Kyung In Kim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4704586/publications.pdf

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		1163117	
13	746	8	13
papers	citations	h-index	g-index
13	13	13	1597
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Effects of dependence in high-dimensional multiple testing problems. BMC Bioinformatics, 2008, 9, 114.	2.6	267
2	CGHcall: calling aberrations for array CGH tumor profiles. Bioinformatics, 2007, 23, 892-894.	4.1	208
3	IL1 Receptor Antagonist Controls Transcriptional Signature of Inflammation in Patients with Metastatic Breast Cancer. Cancer Research, 2018, 78, 5243-5258.	0.9	119
4	Using single cell sequencing data to model the evolutionary history of a tumor. BMC Bioinformatics, 2014, 15, 27.	2.6	58
5	Probabilistic classifiers with high-dimensional data. Biostatistics, 2011, 12, 399-412.	1.5	27
6	A pan-cancer analysis of driver gene mutations, DNA methylation and gene expressions reveals that chromatin remodeling is a major mechanism inducing global changes in cancer epigenomes. BMC Medical Genomics, 2018, 11, 98.	1. 5	21
7	Transcriptional profiling of macrophages in situ in metastatic melanoma reveals localization-dependent phenotypes and function. Cell Reports Medicine, 2022, 3, 100621.	6.5	15
8	Estimating the False Discovery Rate Using Nonparametric Deconvolution. Biometrics, 2007, 63, 806-815.	1.4	14
9	Overfitting, generalization, and MSE in class probability estimation with highâ€dimensional data. Biometrical Journal, 2014, 56, 256-269.	1.0	6
10	Human KIT+ myeloid cells facilitate visceral metastasis by melanoma. Journal of Experimental Medicine, 2021, 218, .	8.5	5
11	Spatial Clustering of Array CGH Features in Combination with Hierarchical Multiple Testing. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article40.	0.6	3
12	Modeling performance of sample collection sites using whole exome sequencing metrics. BioTechniques, 2020, 69, 420-426.	1.8	2
13	SOME COMMENTS ON FALSE DISCOVERY RATE. Journal of Bioinformatics and Computational Biology, 2007, 05, 987-990.	0.8	1