

# Alberto Cassese

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/397462/publications.pdf>

Version: 2024-02-01

12  
papers

174  
citations

1307594

7  
h-index

1199594

12  
g-index

12  
all docs

12  
docs citations

12  
times ranked

490  
citing authors

#	ARTICLE	IF	CITATIONS
1	REMAXINT: a two-mode clustering-based method for statistical inference on two-way interaction. <i>Advances in Data Analysis and Classification</i> , 2021, 15, 987-1013.	1.4	1
2	Bayesian Negative Binomial Mixture Regression Models for the Analysis of Sequence Count and Methylation Data. <i>Biometrics</i> , 2019, 75, 183-192.	1.4	10
3	A Bayesian Nonparametric Spiked Process Prior for Dynamic Model Selection. <i>Bayesian Analysis</i> , 2019, 14, .	3.0	10
4	Round robin study of formalin-fixed paraffin-embedded tissues in mass spectrometry imaging. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 5969-5980.	3.7	39
5	Spatial Autocorrelation in Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2016, 88, 5871-5878.	6.5	29
6	Time-dependence of graph theory metrics in functional connectivity analysis. <i>NeuroImage</i> , 2016, 125, 601-615.	4.2	50
7	A Network Biology Approach Identifies Molecular Cross-Talk between Normal Prostate Epithelial and Prostate Carcinoma Cells. <i>PLoS Computational Biology</i> , 2016, 12, e1004884.	3.2	5
8	iBATCGH: Integrative Bayesian Analysis of Transcriptomic and CGH Data. <i>Abel Symposia</i> , 2016, , 105-123.	0.3	2
9	A Bayesian model for the identification of differentially expressed genes in <i>Daphnia magna</i> exposed to munition pollutants. <i>Biometrics</i> , 2015, 71, 803-811.	1.4	3
10	A hierarchical Bayesian model for inference of copy number variants and their association to gene expression. <i>Annals of Applied Statistics</i> , 2014, 8, 148-175.	1.1	12
11	A Bayesian Integrative Model for Genetical Genomics with Spatially Informed Variable Selection. <i>Cancer Informatics</i> , 2014, 13s2, CIN.S13784.	1.9	3
12	sdef: an R package to synthesize lists of significant features in related experiments. <i>BMC Bioinformatics</i> , 2010, 11, 270.	2.6	10