# David Rossell

List of Publications by Year
in descending order

| 42 papers | 5,123 citations | 361413 20 h-index | 330143 37 g-index |
|---|---|---|---|
| 44 all docs | 44 docs citations | 44 times ranked | 10334 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Dependency of Colorectal Cancer on a TGF-β-Driven Program in Stromal Cells for Metastasis Initiation. Cancer Cell, 2012, 22, 571-584. | 16.8 | 881 |
| 2 | Stromal gene expression defines poor-prognosis subtypes in colorectal cancer. Nature Genetics, 2015, 47, 320-329. | 21.4 | 858 |
| 3 | The Intestinal Stem Cell Signature Identifies Colorectal Cancer Stem Cells and Predicts Disease Relapse. Cell Stem Cell, 2011, 8, 511-524. | 11.1 | 811 |
| 4 | Isolation and in vitro expansion of human colonic stem cells. Nature Medicine, 2011, 17, 1225-1227. | 30.7 | 616 |
| 5 | Hybrid Periportal Hepatocytes Regenerate the Injured Liver without Giving Rise to Cancer. Cell, 2015, 162, 766-779. | 28.9 | 394 |
| 6 | MHC-I Genotype Restricts the Oncogenic Mutational Landscape. Cell, 2017, 171, 1272-1283.e15. | 28.9 | 307 |
| 7 | Ectopic Expression of Germline Genes Drives Malignant Brain Tumor Growth in <i>Drosophila</i>. Science, 2010, 330, 1824-1827. | 12.6 | 252 |
| 8 | 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 |
| 9 | Bayesian Model Selection in High-Dimensional Settings. Journal of the American Statistical Association, 2012, 107, 649-660. | 3.1 | 167 |
| 10 | 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 |
| 11 | <tt>htSeqTools</tt>: high-throughput sequencing quality control, processing and visualization in R. Bioinformatics, 2012, 28, 589-590. | 4.1 | 67 |
| 12 | 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 |
| 13 | Nonlocal Priors for High-Dimensional Estimation. Journal of the American Statistical Association, 2017, 112, 254-265. | 3.1 | 58 |
| 14 | 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 |
| 15 | 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 |
| 16 | Chimeric tRNAs as tools to induce proteome damage and identify components of stress responses. Nucleic Acids Research, 2010, 38, e30-e30. | 14.5 | 38 |
| 17 | Quantifying alternative splicing from paired-end RNA-sequencing data. Annals of Applied Statistics, 2014, 8, 309-330. | 1.1 | 38 |
| 18 | Screening designs for drug development. Biostatistics, 2007, 8, 595-608. | 1.5 | 25 |

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|---|---------|-----|-----------|
| 19 | A chemo-centric view of human health and disease. Nature Communications, 2014, 5, 5676. | 12.8 | 23 |
| 20 | Tractable Bayesian Variable Selection: Beyond Normality. Journal of the American Statistical Association, 2018, 113, 1742-1758. | 3.1 | 20 |
| 21 | KairosMS: A New Solution for the Processing of Hyphenated Ultrahigh Resolution Mass Spectrometry Data. Analytical Chemistry, 2020, 92, 3775-3786. | 6.5 | 20 |
| 22 | An Integrated Model of the Transcriptome of HER2-Positive Breast Cancer. PLoS ONE, 2013, 8, e79298. | 2.5 | 18 |
| 23 | Themis: Batch Preprocessing for Ultrahigh-Resolution Mass Spectra of Complex Mixtures. Analytical Chemistry, 2017, 89, 11383-11390. | 6.5 | 17 |
| 24 | GaGa: A parsimonious and flexible model for differential expression analysis. Annals of Applied Statistics, 2009, 3, . | 1.1 | 14 |
| 25 | High-Dimensional Bayesian Classifiers Using Non-Local Priors. Studies in Classification, Data Analysis, and Knowledge Organization, 2013, , 305-313. | 0.2 | 11 |
| 26 | Semi-Parametric Differential Expression Analysis via Partial Mixture Estimation. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article15. | 0.6 | 10 |
| 27 | Approximate Laplace Approximations for Scalable Model Selection. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2021, 83, 853-879. | 2.2 | 9 |
| 28 | Sequential stopping for high-throughput experiments. Biostatistics, 2013, 14, 75-86. | 1.5 | 8 |
| 29 | Rhapso: Automatic Stitching of Mass Segments from Fourier Transform Ion Cyclotron Resonance Mass Spectra. Analytical Chemistry, 2019, 91, 15130-15137. | 6.5 | 8 |
| 30 | Designing alternative splicing RNA-seq studies. Beyond generic guidelines. Bioinformatics, 2015, 31, 3631-3637. | 4.1 | 7 |
| 31 | 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 |
| 32 | 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 |
| 33 | Heterogeneous Large Datasets Integration Using Bayesian Factor Regression. Bayesian Analysis, 2022, 17, . | 3.0 | 6 |
| 34 | 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 |
| 35 | Concentration of Posterior Model Probabilities and Normalized L0 Criteria. Bayesian Analysis, 2021, -1, . | 3.0 | 4 |
| 36 | Dades massives i estadística: La perspectiva d'un estadístic. Metode, 2014, 5, 143-149. | 0.1 | 2 |

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|---|---------|-----|-----------|
| 37 | Characterizing MHC-I Genotype Predictive Power for Oncogenic Mutation Probability in Cancer Patients. Methods in Molecular Biology, 2020, 2131, 185-198. | 0.9 | 1 |
| 38 | Continuous Mixtures with Skewness and Heavy Tails. , 2019, , 219-237. | | 1 |
| 39 | Abstract 4975: Next generation sequencing reveals a connection between KRAS mutation and the NFkB pathway in lung adenocarcinoma samples. , 2011, , . | | 0 |
| 40 | Abstract 4926: Modeling the transcriptome landscape of HER2+ breast cancer. , 2012, , . | | 0 |
| 41 | Immunostaining Protocol: P-Stat3 (Xenograft and Mice). Bio-protocol, 2014, 4, . | 0.4 | 0 |
| 42 | 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 |