

# Rafael A Irizarry

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

32,248  
citations

94433

37  
h-index

161849

54  
g-index

78  
all docs

78  
docs citations

78  
times ranked

55650  
citing authors

#	ARTICLE	IF	CITATIONS
1	Salmon provides fast and bias-aware quantification of transcript expression. <i>Nature Methods</i> , 2017, 14, 417-419.	19.0	7,460
2	affyâ€™ analysis of <i>Affymetrix GeneChip</i> data at the probe level. <i>Bioinformatics</i> , 2004, 20, 307-315.	4.1	4,830
3	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014, 30, 1363-1369.	4.1	3,192
4	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
5	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. <i>Nature Genetics</i> , 2009, 41, 178-186.	21.4	1,977
6	Tackling the widespread and critical impact of batch effects in high-throughput data. <i>Nature Reviews Genetics</i> , 2010, 11, 733-739.	16.3	1,641
7	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011, 43, 768-775.	21.4	968
8	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. <i>Genome Biology</i> , 2014, 15, R31.	9.6	880
9	Multiple-laboratory comparison of microarray platforms. <i>Nature Methods</i> , 2005, 2, 345-350.	19.0	814
10	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017, 8, 1784.	12.8	714
11	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. <i>Genome Biology</i> , 2012, 13, R83.	9.6	650
12	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. <i>International Journal of Epidemiology</i> , 2012, 41, 200-209.	1.9	567
13	Removing technical variability in RNA-seq data using conditional quantile normalization. <i>Biostatistics</i> , 2012, 13, 204-216.	1.5	532
14	Mortality in Puerto Rico after Hurricane Maria. <i>New England Journal of Medicine</i> , 2018, 379, 162-170.	27.0	462
15	Missing data and technical variability in single-cell RNA-sequencing experiments. <i>Biostatistics</i> , 2018, 19, 562-578.	1.5	388
16	Comprehensive high-throughput arrays for relative methylation (CHARM). <i>Genome Research</i> , 2008, 18, 780-790.	5.5	379
17	Robust decomposition of cell type mixtures in spatial transcriptomics. <i>Nature Biotechnology</i> , 2022, 40, 517-526.	17.5	376
18	Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. <i>Genome Biology</i> , 2019, 20, 295.	8.8	288

#	ARTICLE	IF	CITATIONS
19	Excess deaths associated with covid-19 pandemic in 2020: age and sex disaggregated time series analysis in 29 high income countries. BMJ, The, 2021, 373, n1137.	6.0	281
20	Challenges and emerging directions in single-cell analysis. Genome Biology, 2017, 18, 84.	8.8	258
21	Progressive immune dysfunction with advancing disease stage in renal cell carcinoma. Cancer Cell, 2021, 39, 632-648.e8.	16.8	230
22	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. Nature Genetics, 2017, 49, 1613-1623.	21.4	207
23	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. Genome Medicine, 2014, 6, 61.	8.2	170
24	Gene set enrichment analysis made simple. Statistical Methods in Medical Research, 2009, 18, 565-575.	1.5	166
25	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	8.8	160
26	Modeling of RNA-seq fragment sequence bias reduces systematic errors in transcript abundance estimation. Nature Biotechnology, 2016, 34, 1287-1291.	17.5	159
27	Large-Scale Topological Changes Restrained Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	28.9	126
28	Detection and accurate false discovery rate control of differentially methylated regions from whole genome bisulfite sequencing. Biostatistics, 2019, 20, 367-383.	1.5	118
29	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. Genome Biology, 2015, 16, 80.	8.8	111
30	High-throughput identification of <scp>RNA</scp> nuclear enrichment sequences. EMBO Journal, 2018, 37, .	7.8	99
31	Stem-like intestinal Th17 cells give rise to pathogenic effector T cells during autoimmunity. Cell, 2021, 184, 6281-6298.e23.	28.9	99
32	Smooth quantile normalization. Biostatistics, 2018, 19, 185-198.	1.5	78
33	quantro: a data-driven approach to guide the choice of an appropriate normalization method. Genome Biology, 2015, 16, 117.	9.6	76
34	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. Nature Methods, 2017, 14, 216-217.	19.0	59
35	Flexible expressed region analysis for RNA-seq with <tt>derfinder</tt>. Nucleic Acids Research, 2017, 45, e9-e9.	14.5	54
36	A species-generalized probabilistic model-based definition of CpG islands. Mammalian Genome, 2009, 20, 674-80.	2.2	52

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37	A Guide to Teaching Data Science. American Statistician, 2018, 72, 382-391.	1.6	52
38	A multi-omic analysis of human na <sup>+</sup> ve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
39	Quantifying the dynamics of migration after Hurricane Maria in Puerto Rico. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32772-32778.	7.1	32
40	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. Nucleic Acids Research, 2017, 45, gkx026.	14.5	31
41	Accounting for GC-content bias reduces systematic errors and batch effects in ChIP-seq data. Genome Research, 2017, 27, 1930-1938.	5.5	29
42	Genome-wide methylation profiling reveals Zinc finger protein 516 (ZNF516) and FK-506-binding protein 6 (FKBP6) promoters frequently methylated in cervical neoplasia, associated with HPV status and ethnicity in a Chilean population. Epigenetics, 2014, 9, 308-317.	2.7	28
43	Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers. Genome Biology, 2020, 21, 160.	8.8	25
44	The Role of Academia in Data Science Education. , 0, , .		22
45	Effectiveness estimates of three COVID-19 vaccines based on observational data from Puerto Rico. The Lancet Regional Health Americas, 2022, 9, 100212.	2.6	17
46	methyICC: technology-independent estimation of cell type composition using differentially methylated regions. Genome Biology, 2019, 20, 261.	8.8	13
47	A probabilistic gene expression barcode for annotation of cell types from single-cell RNA-seq data. Biostatistics, 0, , .	1.5	11
48	Visualization and probability-based scoring of structural variants within repetitive sequences. Bioinformatics, 2014, 30, 1514-1521.	4.1	5
49	Vaginal microbiome topic modeling of laboring Ugandan women with and without fever. Npj Biofilms and Microbiomes, 2021, 7, 75.	6.4	5
50	Characterizing batch effects and binding site-specific variability in ChIP-seq data. NAR Genomics and Bioinformatics, 2021, 3, lqab098.	3.2	3
51	Selection-Corrected Statistical Inference for Region Detection With High-Throughput Assays. Journal of the American Statistical Association, 2019, 114, 1351-1365.	3.1	2
52	Capturing discrete latent structures: choose LDs over PCs. Biostatistics, 2021, , .	1.5	2
53	Promoter Hypermethylation in MLL-r Leukemia: Biology and Therapeutic Targeting.. Blood, 2009, 114, 3472-3472.	1.4	0