

# Wolfgang Huber

## List of Publications by Year in descending order

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Version: 2024-02-01

174  
papers

145,325  
citations

8172

76  
h-index

5677

162  
g-index

209  
all docs

209  
docs citations

209  
times ranked

177504  
citing authors

#	ARTICLE	IF	CITATIONS
1	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. <i>Genome Biology</i> , 2014, 15, 550.	3.8	58,325
2	HTSeq—a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, 166-169.	1.8	17,270
3	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010, 11, R106.	3.8	13,707
4	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004, 5, R80.	13.9	10,796
5	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
6	Software for Computing and Annotating Genomic Ranges. <i>PLoS Computational Biology</i> , 2013, 9, e1003118.	1.5	3,262
7	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. <i>Nature Protocols</i> , 2009, 4, 1184-1191.	5.5	3,084
8	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	9.0	3,070
9	Variance stabilization applied to microarray data calibration and to the quantification of differential expression. <i>Bioinformatics</i> , 2002, 18, S96-S104.	1.8	2,012
10	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. <i>Bioinformatics</i> , 2005, 21, 3439-3440.	1.8	1,781
11	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012, 22, 2008-2017.	2.4	1,341
12	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013, 8, 1765-1786.	5.5	1,124
13	arrayQualityMetrics—a bioconductor package for quality assessment of microarray data. <i>Bioinformatics</i> , 2009, 25, 415-416.	1.8	885
14	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009, 457, 1033-1037.	13.7	872
15	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010, 464, 721-727.	13.7	768
16	Independent filtering increases detection power for high-throughput experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9546-9551.	3.3	720
17	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017, 19, 271-281.	4.6	709
18	Multi-Omics Factor Analysis—a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , 2018, 14, e8124.	3.2	659

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19	EImageR an R package for image processing with applications to cellular phenotypes. <i>Bioinformatics</i> , 2010, 26, 979-981.	1.8	616
20	A high-resolution map of transcription in the yeast genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5320-5325.	3.3	613
21	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , 2008, 454, 479-485.	13.7	554
22	Expression Atlas update an integrated database of gene and protein expression in humans, animals and plants. <i>Nucleic Acids Research</i> , 2016, 44, D746-D752.	6.5	526
23	Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235.	6.0	521
24	Gene expression across mammalian organ development. <i>Nature</i> , 2019, 571, 505-509.	13.7	490
25	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	9.0	488
26	Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. <i>Nature Methods</i> , 2016, 13, 577-580.	9.0	483
27	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , 2015, 10, 1567-1593.	5.5	481
28	Addressing Accuracy and Precision Issues in iTRAQ Quantitation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1885-1897.	2.5	471
29	Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , 2018, 13, 530-550.	5.5	454
30	Enhancer loops appear stable during development and are associated with paused polymerase. <i>Nature</i> , 2014, 512, 96-100.	13.7	450
31	Model-based variance-stabilizing transformation for Illumina microarray data. <i>Nucleic Acids Research</i> , 2008, 36, e11-e11.	6.5	447
32	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. <i>Cell Stem Cell</i> , 2014, 15, 507-522.	5.2	439
33	The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. <i>Nature Communications</i> , 2015, 6, 10127.	5.8	385
34	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018, 46, D246-D251.	6.5	365
35	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1213-1224.	0.8	355
36	Directional tissue migration through a self-generated chemokine gradient. <i>Nature</i> , 2013, 503, 285-289.	13.7	320

#	ARTICLE	IF	CITATIONS
37	A global map of human gene expression. <i>Nature Biotechnology</i> , 2010, 28, 322-324.	9.4	315
38	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 2015, 4, 1070.	0.8	304
39	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	13.5	304
40	SomaticSignatures: inferring mutational signatures from single-nucleotide variants. <i>Bioinformatics</i> , 2015, 31, 3673-3675.	1.8	284
41	Analysis of cell-based RNAi screens. <i>Genome Biology</i> , 2006, 7, R66.	13.9	271
42	Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages. <i>Nature Cell Biology</i> , 2014, 16, 27-37.	4.6	262
43	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015, 12, 1129-1131.	9.0	244
44	Tandem fluorescent protein timers for in vivo analysis of protein dynamics. <i>Nature Biotechnology</i> , 2012, 30, 708-714.	9.4	239
45	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	13.7	233
46	Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2012, 2, 1579-1592.	2.9	216
47	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , 2018, 46, 582-592.	6.5	209
48	The Shh Topological Domain Facilitates the Action of Remote Enhancers by Reducing the Effects of Genomic Distances. <i>Developmental Cell</i> , 2016, 39, 529-543.	3.1	194
49	Protein quality control at the inner nuclear membrane. <i>Nature</i> , 2014, 516, 410-413.	13.7	188
50	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , 2019, 10, 1155.	5.8	181
51	Differential expression analysis for sequence count data. <i>Nature Precedings</i> , 0, , .	0.1	180
52	Mapping of signaling networks through synthetic genetic interaction analysis by RNAi. <i>Nature Methods</i> , 2011, 8, 341-346.	9.0	173
53	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.	3.2	173
54	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.	9.0	159

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55	Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , 2016, 61, 260-273.	4.5	155
56	Ringo – an R/Bioconductor package for analyzing ChIP-chip readouts. <i>BMC Bioinformatics</i> , 2007, 8, 221.	1.2	148
57	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , 2015, 16, 933-941.	7.0	148
58	Clustering phenotype populations by genome-wide RNAi and multiparametric imaging. <i>Molecular Systems Biology</i> , 2010, 6, 370.	3.2	141
59	Transcript mapping with high-density oligonucleotide tiling arrays. <i>Bioinformatics</i> , 2006, 22, 1963-1970.	1.8	134
60	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. <i>Molecular Systems Biology</i> , 2020, 16, e9596.	3.2	131
61	Parameter estimation for the calibration and variance stabilization of microarray data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article3.	0.2	128
62	The Small Non-coding Vault RNA1-1 Acts as a Riboregulator of Autophagy. <i>Cell</i> , 2019, 176, 1054-1067.e12.	13.5	125
63	Genome-wide analysis of mRNA decay patterns during early Drosophila development. <i>Genome Biology</i> , 2010, 11, R93.	13.9	124
64	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	3.9	124
65	Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping. <i>Nature Methods</i> , 2013, 10, 427-431.	9.0	122
66	glmGamPoi: fitting Gamma-Poisson generalized linear models on single cell count data. <i>Bioinformatics</i> , 2021, 36, 5701-5702.	1.8	116
67	Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size. <i>Bioinformatics</i> , 2013, 29, 1275-1282.	1.8	113
68	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020, 38, 303-308.	9.4	111
69	Relating CNVs to transcriptome data at fine resolution: Assessment of the effect of variant size, type, and overlap with functional regions. <i>Genome Research</i> , 2011, 21, 2004-2013.	2.4	109
70	Graphs in molecular biology. <i>BMC Bioinformatics</i> , 2007, 8, S8.	1.2	106
71	miR-16 and miR-125b are involved in barrier function dysregulation through the modulation of claudin-2 and cingulin expression in the jejunum in IBS with diarrhoea. <i>Gut</i> , 2017, 66, 1537.1-1538.	6.1	105
72	cAMP Response Element-Binding Protein Is a Primary Hub of Activity-Driven Neuronal Gene Expression. <i>Journal of Neuroscience</i> , 2011, 31, 18237-18250.	1.7	103

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73	Multi-domain protein families and domain pairs: comparison with known structures and a random model of domain recombination. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 67-78.	1.2	100
74	Importing ArrayExpress datasets into R/Bioconductor. <i>Bioinformatics</i> , 2009, 25, 2092-2094.	1.8	100
75	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.	13.9	99
76	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. <i>Nature Cell Biology</i> , 2020, 22, 896-906.	4.6	93
77	Alternative polyadenylation diversifies post-transcriptional regulation by selective <i>scRNA</i> protein interactions. <i>Molecular Systems Biology</i> , 2014, 10, 719.	3.2	91
78	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , 2015, 31, 3085-3091.	1.8	91
79	Microarray data quality control improves the detection of differentially expressed genes. <i>Genomics</i> , 2010, 95, 138-142.	1.3	88
80	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015, 126, 1005-1008.	0.6	88
81	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. <i>Cell Reports</i> , 2019, 29, 3147-3159.e12.	2.9	84
82	Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. <i>BMC Genomics</i> , 2004, 5, 29.	1.2	79
83	A chemical-genetic interaction map of small molecules using high-throughput imaging in cancer cells. <i>Molecular Systems Biology</i> , 2015, 11, 846.	3.2	79
84	A map of directional genetic interactions in a metazoan cell. <i>ELife</i> , 2015, 4, .	2.8	78
85	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. <i>Leukemia</i> , 2018, 32, 774-787.	3.3	75
86	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2506-2515.	2.5	75
87	A Compendium to Ensure Computational Reproducibility in High-Dimensional Classification Tasks. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-24.	0.2	72
88	Assessing affymetrix GeneChip microarray quality. <i>BMC Bioinformatics</i> , 2011, 12, 137.	1.2	71
89	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010, 11, 349.	1.2	68
90	Bioconductor Case Studies. , 2008, , .		65

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91	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. <i>Clinical Cancer Research</i> , 2005, 11, 646-55.	3.2	64
92	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018, 7, 482-495.e10.	2.9	62
93	In situ analysis of cross-hybridisation on microarrays and the inference of expression correlation. <i>BMC Bioinformatics</i> , 2007, 8, 461.	1.2	61
94	Functional Outcomes and Quality of Life After Radical Prostatectomy Only Versus a Combination of Prostatectomy with Radiation and Hormonal Therapy. <i>European Urology</i> , 2017, 71, 330-336.	0.9	57
95	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007, 89, 580-587.	1.3	56
96	A Discrete Transition Zone Organizes the Topological and Regulatory Autonomy of the Adjacent <i>Tfap2c</i> and <i>Bmp7</i> Genes. <i>PLoS Genetics</i> , 2015, 11, e1004897.	1.5	56
97	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 0, 4, 1070.	0.8	55
98	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	1.3	54
99	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.	3.2	52
100	High-Content siRNA Screen Reveals Global ENaC Regulators and Potential Cystic Fibrosis Therapy Targets. <i>Cell</i> , 2013, 154, 1390-1400.	13.5	50
101	Identifying splits with clear separation: a new class discovery method for gene expression data. <i>Bioinformatics</i> , 2001, 17, S107-S114.	1.8	49
102	arrayMagic: two-colour cDNA microarray quality control and preprocessing. <i>Bioinformatics</i> , 2005, 21, 554-556.	1.8	48
103	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , 2019, 27, 3097-3106.e5.	2.9	47
104	Developmental Gene Expression Differences between Humans and Mammalian Models. <i>Cell Reports</i> , 2020, 33, 108308.	2.9	46
105	Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , 2008, 91, 41-51.	1.3	45
106	Quality Assessment and Data Analysis for microRNA Expression Arrays. <i>Nucleic Acids Research</i> , 2009, 37, e17-e17.	6.5	45
107	From ORFeome to Biology: A Functional Genomics Pipeline. <i>Genome Research</i> , 2004, 14, 2136-2144.	2.4	44
108	Systematic comparison of surface coatings for protein microarrays. <i>Proteomics</i> , 2005, 5, 4705-4712.	1.3	42

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109	Making the most of high-throughput protein-interaction data. <i>Genome Biology</i> , 2007, 8, 112.	13.9	41
110	A Large-Scale RNAi Screen Identifies <i>Deaf1</i> as a Regulator of Innate Immune Responses in <i>Drosophila</i> . <i>Journal of Innate Immunity</i> , 2010, 2, 181-194.	1.8	39
111	Timer-based proteomic profiling of the ubiquitin-proteasome system reveals a substrate receptor of the GID ubiquitin ligase. <i>Molecular Cell</i> , 2021, 81, 2460-2476.e11.	4.5	39
112	Coverage and error models of protein-protein interaction data by directed graph analysis. <i>Genome Biology</i> , 2007, 8, R186.	13.9	37
113	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D415-D418.	6.5	36
114	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020, 11, 5783.	5.8	34
115	gscreeend: modelling asymmetric count ratios in CRISPR screens to decrease experiment size and improve phenotype detection. <i>Genome Biology</i> , 2020, 21, 53.	3.8	34
116	Comparative analysis of structured RNAs in <i>S. cerevisiae</i> indicates a multitude of different functions. <i>BMC Biology</i> , 2007, 5, 25.	1.7	32
117	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. <i>Stem Cell Reports</i> , 2014, 3, 858-875.	2.3	32
118	Multi-omics reveals clinically relevant proliferative drive associated with mTOR-MYC-OXPHOS activity in chronic lymphocytic leukemia. <i>Nature Cancer</i> , 2021, 2, 853-864.	5.7	32
119	matchprobes: a Bioconductor package for the sequence-matching of microarray probe elements. <i>Bioinformatics</i> , 2004, 20, 1651-1652.	1.8	31
120	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009, 5, 274.	3.2	31
121	Covariate Powered Cross-Weighted Multiple Testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2021, 83, 720-751.	1.1	26
122	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. <i>Blood</i> , 2018, 131, 2789-2802.	0.6	25
123	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.	5.8	23
124	Statistical methods and software for the analysis of highthroughput reverse genetic assays using flow cytometry readouts. <i>Genome Biology</i> , 2006, 7, R77.	13.9	22
125	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011, 12, R36.	3.8	22
126	A genetic interaction map of cell cycle regulators. <i>Molecular Biology of the Cell</i> , 2016, 27, 1397-1407.	0.9	22



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127	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018, 8, 12046.	1.6	22
128	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	21
129	Functional Profiling: From Microarrays via Cell-Based Assays to Novel Tumor Relevant Modulators of the Cell Cycle. <i>Cancer Research</i> , 2005, 65, 7733-7742.	0.4	19
130	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011, 12, R101.	13.9	19
131	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019, 79, 3125-3138.	0.4	19
132	Analyzing ChIP-chip Data Using Bioconductor. <i>PLoS Computational Biology</i> , 2008, 4, e1000227.	1.5	17
133	Estimating node degree in bait-prey graphs. <i>Bioinformatics</i> , 2008, 24, 218-224.	1.8	17
134	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	17
135	Energy metabolism is co-determined by genetic variants in chronic lymphocytic leukemia and influences drug sensitivity. <i>Haematologica</i> , 2019, 104, 1830-1840.	1.7	17
136	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021, , .	0.6	17
137	Top-down standards will not serve systems biology. <i>Nature</i> , 2006, 440, 24-24.	13.7	16
138	Measuring genetic interactions in human cells by RNAi and imaging. <i>Nature Protocols</i> , 2014, 9, 2341-2353.	5.5	16
139	Survey of ex vivo drug combination effects in chronic lymphocytic leukemia reveals synergistic drug effects and genetic dependencies. <i>Leukemia</i> , 2020, 34, 2934-2950.	3.3	16
140	Control of PD-L1 expression in CLL-cells by stromal triggering of the Notch-c-Myc-EZH2 oncogenic signaling axis. , 2021, 9, e001889.		15
141	Extracting quantitative genetic interaction phenotypes from matrix combinatorial RNAi. <i>BMC Bioinformatics</i> , 2011, 12, 342.	1.2	14
142	Research Techniques Made Simple: Bioinformatics for Genome-Scale Biology. <i>Journal of Investigative Dermatology</i> , 2017, 137, e163-e168.	0.3	14
143	Analysis of Microarray Gene Expression Data. , 2004, , .		13
144	Reply to Talloen et al.: Independent filtering is a generic approach that needs domain specific adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, E175-E175.	3.3	13

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145	Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. BMC Bioinformatics, 2013, 14, 308.	1.2	13
146	CellH5: a format for data exchange in high-content screening. Bioinformatics, 2013, 29, 1580-1582.	1.8	13
147	Dissection of CD20 regulation in lymphoma using RNAi. Leukemia, 2016, 30, 2409-2412.	3.3	13
148	TimerQuant: A modelling approach to tandem fluorescent timer design and data interpretation for measuring protein turnover in embryos. Development (Cambridge), 2015, 143, 174-9.	1.2	12
149	Miniaturized Drug Sensitivity and Resistance Test on Patient-Derived Cells Using Droplet-Microarray. SLAS Technology, 2021, 26, 274-286.	1.0	11
150	Contributions of the EMERALD project to assessing and improving microarray data quality. BioTechniques, 2011, 50, 27-31.	0.8	11
151	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. Bioinformatics, 2008, 24, 1100-1101.	1.8	9
152	A clash of cultures in discussions of the P value. Nature Methods, 2016, 13, 607-607.	9.0	9
153	An autologous culture model of nodal B-cell lymphoma identifies ex vivo determinants of response to bispecific antibodies. Blood Advances, 2021, 5, 5060-5071.	2.5	9
154	Adaptive penalization in high-dimensional regression and classification with external covariates using variational Bayes. Biostatistics, 2021, 22, 348-364.	0.9	8
155	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. Bioinformatics, 2009, 25, 1056-1062.	1.8	7
156	High-Throughput Flow Cytometry-Based Assay to Identify Apoptosis-Inducing Proteins. Journal of Biomolecular Screening, 2007, 12, 510-520.	2.6	6
157	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	0.8	6
158	Pairwise effects between lipid GWAS genes modulate lipid plasma levels and cellular uptake. Nature Communications, 2021, 12, 6411.	5.8	6
159	MatrixQCvis: shiny-based interactive data quality exploration for omics data. Bioinformatics, 2022, 38, 1181-1182.	1.8	6
160	Upregulation of SPS100 gene expression by an antisense RNA via a switch of mRNA isoforms with different stabilities. Nucleic Acids Research, 2017, 45, 11144-11158.	6.5	5
161	Fast Monte Carlo algorithm for nonequilibrium systems. Physical Review E, 1996, 53, 4232-4235.	0.8	4
162	h5vc: scalable nucleotide tallies with HDF5. Bioinformatics, 2014, 30, 1464-1466.	1.8	4

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163	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	0.8	4
164	Mutational landscape and complexity in CLL. Blood, 2015, 126, 2078-2079.	0.6	3
165	Reporting p Values. Cell Systems, 2019, 8, 170-171.	2.9	3
166	Asymptomatic Multiple Myeloma - Background of Progression, Evolution, and Prognosis. Blood, 2016, 128, 235-235.	0.6	3
167	DRUG PERTURBATION BASED STRATIFICATION OF LYMPHOPROLIFERATIVE DISORDERS. Hematological Oncology, 2017, 35, 56-56.	0.8	2
168	Systematic Investigation of Microenvironmental Drug Resistance Mechanisms in Chronic Lymphocytic Leukemia. Blood, 2019, 134, 3363-3363.	0.6	2
169	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. Bioinformatics, 2007, 23, 771-773.	1.8	0
170	Analysis of Microarray Gene Expression Data. , 2008, , 201-230.		0
171	THE LANDSCAPE OF DRUG PERTURBATION EFFECTS IN LEUKEMIA AND LYMPHOMA. Hematological Oncology, 2019, 37, 127-127.	0.8	0
172	Systematic Mapping Of Drug and Pathway Sensitivity In Chronic Lymphocytic Leukemia Identifies Synthetic Lethal Interactions Of Mutant p53. Blood, 2013, 122, 173-173.	0.6	0
173	Discovery of Novel Drug Sensitivities in T-Prolymphocytic Leukemia (T-PLL) By High-Throughput Ex Vivo Drug Testing and Genetic Profiling. Blood, 2014, 124, 917-917.	0.6	0
174	Authoring Bioconductor workflows with BiocWorkflowTools. F1000Research, 0, 7, 431.	0.8	0