

Wolfgang Huber

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

188
papers

87,890
citations

72
h-index

209
g-index

209
ext. papers

123,690
ext. citations

14.1
avg, IF

8.8
L-index

#	Paper	IF	Citations
188	Pairwise effects between lipid GWAS genes modulate lipid plasma levels and cellular uptake. <i>Nature Communications</i> , 2021 , 12, 6411	17.4	0
187	glmGamPoi: fitting Gamma-Poisson generalized linear models on single cell count data. <i>Bioinformatics</i> , 2021 , 36, 5701-5702	7.2	17
186	Control of PD-L1 expression in CLL-cells by stromal triggering of the Notch-c-Myc-EZH2 oncogenic signaling axis 2021 , 9,		1
185	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021 ,	2.2	6
184	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	17.6	15
183	Multi-omics reveals clinically relevant proliferative drive associated with mTOR-MYC-OXPPOS activity in chronic lymphocytic leukemia. <i>Nature Cancer</i> , 2021 , 2, 853-864	15.4	2
182	Miniaturized Drug Sensitivity and Resistance Test on Patient-Derived Cells Using Droplet-Microarray. <i>SLAS Technology</i> , 2021 , 26, 274-286	3	4
181	Adaptive penalization in high-dimensional regression and classification with external covariates using variational Bayes. <i>Biostatistics</i> , 2021 , 22, 348-364	3.7	5
180	Covariate powered cross-weighted multiple testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2021 , 83, 720-751	3.9	4
179	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	7.8	1
178	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	10.7	5
177	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	23.4	30
176	gscrend: modelling asymmetric count ratios in CRISPR screens to decrease experiment size and improve phenotype detection. <i>Genome Biology</i> , 2020 , 21, 53	18.3	14
175	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020 , 11, 3400	17.4	7
174	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020 , 38, 303-308	44.5	46
173	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020 , 17, 137-145	21.6	174
172	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020 , 586, E14-E16	50.4	85

171	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020 , 11, 5783	17.4	8
170	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. <i>Molecular Systems Biology</i> , 2020 , 16, e9596	12.2	37
169	Developmental Gene Expression Differences between Humans and Mammalian Models. <i>Cell Reports</i> , 2020 , 33, 108308	10.6	11
168	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2506-2515	7.6	34
167	Gene expression across mammalian organ development. <i>Nature</i> , 2019 , 571, 505-509	50.4	179
166	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , 2019 , 27, 3097-3106.e5	10.6	23
165	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019 , 79, 3125-3138	10.3	8
164	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , 2019 , 10, 1155	17.4	88
163	Energy metabolism is co-determined by genetic variants in chronic lymphocytic leukemia and influences drug sensitivity. <i>Haematologica</i> , 2019 , 104, 1830-1840	6.6	8
162	THE LANDSCAPE OF DRUG PERTURBATION EFFECTS IN LEUKEMIA AND LYMPHOMA. <i>Hematological Oncology</i> , 2019 , 37, 127-127	1.3	
161	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019 , 16, 1087-1093	21.6	94
160	Systematic Investigation of Microenvironmental Drug Resistance Mechanisms in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2019 , 134, 3363-3363	2.2	1
159	The Small Non-coding Vault RNA1-1 Acts as a Riboregulator of Autophagy. <i>Cell</i> , 2019 , 176, 1054-1067.e13	36.2	73
158	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. <i>Cell Reports</i> , 2019 , 29, 3147-3159.e12	10.6	26
157	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. <i>Blood</i> , 2018 , 131, 2789-2802	2.2	17
156	Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , 2018 , 13, 530-550	18.8	151
155	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018 , 46, D246-D251	20.1	222
154	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , 2018 , 46, 582-592	20.1	113

153	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018 , 8, 12046	4.9	15
152	Multi-Omics Factor Analysis-a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , 2018 , 14, e8124	12.2	287
151	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2018 , 128, 427-445	4.9	72
150	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	10.7	56
149	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018 , 7, 482-495.e10	10.6	37
148	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, 1537-1538	19.2	65
147	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017 , 19, 271-281	23.4	441
146	Research Techniques Made Simple: Bioinformatics for Genome-Scale Biology. <i>Journal of Investigative Dermatology</i> , 2017 , 137, e163-e168	4.3	8
145	DRUG PERTURBATION BASED STRATIFICATION OF LYMPHOPROLIFERATIVE DISORDERS. <i>Hematological Oncology</i> , 2017 , 35, 56-56	1.3	1
144	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	10.2	42
143	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	20.1	4
142	Dissection of CD20 regulation in lymphoma using RNAi. <i>Leukemia</i> , 2016 , 30, 2409-2412	10.7	7
141	Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. <i>Nature Methods</i> , 2016 , 13, 577-80	21.6	219
140	Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , 2016 , 61, 260-73	17.6	111
139	Expression Atlas update--an integrated database of gene and protein expression in humans, animals and plants. <i>Nucleic Acids Research</i> , 2016 , 44, D746-52	20.1	404
138	A genetic interaction map of cell cycle regulators. <i>Molecular Biology of the Cell</i> , 2016 , 27, 1397-407	3.5	13
137	TimerQuant: a modelling approach to tandem fluorescent timer design and data interpretation for measuring protein turnover in embryos. <i>Development (Cambridge)</i> , 2016 , 143, 174-9	6.6	9
136	Asymptomatic Multiple Myeloma - Background of Progression, Evolution, and Prognosis. <i>Blood</i> , 2016 , 128, 235-235	2.2	3

135	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	10.2	134
134	A clash of cultures in discussions of the P value. <i>Nature Methods</i> , 2016 , 13, 607	21.6	6
133	HTSeq--a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , 2015 , 31, 166-9	7.2	10519
132	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , 2015 , 16, 933-41	19.1	88
131	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015 , 126, 1005-8	2.2	66
130	A discrete transition zone organizes the topological and regulatory autonomy of the adjacent tfap2c and bmp7 genes. <i>PLoS Genetics</i> , 2015 , 11, e1004897	6	46
129	SomaticSignatures: inferring mutational signatures from single-nucleotide variants. <i>Bioinformatics</i> , 2015 , 31, 3673-5	7.2	174
128	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015 , 12, 1129-31	21.6	173
127	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , 2015 , 31, 3085-91	7.2	74
126	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015 , 162, 1051-65	56.2	240
125	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , 2015 , 10, 1567-93	18.8	293
124	Mutational landscape and complexity in CLL. <i>Blood</i> , 2015 , 126, 2078-9	2.2	2
123	A chemical-genetic interaction map of small molecules using high-throughput imaging in cancer cells. <i>Molecular Systems Biology</i> , 2015 , 11, 846	12.2	51
122	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015 , 11, 812	12.2	40
121	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 2015 , 4, 1070	3.6	181
120	The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. <i>Nature Communications</i> , 2015 , 6, 10127	17.4	286
119	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015 , 12, 115-21	21.6	1949
118	The Bioconductor channel in F1000Research. <i>F1000Research</i> , 2015 , 4, 217	3.6	4

117	The Bioconductor channel in F1000Research. <i>F1000Research</i> , 2015 , 4, 217	3.6	3
116	A map of directional genetic interactions in a metazoan cell. <i>ELife</i> , 2015 , 4,	8.9	59
115	Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages. <i>Nature Cell Biology</i> , 2014 , 16, 27-37	23.4	213
114	Enhancer loops appear stable during development and are associated with paused polymerase. <i>Nature</i> , 2014 , 512, 96-100	50.4	332
113	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	18	320
112	Measuring genetic interactions in human cells by RNAi and imaging. <i>Nature Protocols</i> , 2014 , 9, 2341-53	18.8	15
111	Protein quality control at the inner nuclear membrane. <i>Nature</i> , 2014 , 516, 410-3	50.4	134
110	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , 2014 , 10, 719	12.2	64
109	Transcriptome-wide profiling and posttranscriptional analysis of hematopoietic stem/progenitor cell differentiation toward myeloid commitment. <i>Stem Cell Reports</i> , 2014 , 3, 858-75	8	25
108	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. <i>Genome Biology</i> , 2014 , 15, 550	18.3	28138
107	h5vc: scalable nucleotide tallies with HDF5. <i>Bioinformatics</i> , 2014 , 30, 1464-6	7.2	2
106	Discovery of Novel Drug Sensitivities in T-Prolymphocytic Leukemia (T-PLL) By High-Throughput Ex Vivo Drug Testing and Genetic Profiling. <i>Blood</i> , 2014 , 124, 917-917	2.2	
105	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013 , 8, 1765-86	18.8	788
104	High-content siRNA screen reveals global ENaC regulators and potential cystic fibrosis therapy targets. <i>Cell</i> , 2013 , 154, 1390-400	56.2	42
103	Directional tissue migration through a self-generated chemokine gradient. <i>Nature</i> , 2013 , 503, 285-9	50.4	252
102	Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping. <i>Nature Methods</i> , 2013 , 10, 427-31	21.6	94
101	Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. <i>BMC Bioinformatics</i> , 2013 , 14, 308	3.6	10
100	Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size. <i>Bioinformatics</i> , 2013 , 29, 1275-82	7.2	73

99	Software for computing and annotating genomic ranges. <i>PLoS Computational Biology</i> , 2013 , 9, e1003118		1845
98	The genomic and transcriptomic landscape of a HeLa cell line. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1213-24	3.2	269
97	CellH5: a format for data exchange in high-content screening. <i>Bioinformatics</i> , 2013 , 29, 1580-2	7.2	11
96	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	2.2	
95	Highly coordinated proteome dynamics during reprogramming of somatic cells to pluripotency. <i>Cell Reports</i> , 2012 , 2, 1579-92	10.6	183
94	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 2012 ,		11
93	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 2012 ,		8
92	Tandem fluorescent protein timers for in vivo analysis of protein dynamics. <i>Nature Biotechnology</i> , 2012 , 30, 708-14	44.5	172
91	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012 , 22, 2008-17	9.7	882
90	Assessing affymetrix GeneChip microarray quality. <i>BMC Bioinformatics</i> , 2011 , 12, 137	3.6	59
89	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011 , 12, R101	18.3	15
88	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011 , 12, R36	18.3	17
87	Mapping of signaling networks through synthetic genetic interaction analysis by RNAi. <i>Nature Methods</i> , 2011 , 8, 341-6	21.6	150
86	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
85	Extracting quantitative genetic interaction phenotypes from matrix combinatorial RNAi. <i>BMC Bioinformatics</i> , 2011 , 12, 342	3.6	12
84	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, 2004-13	9.7	80
83	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011 , 7, 468	12.2	131
82	cAMP response element-binding protein is a primary hub of activity-driven neuronal gene expression. <i>Journal of Neuroscience</i> , 2011 , 31, 18237-50	6.6	83

81	Contributions of the EMERALD project to assessing and improving microarray data quality. <i>BioTechniques</i> , 2011 , 50, 27-31	2.5	9
80	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010 , 464, 721-7	50.4	668
79	A global map of human gene expression. <i>Nature Biotechnology</i> , 2010 , 28, 322-4	44.5	271
78	Differential expression analysis for sequence count data. <i>Nature Precedings</i> , 2010 ,		59
77	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	11.5	9
76	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, 9546-51	11.5	499
75	EBImage--an R package for image processing with applications to cellular phenotypes. <i>Bioinformatics</i> , 2010 , 26, 979-81	7.2	425
74	A large-scale RNAi screen identifies Deaf1 as a regulator of innate immune responses in <i>Drosophila</i> . <i>Journal of Innate Immunity</i> , 2010 , 2, 181-94	6.9	34
73	Variation in transcription factor binding among humans. <i>Science</i> , 2010 , 328, 232-5	33.3	447
72	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010 , 11, R106	18.3	9952
71	Microarray data quality control improves the detection of differentially expressed genes. <i>Genomics</i> , 2010 , 95, 138-42	4.3	65
70	Genome-wide analysis of mRNA decay patterns during early <i>Drosophila</i> development. <i>Genome Biology</i> , 2010 , 11, R93	18.3	92
69	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010 , 11, R24	18.3	81
68	Addressing accuracy and precision issues in iTRAQ quantitation. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1885-97	7.6	400
67	Clustering phenotype populations by genome-wide RNAi and multiparametric imaging. <i>Molecular Systems Biology</i> , 2010 , 6, 370	12.2	119
66	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010 , 11, 349	4.5	60
65	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010 , 10, 3957-69	4.8	44
64	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009 , 5, 274	12.2	28

63	Quality assessment and data analysis for microRNA expression arrays. <i>Nucleic Acids Research</i> , 2009 , 37, e17	20.1	41
62	Importing ArrayExpress datasets into R/Bioconductor. <i>Bioinformatics</i> , 2009 , 25, 2092-4	7.2	68
61	arrayQualityMetrics--a bioconductor package for quality assessment of microarray data. <i>Bioinformatics</i> , 2009 , 25, 415-6	7.2	635
60	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. <i>Bioinformatics</i> , 2009 , 25, 1056-62	7.2	5
59	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009 , 457, 1033-7	50.4	725
58	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. <i>Nature Protocols</i> , 2009 , 4, 1184-91	18.8	1626
57	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , 2008 , 454, 479-85	50.4	441
56	Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , 2008 , 91, 41-51	4.3	38
55	Model-based variance-stabilizing transformation for Illumina microarray data. <i>Nucleic Acids Research</i> , 2008 , 36, e11	20.1	390
54	Analyzing ChIP-chip data using bioconductor. <i>PLoS Computational Biology</i> , 2008 , 4, e1000227	5	17
53	Estimating node degree in bait-prey graphs. <i>Bioinformatics</i> , 2008 , 24, 218-24	7.2	15
52	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. <i>Bioinformatics</i> , 2008 , 24, 1100-1	7.2	9
51	Bioconductor Case Studies 2008 ,		46
50	Analysis of Microarray Gene Expression Data 2008 , 201-230		
49	Comparative analysis of structured RNAs in <i>S. cerevisiae</i> indicates a multitude of different functions. <i>BMC Biology</i> , 2007 , 5, 25	7.3	31
48	Ringo--an R/Bioconductor package for analyzing ChIP-chip readouts. <i>BMC Bioinformatics</i> , 2007 , 8, 221	3.6	134
47	In situ analysis of cross-hybridisation on microarrays and the inference of expression correlation. <i>BMC Bioinformatics</i> , 2007 , 8, 461	3.6	55
46	Graphs in molecular biology. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 6, S8	3.6	76

45	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. <i>Bioinformatics</i> , 2007 , 23, 771-3	7.2	
44	High-throughput flow cytometry-based assay to identify apoptosis-inducing proteins. <i>Journal of Biomolecular Screening</i> , 2007 , 12, 510-20		6
43	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007 , 89, 580-7	4.3	50
42	Making the most of high-throughput protein-interaction data. <i>Genome Biology</i> , 2007 , 8, 112	18.3	36
41	Coverage and error models of protein-protein interaction data by directed graph analysis. <i>Genome Biology</i> , 2007 , 8, R186	18.3	32
40	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D415-8	20.1	33
39	Transcript mapping with high-density oligonucleotide tiling arrays. <i>Bioinformatics</i> , 2006 , 22, 1963-70	7.2	120
38	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, 5320-5	11.5	546
37	Statistical methods and software for the analysis of highthroughput reverse genetic assays using flow cytometry readouts. <i>Genome Biology</i> , 2006 , 7, R77	18.3	19
36	Analysis of cell-based RNAi screens. <i>Genome Biology</i> , 2006 , 7, R66	18.3	234
35	Top-down standards will not serve systems biology. <i>Nature</i> , 2006 , 440, 24	50.4	15
34	Functional profiling: from microarrays via cell-based assays to novel tumor relevant modulators of the cell cycle. <i>Cancer Research</i> , 2005 , 65, 7733-42	10.1	18
33	Systematic comparison of surface coatings for protein microarrays. <i>Proteomics</i> , 2005 , 5, 4705-12	4.8	40
32	Large error models for microarray intensities 2005 ,		1
31	arrayMagic: two-colour cDNA microarray quality control and preprocessing. <i>Bioinformatics</i> , 2005 , 21, 554-6	7.2	46
30	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. <i>Bioinformatics</i> , 2005 , 21, 3439-40	7.2	1069
29	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. <i>Clinical Cancer Research</i> , 2005 , 11, 646-55	12.9	61
28	matchprobes: a Bioconductor package for the sequence-matching of microarray probe elements. <i>Bioinformatics</i> , 2004 , 20, 1651-2	7.2	30

27	From ORFeome to biology: a functional genomics pipeline. <i>Genome Research</i> , 2004 , 14, 2136-44	9.7	40
26	Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. <i>BMC Genomics</i> , 2004 , 5, 29	4.5	66
25	A compendium to ensure computational reproducibility in high-dimensional classification tasks. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004 , 3, Article37	1.2	61
24	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004 , 5, R80	18.3	9148
23	Analysis of Microarray Gene Expression Data 2004 ,		3
22	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		74
21	Parameter estimation for the calibration and variance stabilization of microarray data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003 , 2, Article3	1.2	103
20	Variance stabilization applied to microarray data calibration and to the quantification of differential expression. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S96-104	7.2	1554
19	Identifying splits with clear separation: a new class discovery method for gene expression data. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S107-14	7.2	44
18	Fast Monte Carlo algorithm for nonequilibrium systems. <i>Physical Review E</i> , 1996 , 53, 4232-4235	2.4	3
17	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 4 , 1070	3.6	28
16	Authoring Bioconductor workflows with BiocWorkflowTools. <i>F1000Research</i> , 7 , 431	3.6	
15	HTSeq - A Python framework to work with high-throughput sequencing data		227
14	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2		151
13	SomaticSignatures: Inferring Mutational Signatures from Single Nucleotide Variants		3
12	Data-driven hypothesis weighting increases detection power in multiple testing		5
11	Transcript isoform differences across human tissues are predominantly driven by alternative start and termination sites of transcription		1
10	The small non-coding vault RNA1-1 acts as a riboregulator of autophagy		1

9	Computational analysis of ligand dose range thermal proteome profiles	1
8	Single cell 3UTR analysis identifies changes in alternative polyadenylation throughout neuronal differentiation and in autism	3
7	glmGamPoi: Fitting Gamma-Poisson Generalized Linear Models on Single Cell Count Data	2
6	Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins	2
5	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation	4
4	Orchestrating Single-Cell Analysis with Bioconductor	9
3	Biological Plasticity Rescues Target Activity in CRISPR Knockouts	4
2	Subgroup-specific gene expression profiles and mixed epistasis in chronic lymphocytic leukemia	1
1	Transformation and Preprocessing of Single-Cell RNA-Seq Data	9