Biology, 2011, 7, 531.	7.2	22
24	Fewer permutations, more accurate *P*-values. Bioinformatics, 2009, 25, i161-i168.	4.1	183