

Arief Gusnanto

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11023906/publications.pdf>

Version: 2024-02-01

28
papers

1,500
citations

687363

13
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

3034
citing authors

#	ARTICLE	IF	CITATIONS
1	False discovery rate, sensitivity and sample size for microarray studies. <i>Bioinformatics</i> , 2005, 21, 3017-3024.	4.1	410
2	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , 2009, 113, e1-e9.	1.4	215
3	Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next-generation sequence data. <i>Bioinformatics</i> , 2012, 28, 40-47.	4.1	173
4	Comparative gene expression profiling of in vitro differentiated megakaryocytes and erythroblasts identifies novel activatory and inhibitory platelet membrane proteins. <i>Blood</i> , 2007, 109, 3260-3269.	1.4	153
5	Platelet genomics and proteomics in human health and disease. <i>Journal of Clinical Investigation</i> , 2005, 115, 3370-3377.	8.2	146
6	Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. <i>Blood</i> , 2010, 116, 4646-4656.	1.4	90
7	Multidimensional local false discovery rate for microarray studies. <i>Bioinformatics</i> , 2006, 22, 556-565.	4.1	69
8	A DNA microarray for fission yeast: minimal changes in global gene expression after temperature shift. <i>Yeast</i> , 2004, 21, 25-39.	1.7	39
9	Identification of differentially expressed genes and false discovery rate in microarray studies. <i>Current Opinion in Lipidology</i> , 2007, 18, 187-193.	2.7	39
10	Robust smooth segmentation approach for array CGH data analysis. <i>Bioinformatics</i> , 2007, 23, 2463-2469.	4.1	35
11	Variable selection in random calibration of near-infrared instruments: ridge regression and partial least squares regression settings. <i>Journal of Chemometrics</i> , 2003, 17, 174-185.	1.3	26
12	Identification of candidate genes linking systemic inflammation to atherosclerosis; results of a human in vivo LPS infusion study. <i>BMC Medical Genomics</i> , 2011, 4, 64.	1.5	25
13	Estimating optimal window size for analysis of low-coverage next-generation sequence data. <i>Bioinformatics</i> , 2014, 30, 1823-1829.	4.1	24
14	Fold-Change Estimation of Differentially Expressed Genes using Mixture Mixed-Model. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article26.	0.6	11
15	DNA ADDUCTS OF BENZO[A]PYRENE- AND DIBENZO[A,L]PYRENE-DIOL EPOXIDES IN HUMAN LUNG EPITHELIAL CELLS: KINETICS OF ADDUCT REMOVAL, EFFECTS ON CELL CYCLE CHECKPOINTS, AND GENE EXPRESSION. <i>Polycyclic Aromatic Compounds</i> , 2004, 24, 549-566.	2.6	9
16	Identification of variation in the platelet transcriptome associated with Glycoprotein 6 haplotype. <i>Platelets</i> , 2008, 19, 258-267.	2.3	9
17	Stratifying tumour subtypes based on copy number alteration profiles using next-generation sequence data. <i>Bioinformatics</i> , 2015, 31, 2713-2720.	4.1	9
18	Partial least squares and logistic regression random-effects estimates for gene selection in supervised classification of gene expression data. <i>Journal of Biomedical Informatics</i> , 2013, 46, 697-709.	4.3	8

#	ARTICLE	IF	CITATIONS
19	Improving the power to detect differentially expressed genes in comparative microarray experiments by including information from self-self hybridizations. Computational Biology and Chemistry, 2007, 31, 178-185.	2.3	1
20	Sparse alternatives to ridge regression: a random effects approach. Journal of Applied Statistics, 2015, 42, 12-26.	1.3	1
21	Method for Automatic Selection of Parameters in Normal Tissue Complication Probability Modeling. International Journal of Radiation Oncology Biology Physics, 2018, 101, 704-712.	0.8	1
22	Properties and approximate p-value calculation of the Cramer test. Journal of Statistical Computation and Simulation, 2020, 90, 1965-1981.	1.2	1
23	Geometry-based distance for clustering amino acids. Journal of Applied Statistics, 2020, 47, 1235-1250.	1.3	1
24	Sparse modelling of cancer patients' survival based on genomic copy number alterations. Journal of Biomedical Informatics, 2022, 128, 104025.	4.3	1
25	Identification of transcript regulatory patterns in cell differentiation. Bioinformatics, 2017, 33, 3235-3242.	4.1	0
26	Prediction of tumour pathological subtype from genomic profile using sparse logistic regression with random effects. Journal of Applied Statistics, 2021, 48, 605-622.	1.3	0
27	Classification of form under heterogeneity and non-isotropic errors. Journal of Applied Statistics, 2017, 44, 1495-1508.	1.3	0
28	Use of shared gamma frailty model in analysis of survival data in twins.. Theoretical Biology Forum, 2021, 114, 45-58.	0.2	0