

Guillemette Marot

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,953
citations

516710

16
h-index

501196

28
g-index

32
all docs

32
docs citations

32
times ranked

3941
citing authors

#	ARTICLE	IF	CITATIONS
1	TgAP2IX-5 is a key transcriptional regulator of the asexual cell cycle division in <i>Toxoplasma gondii</i> . <i>Nature Communications</i> , 2021, 12, 116.	12.8	24
2	Transient Receptor Potential Channel Expression Signatures in Tumor-Derived Endothelial Cells: Functional Roles in Prostate Cancer Angiogenesis. <i>Cancers</i> , 2019, 11, 956.	3.7	27
3	SMAGEXP: a galaxy tool suite for transcriptomics data meta-analysis. <i>GigaScience</i> , 2019, 8, .	6.4	5
4	Metabolic and Innate Immune Cues Merge into a Specific Inflammatory Response via the UPR. <i>Cell</i> , 2019, 177, 1201-1216.e19.	28.9	100
5	The miRNA-targeted transcriptome of porcine alveolar macrophages upon infection with Porcine Reproductive and Respiratory Syndrome Virus. <i>Scientific Reports</i> , 2019, 9, 3160.	3.3	9
6	Circulating proteomic signature of early death in heart failure patients with reduced ejection fraction. <i>Scientific Reports</i> , 2019, 9, 19202.	3.3	21
7	Abstract 2671: Omics unveils a specific signature of tumor dormancy in two murine models of leukemia and melanoma. , 2019, , .		0
8	Pre-malignant transformation by senescence evasion is prevented by the PERK and ATF6alpha branches of the Unfolded Protein Response. <i>Cancer Letters</i> , 2018, 438, 187-196.	7.2	5
9	New efficient algorithms for multiple change-point detection with reproducing kernels. <i>Computational Statistics and Data Analysis</i> , 2018, 128, 200-220.	1.2	32
10	The logic of transcriptional regulator recruitment architecture at cis-regulatory modules controlling liver functions. <i>Genome Research</i> , 2017, 27, 985-996.	5.5	22
11	BACH2 promotes indolent clinical presentation in Waldenström macroglobulinemia. <i>Oncotarget</i> , 2017, 8, 57451-57459.	1.8	2
12	Genomic Landscape of CXCR4 Mutations in Waldenström Macroglobulinemia. <i>Clinical Cancer Research</i> , 2016, 22, 1480-1488.	7.0	102
13	MPAgenomics: an R package for multi-patient analysis of genomic markers. <i>BMC Bioinformatics</i> , 2014, 15, 394.	2.6	2
14	Identification of a gene signature of a pre-transformation process by senescence evasion in normal human epidermal keratinocytes. <i>Molecular Cancer</i> , 2014, 13, 151.	19.2	12
15	Differential meta-analysis of RNA-seq data from multiple studies. <i>BMC Bioinformatics</i> , 2014, 15, 91.	2.6	99
16	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	6.5	1,064
17	Wavelet-Based Clustering for Mixed-Effects Functional Models in High Dimension. <i>Biometrics</i> , 2013, 69, 31-40.	1.4	66
18	<i>Toxoplasma</i> Transcription Factor TgAP2XI-5 Regulates the Expression of Genes Involved in Parasite Virulence and Host Invasion*. <i>Journal of Biological Chemistry</i> , 2013, 288, 31127-31138.	3.4	53

#	ARTICLE	IF	CITATIONS
19	Pre- and Postpartum Mild Underfeeding Influences Gene Expression in the Reproductive Tract of Cyclic Dairy Cows. <i>Reproduction in Domestic Animals</i> , 2013, 48, 484-499.	1.4	21
20	B-Cell-Specific Transcription Factor BACH2 Involved in the Clinical Behavior Heterogeneity of Waldenström Macroglobulinemia. <i>Blood</i> , 2012, 120, 1288-1288.	1.4	0
21	Sequential Analysis for Microarray Data Based on Sensitivity and Meta-Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-33.	0.6	14
22	Moderated effect size and <i>P</i> -value combinations for microarray meta-analyses. <i>Bioinformatics</i> , 2009, 25, 2692-2699.	4.1	139
23	The adult boar testicular and epididymal transcriptomes. <i>BMC Genomics</i> , 2009, 10, 369.	2.8	52
24	A structural mixed model to shrink covariance matrices for time-course differential gene expression studies. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1630-1638.	1.2	2
25	A structural mixed model for variances in differential gene expression studies. <i>Genetical Research</i> , 2007, 89, 19-25.	0.9	31
26	Analysis of a simulated microarray dataset: Comparison of methods for data normalisation and detection of differential expression (Open Access publication). <i>Genetics Selection Evolution</i> , 2007, 39, 669.	3.0	5
27	The EADGENE Microarray Data Analysis Workshop (Open Access publication). <i>Genetics Selection Evolution</i> , 2007, 39, 621-631.	3.0	2
28	Analysis of the real EADGENE data set: Comparison of methods and guidelines for data normalisation and selection of differentially expressed genes (Open Access publication). <i>Genetics Selection Evolution</i> , 2007, 39, 633-650.	3.0	0
29	Analysis of a simulated microarray dataset: Comparison of methods for data normalisation and detection of differential expression (Open Access publication). <i>Genetics Selection Evolution</i> , 2007, 39, 669-683.	3.0	1