

# Wolfgang Huber

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2621498/publications.pdf>

Version: 2024-02-01

174  
papers

145,325  
citations

8181

76  
h-index

5679

162  
g-index

209  
all docs

209  
docs citations

209  
times ranked

177504  
citing authors

#	ARTICLE	IF	CITATIONS
1	MatrixQCvis: shiny-based interactive data quality exploration for omics data. <i>Bioinformatics</i> , 2022, 38, 1181-1182.	4.1	6
2	Miniaturized Drug Sensitivity and Resistance Test on Patient-Derived Cells Using Droplet-Microarray. <i>SLAS Technology</i> , 2021, 26, 274-286.	1.9	11
3	Adaptive penalization in high-dimensional regression and classification with external covariates using variational Bayes. <i>Biostatistics</i> , 2021, 22, 348-364.	1.5	8
4	Control of PD-L1 expression in CLL-cells by stromal triggering of the Notch-c-Myc-EZH2 oncogenic signaling axis. , 2021, 9, e001889.		15
5	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021, , .	1.4	17
6	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.	9.7	39
7	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.	13.2	32
8	Covariate Powered Cross-Weighted Multiple Testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2021, 83, 720-751.	2.2	26
9	An autologous culture model of nodal B-cell lymphoma identifies ex vivo determinants of response to bispecific antibodies. <i>Blood Advances</i> , 2021, 5, 5060-5071.	5.2	9
10	glmGamPoi: fitting Gamma-Poisson generalized linear models on single cell count data. <i>Bioinformatics</i> , 2021, 36, 5701-5702.	4.1	116
11	Pairwise effects between lipid GWAS genes modulate lipid plasma levels and cellular uptake. <i>Nature Communications</i> , 2021, 12, 6411.	12.8	6
12	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
13	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	27.8	233
14	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020, 11, 5783.	12.8	34
15	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. <i>Molecular Systems Biology</i> , 2020, 16, e9596.	7.2	131
16	Developmental Gene Expression Differences between Humans and Mammalian Models. <i>Cell Reports</i> , 2020, 33, 108308.	6.4	46
17	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.	7.2	16
18	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.	10.3	93

#	ARTICLE	IF	CITATIONS
19	gscreeend: modelling asymmetric count ratios in CRISPR screens to decrease experiment size and improve phenotype detection. <i>Genome Biology</i> , 2020, 21, 53.	8.8	34
20	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.	12.8	23
21	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020, 38, 303-308.	17.5	111
22	THE LANDSCAPE OF DRUG PERTURBATION EFFECTS IN LEUKEMIA AND LYMPHOMA. <i>Hematological Oncology</i> , 2019, 37, 127-127.	1.7	0
23	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.	19.0	159
24	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2506-2515.	3.8	75
25	Gene expression across mammalian organ development. <i>Nature</i> , 2019, 571, 505-509.	27.8	490
26	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , 2019, 27, 3097-3106.e5.	6.4	47
27	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019, 79, 3125-3138.	0.9	19
28	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , 2019, 10, 1155.	12.8	181
29	Reporting p Values. <i>Cell Systems</i> , 2019, 8, 170-171.	6.2	3
30	Energy metabolism is co-determined by genetic variants in chronic lymphocytic leukemia and influences drug sensitivity. <i>Haematologica</i> , 2019, 104, 1830-1840.	3.5	17
31	The Small Non-coding Vault RNA1-1 Acts as a Riboregulator of Autophagy. <i>Cell</i> , 2019, 176, 1054-1067.e12.	28.9	125
32	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. <i>Cell Reports</i> , 2019, 29, 3147-3159.e12.	6.4	84
33	Systematic Investigation of Microenvironmental Drug Resistance Mechanisms in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2019, 134, 3363-3363.	1.4	2
34	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. <i>Blood</i> , 2018, 131, 2789-2802.	1.4	25
35	Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , 2018, 13, 530-550.	12.0	454
36	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018, 46, D246-D251.	14.5	365

#	ARTICLE	IF	CITATIONS
37	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , 2018, 46, 582-592.	14.5	209
38	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.	7.2	75
39	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018, 7, 482-495.e10.	6.2	62
40	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018, 8, 12046.	3.3	22
41	Multi-Omics Factor Analysis—a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , 2018, 14, e8124.	7.2	659
42	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.	12.1	105
43	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017, 19, 271-281.	10.3	709
44	Research Techniques Made Simple: Bioinformatics for Genome-Scale Biology. <i>Journal of Investigative Dermatology</i> , 2017, 137, e163-e168.	0.7	14
45	DRUG PERTURBATION BASED STRATIFICATION OF LYMPHOPROLIFERATIVE DISORDERS. <i>Hematological Oncology</i> , 2017, 35, 56-56.	1.7	2
46	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.	1.9	57
47	Upregulation of SPS100 gene expression by an antisense RNA via a switch of mRNA isoforms with different stabilities. <i>Nucleic Acids Research</i> , 2017, 45, 11144-11158.	14.5	5
48	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	8.2	124
49	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.	7.0	194
50	A clash of cultures in discussions of the P value. <i>Nature Methods</i> , 2016, 13, 607-607.	19.0	9
51	Dissection of CD20 regulation in lymphoma using RNAi. <i>Leukemia</i> , 2016, 30, 2409-2412.	7.2	13
52	Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. <i>Nature Methods</i> , 2016, 13, 577-580.	19.0	483
53	Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , 2016, 61, 260-273.	9.7	155
54	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.	14.5	526

#	ARTICLE	IF	CITATIONS
55	A genetic interaction map of cell cycle regulators. <i>Molecular Biology of the Cell</i> , 2016, 27, 1397-1407.	2.1	22
56	Asymptomatic Multiple Myeloma - Background of Progression, Evolution, and Prognosis. <i>Blood</i> , 2016, 128, 235-235.	1.4	3
57	TimerQuant: A modelling approach to tandem fluorescent timer design and data interpretation for measuring protein turnover in embryos. <i>Development (Cambridge)</i> , 2015, 143, 174-9.	2.5	12
58	Mutational landscape and complexity in CLL. <i>Blood</i> , 2015, 126, 2078-2079.	1.4	3
59	A chemicalâ€“genetic interaction map of small molecules using highâ€“throughput imaging in cancer cells. <i>Molecular Systems Biology</i> , 2015, 11, 846.	7.2	79
60	Singleâ€“cell polyadenylation site mapping reveals 3â€“ isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.	7.2	52
61	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 2015, 4, 1070.	1.6	304
62	The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. <i>Nature Communications</i> , 2015, 6, 10127.	12.8	385
63	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
64	HTSeqâ€“a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, 166-169.	4.1	17,270
65	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , 2015, 16, 933-941.	14.5	148
66	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015, 126, 1005-1008.	1.4	88
67	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.	3.5	56
68	SomaticSignatures: inferring mutational signatures from single-nucleotide variants. <i>Bioinformatics</i> , 2015, 31, 3673-3675.	4.1	284
69	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015, 12, 1129-1131.	19.0	244
70	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , 2015, 31, 3085-3091.	4.1	91
71	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	28.9	304
72	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.	12.0	481

#	ARTICLE	IF	CITATIONS
73	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	1.6	6
74	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	1.6	4
75	A map of directional genetic interactions in a metazoan cell. ELife, 2015, 4, .	6.0	78
76	Protein quality control at the inner nuclear membrane. Nature, 2014, 516, 410-413.	27.8	188
77	Alternative polyadenylation diversifies posttranscriptional regulation by selective RNA-protein interactions. Molecular Systems Biology, 2014, 10, 719.	7.2	91
78	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. Stem Cell Reports, 2014, 3, 858-875.	4.8	32
79	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 2014, 15, 550.	8.8	58,325
80	h5vc: scalable nucleotide tallies with HDF5. Bioinformatics, 2014, 30, 1464-1466.	4.1	4
81	Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages. Nature Cell Biology, 2014, 16, 27-37.	10.3	262
82	Enhancer loops appear stable during development and are associated with paused polymerase. Nature, 2014, 512, 96-100.	27.8	450
83	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methyome Analysis. Cell Stem Cell, 2014, 15, 507-522.	11.1	439
84	Measuring genetic interactions in human cells by RNAi and imaging. Nature Protocols, 2014, 9, 2341-2353.	12.0	16
85	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.	1.4	0
86	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. Nature Protocols, 2013, 8, 1765-1786.	12.0	1,124
87	High-Content siRNA Screen Reveals Global ENaC Regulators and Potential Cystic Fibrosis Therapy Targets. Cell, 2013, 154, 1390-1400.	28.9	50
88	Directional tissue migration through a self-generated chemokine gradient. Nature, 2013, 503, 285-289.	27.8	320
89	Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping. Nature Methods, 2013, 10, 427-431.	19.0	122
90	Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. BMC Bioinformatics, 2013, 14, 308.	2.6	13

#	ARTICLE	IF	CITATIONS
91	Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size. <i>Bioinformatics</i> , 2013, 29, 1275-1282.	4.1	113
92	Software for Computing and Annotating Genomic Ranges. <i>PLoS Computational Biology</i> , 2013, 9, e1003118.	3.2	3,262
93	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1213-1224.	1.8	355
94	CellH5: a format for data exchange in high-content screening. <i>Bioinformatics</i> , 2013, 29, 1580-1582.	4.1	13
95	Systematic Mapping Of Drug and Pathway Sensitivity In Chronic Lymphocytic Leukemia Identifies Synthetic Lethal Interactions Of Mutant p53. <i>Blood</i> , 2013, 122, 173-173.	1.4	0
96	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012, 22, 2008-2017.	5.5	1,341
97	Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2012, 2, 1579-1592.	6.4	216
98	Tandem fluorescent protein timers for in vivo analysis of protein dynamics. <i>Nature Biotechnology</i> , 2012, 30, 708-714.	17.5	239
99	Assessing affymetrix GeneChip microarray quality. <i>BMC Bioinformatics</i> , 2011, 12, 137.	2.6	71
100	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011, 12, R101.	9.6	19
101	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011, 12, R36.	8.8	22
102	Mapping of signaling networks through synthetic genetic interaction analysis by RNAi. <i>Nature Methods</i> , 2011, 8, 341-346.	19.0	173
103	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
104	Extracting quantitative genetic interaction phenotypes from matrix combinatorial RNAi. <i>BMC Bioinformatics</i> , 2011, 12, 342.	2.6	14
105	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.	5.5	109
106	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.	7.2	173
107	cAMP Response Element-Binding Protein Is a Primary Hub of Activity-Driven Neuronal Gene Expression. <i>Journal of Neuroscience</i> , 2011, 31, 18237-18250.	3.6	103
108	Contributions of the EMERALD project to assessing and improving microarray data quality. <i>BioTechniques</i> , 2011, 50, 27-31.	1.8	11

#	ARTICLE	IF	CITATIONS
109	Clustering phenotype populations by genome-wide RNAi and multiparametric imaging. <i>Molecular Systems Biology</i> , 2010, 6, 370.	7.2	141
110	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010, 11, 349.	2.8	68
111	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	2.2	54
112	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010, 464, 721-727.	27.8	768
113	A global map of human gene expression. <i>Nature Biotechnology</i> , 2010, 28, 322-324.	17.5	315
114	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.	7.1	13
115	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.	7.1	720
116	EImage—an R package for image processing with applications to cellular phenotypes. <i>Bioinformatics</i> , 2010, 26, 979-981.	4.1	616
117	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.	3.8	39
118	Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235.	12.6	521
119	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010, 11, R106.	8.8	13,707
120	Microarray data quality control improves the detection of differentially expressed genes. <i>Genomics</i> , 2010, 95, 138-142.	2.9	88
121	Genome-wide analysis of mRNA decay patterns during early <i>Drosophila</i> development. <i>Genome Biology</i> , 2010, 11, R93.	9.6	124
122	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.	9.6	99
123	Addressing Accuracy and Precision Issues in iTRAQ Quantitation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1885-1897.	3.8	471
124	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009, 5, 274.	7.2	31
125	Quality Assessment and Data Analysis for microRNA Expression Arrays. <i>Nucleic Acids Research</i> , 2009, 37, e17-e17.	14.5	45
126	Importing ArrayExpress datasets into R/Bioconductor. <i>Bioinformatics</i> , 2009, 25, 2092-2094.	4.1	100



#	ARTICLE	IF	CITATIONS
127	arrayQualityMetricsâ€”a bioconductor package for quality assessment of microarray data. Bioinformatics, 2009, 25, 415-416.	4.1	885
128	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. Bioinformatics, 2009, 25, 1056-1062.	4.1	7
129	Bidirectional promoters generate pervasive transcription in yeast. Nature, 2009, 457, 1033-1037.	27.8	872
130	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. Nature Protocols, 2009, 4, 1184-1191.	12.0	3,084
131	Analysis of Microarray Gene Expression Data. , 2008, , 201-230.		0
132	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. Nature, 2008, 454, 479-485.	27.8	554
133	Combinatorial effects of four histone modifications in transcription and differentiation. Genomics, 2008, 91, 41-51.	2.9	45
134	Model-based variance-stabilizing transformation for Illumina microarray data. Nucleic Acids Research, 2008, 36, e11-e11.	14.5	447
135	Analyzing ChIP-chip Data Using Bioconductor. PLoS Computational Biology, 2008, 4, e1000227.	3.2	17
136	Estimating node degree in bait-prey graphs. Bioinformatics, 2008, 24, 218-224.	4.1	17
137	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. Bioinformatics, 2008, 24, 1100-1101.	4.1	9
138	Bioconductor Case Studies. , 2008, , .		65
139	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.	4.1	0
140	High-Throughput Flow Cytometryâ€”Based Assay to Identify Apoptosis-Inducing Proteins. Journal of Biomolecular Screening, 2007, 12, 510-520.	2.6	6
141	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. Genomics, 2007, 89, 580-587.	2.9	56
142	Making the most of high-throughput protein-interaction data. Genome Biology, 2007, 8, 112.	9.6	41
143	Coverage and error models of protein-protein interaction data by directed graph analysis. Genome Biology, 2007, 8, R186.	9.6	37
144	Comparative analysis of structured RNAs in <i>S. cerevisiae</i> indicates a multitude of different functions. BMC Biology, 2007, 5, 25.	3.8	32

#	ARTICLE	IF	CITATIONS
145	Ringo – an R/Bioconductor package for analyzing ChIP-chip readouts. BMC Bioinformatics, 2007, 8, 221.	2.6	148
146	In situ analysis of cross-hybridisation on microarrays and the inference of expression correlation. BMC Bioinformatics, 2007, 8, 461.	2.6	61
147	Graphs in molecular biology. BMC Bioinformatics, 2007, 8, S8.	2.6	106
148	Statistical methods and software for the analysis of highthroughput reverse genetic assays using flow cytometry readouts. Genome Biology, 2006, 7, R77.	9.6	22
149	Analysis of cell-based RNAi screens. Genome Biology, 2006, 7, R66.	9.6	271
150	Top-down standards will not serve systems biology. Nature, 2006, 440, 24-24.	27.8	16
151	The LIFEdb database in 2006. Nucleic Acids Research, 2006, 34, D415-D418.	14.5	36
152	Transcript mapping with high-density oligonucleotide tiling arrays. Bioinformatics, 2006, 22, 1963-1970.	4.1	134
153	A high-resolution map of transcription in the yeast genome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5320-5325.	7.1	613
154	Functional Profiling: From Microarrays via Cell-Based Assays to Novel Tumor Relevant Modulators of the Cell Cycle. Cancer Research, 2005, 65, 7733-7742.	0.9	19
155	Systematic comparison of surface coatings for protein microarrays. Proteomics, 2005, 5, 4705-4712.	2.2	42
156	arrayMagic: two-colour cDNA microarray quality control and preprocessing. Bioinformatics, 2005, 21, 554-556.	4.1	48
157	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics, 2005, 21, 3439-3440.	4.1	1,781
158	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. Clinical Cancer Research, 2005, 11, 646-55.	7.0	64
159	matchprobes: a Bioconductor package for the sequence-matching of microarray probe elements. Bioinformatics, 2004, 20, 1651-1652.	4.1	31
160	From ORFeome to Biology: A Functional Genomics Pipeline. Genome Research, 2004, 14, 2136-2144.	5.5	44
161	Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. BMC Genomics, 2004, 5, 29.	2.8	79
162	A Compendium to Ensure Computational Reproducibility in High-Dimensional Classification Tasks. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-24.	0.6	72

#	ARTICLE	IF	CITATIONS
163	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004, 5, R80.	9.6	10,796
164	Analysis of Microarray Gene Expression Data. , 2004, , .		13
165	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
166	Parameter estimation for the calibration and variance stabilization of microarray data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article3.	0.6	128
167	Variance stabilization applied to microarray data calibration and to the quantification of differential expression. <i>Bioinformatics</i> , 2002, 18, S96-S104.	4.1	2,012
168	Identifying splits with clear separation: a new class discovery method for gene expression data. <i>Bioinformatics</i> , 2001, 17, S107-S114.	4.1	49
169	Fast Monte Carlo algorithm for nonequilibrium systems. <i>Physical Review E</i> , 1996, 53, 4232-4235.	2.1	4
170	Differential expression analysis for sequence count data. <i>Nature Precedings</i> , 0, , .	0.1	180
171	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	21
172	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	17
173	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 0, 4, 1070.	1.6	55
174	Authoring Bioconductor workflows with BiocWorkflowTools. <i>F1000Research</i> , 0, 7, 431.	1.6	0