

Florian Rohart

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

3,286
citations

1040056

9
h-index

1199594

12
g-index

16
all docs

16
docs citations

16
times ranked

6644
citing authors

#	ARTICLE	IF	CITATIONS
1	DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays. <i>Bioinformatics</i> , 2019, 35, 3055-3062.	4.1	496
2	MINT: a multivariate integrative method to identify reproducible molecular signatures across independent experiments and platforms. <i>BMC Bioinformatics</i> , 2017, 18, 128.	2.6	83
3	Human hepatocellular carcinomas with a periportal phenotype have the lowest potential for early recurrence after curative resection. <i>Hepatology</i> , 2017, 66, 1502-1518.	7.3	87
4	mixOmics: An R package for omics feature selection and multiple data integration. <i>PLoS Computational Biology</i> , 2017, 13, e1005752.	3.2	2,279
5	Multiple Hypothesis Testing for Variable Selection. <i>Australian and New Zealand Journal of Statistics</i> , 2016, 58, 245-267.	0.9	4
6	Integrating Multi-omics Data to Dissect Mechanisms of DNA repair Dysregulation in Breast Cancer. <i>Scientific Reports</i> , 2016, 6, 34000.	3.3	8
7	Disease surveillance based on Internet-based linear models: an Australian case study of previously unmodeled infection diseases. <i>Scientific Reports</i> , 2016, 6, 38522.	3.3	19
8	A molecular classification of human mesenchymal stromal cells. <i>PeerJ</i> , 2016, 4, e1845.	2.0	41
9	Exploring transcriptomic diversity in muscle revealed that cellular signaling pathways mainly differentiate five Western porcine breeds. <i>BMC Genomics</i> , 2015, 16, 1055.	2.8	9
10	Selection of fixed effects in high dimensional linear mixed models using a multicycle ECM algorithm. <i>Computational Statistics and Data Analysis</i> , 2014, 80, 209-222.	1.2	16
11	YuGene: A simple approach to scale gene expression data derived from different platforms for integrated analyses. <i>Genomics</i> , 2014, 103, 239-251.	2.9	63
12	Phenotypic prediction based on metabolomic data for growing pigs from three main European breeds1. <i>Journal of Animal Science</i> , 2012, 90, 4729-4740.	0.5	33