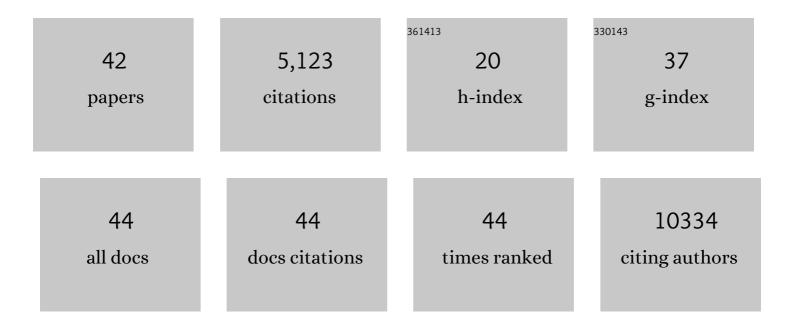
David Rossell

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Heterogeneous Large Datasets Integration Using Bayesian Factor Regression. Bayesian Analysis, 2022, 17, .	3.0	6
2	Revealing the Reactivity of Individual Chemical Entities in Complex Mixtures: the Chemistry Behind Bio-Oil Upgrading. Analytical Chemistry, 2022, 94, 7536-7544.	6.5	5
3	Specification Analysis for Technology Use and Teenager Well-Being: Statistical Validity and a Bayesian Proposal. Journal of the Royal Statistical Society Series C: Applied Statistics, 2022, 71, 1330-1355.	1.0	0
4	Concentration of Posterior Model Probabilities and Normalized LO Criteria. Bayesian Analysis, 2021, -1,	3.0	4
5	Approximate Laplace Approximations for Scalable Model Selection. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2021, 83, 853-879.	2.2	9
6	KairosMS: A New Solution for the Processing of Hyphenated Ultrahigh Resolution Mass Spectrometry Data. Analytical Chemistry, 2020, 92, 3775-3786.	6.5	20
7	Characterizing MHC-I Genotype Predictive Power for Oncogenic Mutation Probability in Cancer Patients. Methods in Molecular Biology, 2020, 2131, 185-198.	0.9	1
8	On Choosing Mixture Components via Non-Local Priors. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2019, 81, 809-837.	2.2	7
9	Pushing the analytical limits: new insights into complex mixtures using mass spectra segments of constant ultrahigh resolving power. Chemical Science, 2019, 10, 6966-6978.	7.4	74
10	Rhapso: Automatic Stitching of Mass Segments from Fourier Transform Ion Cyclotron Resonance Mass Spectra. Analytical Chemistry, 2019, 91, 15130-15137.	6.5	8
11	Continuous Mixtures with Skewness and Heavy Tails. , 2019, , 219-237.		1
12	Tractable Bayesian Variable Selection: Beyond Normality. Journal of the American Statistical Association, 2018, 113, 1742-1758.	3.1	20
13	Nonlocal Priors for High-Dimensional Estimation. Journal of the American Statistical Association, 2017, 112, 254-265.	3.1	58
14	MHC-I Genotype Restricts the Oncogenic Mutational Landscape. Cell, 2017, 171, 1272-1283.e15.	28.9	307
15	Themis: Batch Preprocessing for Ultrahigh-Resolution Mass Spectra of Complex Mixtures. Analytical Chemistry, 2017, 89, 11383-11390.	6.5	17
16	Stromal gene expression defines poor-prognosis subtypes in colorectal cancer. Nature Genetics, 2015, 47, 320-329.	21.4	858
17	Designing alternative splicing RNA-seq studies. Beyond generic guidelines. Bioinformatics, 2015, 31, 3631-3637.	4.1	7
18	Hybrid Periportal Hepatocytes Regenerate the Injured Liver without Giving Rise to Cancer. Cell, 2015, 162, 766-779.	28.9	394

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19	Dades massives i estadÃstica: La perspectiva d'un estadÃstic. Metode, 2014, 5, 143-149.	0.1	2
20	A chemo-centric view of human health and disease. Nature Communications, 2014, 5, 5676.	12.8	23
21	Quantifying alternative splicing from paired-end RNA-sequencing data. Annals of Applied Statistics, 2014, 8, 309-330.	1.1	38
22	chroGPS, a global chromatin positioning system for the functional analysis and visualization of the epigenome. Nucleic Acids Research, 2014, 42, 2126-2137.	14.5	6
23	Immunostaining Protocol: P-Stat3 (Xenograft and Mice). Bio-protocol, 2014, 4, .	0.4	Ο
24	Sequential stopping for high-throughput experiments. Biostatistics, 2013, 14, 75-86.	1.5	8
25	An Integrated Model of the Transcriptome of HER2-Positive Breast Cancer. PLoS ONE, 2013, 8, e79298.	2.5	18
26	High-Dimensional Bayesian Classifiers Using Non-Local Priors. Studies in Classification, Data Analysis, and Knowledge Organization, 2013, , 305-313.	0.2	11
27	dKDM5/LID regulates H3K4me3 dynamics at the transcription-start site (TSS) of actively transcribed developmental genes. Nucleic Acids Research, 2012, 40, 9493-9505.	14.5	47
28	Dependency of Colorectal Cancer on a TGF-Î ² -Driven Program in Stromal Cells for Metastasis Initiation. Cancer Cell, 2012, 22, 571-584.	16.8	881
29	Bayesian Model Selection in High-Dimensional Settings. Journal of the American Statistical Association, 2012, 107, 649-660.	3.1	167
30	Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. Frontiers in Oncology, 2012, 2, 12.	2.8	46
31	<tt>htSeqTools</tt> : high-throughput sequencing quality control, processing and visualization in R. Bioinformatics, 2012, 28, 589-590.	4.1	67
32	Abstract 4926: Modeling the transcriptome landscape of HER2+ breast cancer. , 2012, , .		0
33	The Intestinal Stem Cell Signature Identifies Colorectal Cancer Stem Cells and Predicts Disease Relapse. Cell Stem Cell, 2011, 8, 511-524.	11.1	811
34	Isolation and in vitro expansion of human colonic stem cells. Nature Medicine, 2011, 17, 1225-1227.	30.7	616
35	Abstract 4975: Next generation sequencing reveals a connection between KRAS mutation and the NFkB pathway in lung adenocarcinoma samples. , 2011, , .		0
36	On the use of Non-Local Prior Densities in Bayesian Hypothesis Tests. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2010, 72, 143-170.	2.2	183

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37	Chimeric tRNAs as tools to induce proteome damage and identify components of stress responses. Nucleic Acids Research, 2010, 38, e30-e30.	14.5	38
38	Ectopic Expression of Germline Genes Drives Malignant Brain Tumor Growth in <i>Drosophila</i> . Science, 2010, 330, 1824-1827.	12.6	252
39	GaGa: A parsimonious and flexible model for differential expression analysis. Annals of Applied Statistics, 2009, 3, .	1.1	14
40	Drosophila HP1c isoform interacts with the zinc-finger proteins WOC and Relative-of-WOC to regulate gene expression. Genes and Development, 2008, 22, 3007-3023.	5.9	62
41	Semi-Parametric Differential Expression Analysis via Partial Mixture Estimation. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article15.	0.6	10
42	Screening designs for drug development. Biostatistics, 2007, 8, 595-608.	1.5	25