

# Wolfgang Huber

## List of Publications by Citations

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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	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. <i>Genome Biology</i> , <b>2014</b> , 15, 550	18.3	28138
187	HTSeq--a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , <b>2015</b> , 31, 166-9	7.2	10519
186	Differential expression analysis for sequence count data. <i>Genome Biology</i> , <b>2010</b> , 11, R106	18.3	9952
185	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , <b>2004</b> , 5, R80	18.3	9148
184	Enterotypes of the human gut microbiome. <i>Nature</i> , <b>2011</b> , 473, 174-80	50.4	4240
183	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , <b>2015</b> , 12, 115-21	21.6	1949
182	Software for computing and annotating genomic ranges. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003118	5	1845
181	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. <i>Nature Protocols</i> , <b>2009</b> , 4, 1184-91	18.8	1626
180	Variance stabilization applied to microarray data calibration and to the quantification of differential expression. <i>Bioinformatics</i> , <b>2002</b> , 18 Suppl 1, S96-104	7.2	1554
179	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. <i>Bioinformatics</i> , <b>2005</b> , 21, 3439-40	7.2	1069
178	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , <b>2012</b> , 22, 2008-17	9.7	882
177	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , <b>2013</b> , 8, 1765-86	18.8	788
176	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , <b>2009</b> , 457, 1033-7	50.4	725
175	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , <b>2010</b> , 464, 721-7	50.4	668
174	arrayQualityMetrics--a bioconductor package for quality assessment of microarray data. <i>Bioinformatics</i> , <b>2009</b> , 25, 415-6	7.2	635
173	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> , <b>2006</b> , 103, 5320-5	11.5	546
172	Independent filtering increases detection power for high-throughput experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 9546-51	11.5	499

171	Variation in transcription factor binding among humans. <i>Science</i> , <b>2010</b> , 328, 232-5	33.3	447
170	Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 271-281	23.4	441
169	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , <b>2008</b> , 454, 479-85	50.4	441
168	EBImage--an R package for image processing with applications to cellular phenotypes. <i>Bioinformatics</i> , <b>2010</b> , 26, 979-81	7.2	425
167	Expression Atlas update--an integrated database of gene and protein expression in humans, animals and plants. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D746-52	20.1	404
166	Addressing accuracy and precision issues in iTRAQ quantitation. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 1885-97	7.6	400
165	Model-based variance-stabilizing transformation for Illumina microarray data. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, e11	20.1	390
164	Enhancer loops appear stable during development and are associated with paused polymerase. <i>Nature</i> , <b>2014</b> , 512, 96-100	50.4	332
163	Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. <i>Cell Stem Cell</i> , <b>2014</b> , 15, 507-522	18	320
162	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , <b>2015</b> , 10, 1567-93	18.8	293
161	Multi-Omics Factor Analysis-a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , <b>2018</b> , 14, e8124	12.2	287
160	The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. <i>Nature Communications</i> , <b>2015</b> , 6, 10127	17.4	286
159	A global map of human gene expression. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 322-4	44.5	271
158	The genomic and transcriptomic landscape of a HeLa cell line. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 1213-24	3.2	269
157	Directional tissue migration through a self-generated chemokine gradient. <i>Nature</i> , <b>2013</b> , 503, 285-9	50.4	252
156	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , <b>2015</b> , 162, 1051-65	56.2	240
155	Analysis of cell-based RNAi screens. <i>Genome Biology</i> , <b>2006</b> , 7, R66	18.3	234
154	HTSeq - A Python framework to work with high-throughput sequencing data		227

153	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D246-D251	20.1	222
152	Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. <i>Nature Methods</i> , <b>2016</b> , 13, 577-80	21.6	219
151	Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages. <i>Nature Cell Biology</i> , <b>2014</b> , 16, 27-37	23.4	213
150	Highly coordinated proteome dynamics during reprogramming of somatic cells to pluripotency. <i>Cell Reports</i> , <b>2012</b> , 2, 1579-92	10.6	183
149	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , <b>2015</b> , 4, 1070	3.6	181
148	Gene expression across mammalian organ development. <i>Nature</i> , <b>2019</b> , 571, 505-509	50.4	179
147	SomaticSignatures: inferring mutational signatures from single-nucleotide variants. <i>Bioinformatics</i> , <b>2015</b> , 31, 3673-5	7.2	174
146	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , <b>2020</b> , 17, 137-145	21.6	174
145	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , <b>2015</b> , 12, 1129-31	21.6	173
144	Tandem fluorescent protein timers for in vivo analysis of protein dynamics. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 708-14	44.5	172
143	Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , <b>2018</b> , 13, 530-550	50.8	151
142	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2		151
141	Mapping of signaling networks through synthetic genetic interaction analysis by RNAi. <i>Nature Methods</i> , <b>2011</b> , 8, 341-6	21.6	150
140	Protein quality control at the inner nuclear membrane. <i>Nature</i> , <b>2014</b> , 516, 410-3	50.4	134
139	Ringo--an R/Bioconductor package for analyzing CHIP-chip readouts. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 221	3.6	134
138	The Shh Topological Domain Facilitates the Action of Remote Enhancers by Reducing the Effects of Genomic Distances. <i>Developmental Cell</i> , <b>2016</b> , 39, 529-543	10.2	134
137	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 468	12.2	131
136	Transcript mapping with high-density oligonucleotide tiling arrays. <i>Bioinformatics</i> , <b>2006</b> , 22, 1963-70	7.2	120

135	Clustering phenotype populations by genome-wide RNAi and multiparametric imaging. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 370	12.2	119
134	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 582-592	20.1	113
133	Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , <b>2016</b> , 61, 260-73	17.6	111
132	Parameter estimation for the calibration and variance stabilization of microarray data. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2003</b> , 2, Article3	1.2	103
131	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , <b>2019</b> , 16, 1087-1093	21.6	94
130	Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping. <i>Nature Methods</i> , <b>2013</b> , 10, 427-31	21.6	94
129	Genome-wide analysis of mRNA decay patterns during early Drosophila development. <i>Genome Biology</i> , <b>2010</b> , 11, R93	18.3	92
128	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , <b>2019</b> , 10, 1155	17.4	88
127	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. <i>Nature Immunology</i> , <b>2015</b> , 16, 933-41	19.1	88
126	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , <b>2020</b> , 586, E14-E16	50.4	85
125	cAMP response element-binding protein is a primary hub of activity-driven neuronal gene expression. <i>Journal of Neuroscience</i> , <b>2011</b> , 31, 18237-50	6.6	83
124	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , <b>2010</b> , 11, R24	18.3	81
123	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> , <b>2011</b> , 21, 2004-13	9.7	80
122	Graphs in molecular biology. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 6, S8	3.6	76
121	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , <b>2015</b> , 31, 3085-91	7.2	74
120	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> , <b>2003</b> , 4, 67-78		74
119	Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size. <i>Bioinformatics</i> , <b>2013</b> , 29, 1275-82	7.2	73
118	The Small Non-coding Vault RNA1-1 Acts as a Riboregulator of Autophagy. <i>Cell</i> , <b>2019</b> , 176, 1054-1067.e136.2	36.2	73

117	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , <b>2018</b> , 128, 427-445	4.5	72
116	Importing ArrayExpress datasets into R/Bioconductor. <i>Bioinformatics</i> , <b>2009</b> , 25, 2092-4	7.2	68
115	Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , <b>2015</b> , 126, 1005-8	2.2	66
114	Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. <i>BMC Genomics</i> , <b>2004</b> , 5, 29	4.5	66
113	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> , <b>2017</b> , 66, 1537-1538	19.2	65
112	Microarray data quality control improves the detection of differentially expressed genes. <i>Genomics</i> , <b>2010</b> , 95, 138-42	4.3	65
111	Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA-protein interactions. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 719	12.2	64
110	A compendium to ensure computational reproducibility in high-dimensional classification tasks. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2004</b> , 3, Article37	1.2	61
109	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. <i>Clinical Cancer Research</i> , <b>2005</b> , 11, 646-55	12.9	61
108	Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , <b>2010</b> , 11, 349	4.5	60
107	Assessing affymetrix GeneChip microarray quality. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 137	3.6	59
106	Differential expression analysis for sequence count data. <i>Nature Precedings</i> , <b>2010</b> ,		59
105	A map of directional genetic interactions in a metazoan cell. <i>ELife</i> , <b>2015</b> , 4,	8.9	59
104	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. <i>Leukemia</i> , <b>2018</b> , 32, 774-787	10.7	56
103	In situ analysis of cross-hybridisation on microarrays and the inference of expression correlation. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 461	3.6	55
102	A chemical-genetic interaction map of small molecules using high-throughput imaging in cancer cells. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 846	12.2	51
101	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , <b>2007</b> , 89, 580-7	4.3	50
100	A discrete transition zone organizes the topological and regulatory autonomy of the adjacent tfap2c and bmp7 genes. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1004897	6	46

99	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 303-308	44.5	46
98	Bioconductor Case Studies <b>2008</b> ,		46
97	arrayMagic: two-colour cDNA microarray quality control and preprocessing. <i>Bioinformatics</i> , <b>2005</b> , 21, 554-6	7.2	46
96	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , <b>2010</b> , 10, 3957-69	4.8	44
95	Identifying splits with clear separation: a new class discovery method for gene expression data. <i>Bioinformatics</i> , <b>2001</b> , 17 Suppl 1, S107-14	7.2	44
94	High-content siRNA screen reveals global ENaC regulators and potential cystic fibrosis therapy targets. <i>Cell</i> , <b>2013</b> , 154, 1390-400	56.2	42
93	Functional Outcomes and Quality of Life After Radical Prostatectomy Only Versus a Combination of Prostatectomy with Radiation and Hormonal Therapy. <i>European Urology</i> , <b>2017</b> , 71, 330-336	10.2	42
92	Quality assessment and data analysis for microRNA expression arrays. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e17	20.1	41
91	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 812	12.2	40
90	From ORFeome to biology: a functional genomics pipeline. <i>Genome Research</i> , <b>2004</b> , 14, 2136-44	9.7	40
89	Systematic comparison of surface coatings for protein microarrays. <i>Proteomics</i> , <b>2005</b> , 5, 4705-12	4.8	40
88	Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , <b>2008</b> , 91, 41-51	4.3	38
87	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9596	12.2	37
86	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , <b>2018</b> , 7, 482-495.e10	10.6	37
85	Making the most of high-throughput protein-interaction data. <i>Genome Biology</i> , <b>2007</b> , 8, 112	18.3	36
84	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 2506-2515	7.6	34
83	A large-scale RNAi screen identifies Deaf1 as a regulator of innate immune responses in <i>Drosophila</i> . <i>Journal of Innate Immunity</i> , <b>2010</b> , 2, 181-94	6.9	34
82	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D415-8	20.1	33

81	Coverage and error models of protein-protein interaction data by directed graph analysis. <i>Genome Biology</i> , <b>2007</b> , 8, R186	18.3	32
80	Comparative analysis of structured RNAs in <i>S. cerevisiae</i> indicates a multitude of different functions. <i>BMC Biology</i> , <b>2007</b> , 5, 25	7.3	31
79	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 896-906	23.4	30
78	matchprobes: a Bioconductor package for the sequence-matching of microarray probe elements. <i>Bioinformatics</i> , <b>2004</b> , 20, 1651-2	7.2	30
77	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , <b>2009</b> , 5, 274	12.2	28
76	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , <b>4</b> , 1070	3.6	28
75	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. <i>Cell Reports</i> , <b>2019</b> , 29, 3147-3159.e12	10.6	26
74	Transcriptome-wide profiling and posttranscriptional analysis of hematopoietic stem/progenitor cell differentiation toward myeloid commitment. <i>Stem Cell Reports</i> , <b>2014</b> , 3, 858-75	8	25
73	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , <b>2019</b> , 27, 3097-3106.e5	10.6	23
72	Statistical methods and software for the analysis of highthroughput reverse genetic assays using flow cytometry readouts. <i>Genome Biology</i> , <b>2006</b> , 7, R77	18.3	19
71	Functional profiling: from microarrays via cell-based assays to novel tumor relevant modulators of the cell cycle. <i>Cancer Research</i> , <b>2005</b> , 65, 7733-42	10.1	18
70	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. <i>Blood</i> , <b>2018</b> , 131, 2789-2802	2.2	17
69	Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , <b>2011</b> , 12, R36	18.3	17
68	Analyzing ChIP-chip data using bioconductor. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000227	5	17
67	glmGamPoi: fitting Gamma-Poisson generalized linear models on single cell count data. <i>Bioinformatics</i> , <b>2021</b> , 36, 5701-5702	7.2	17
66	Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , <b>2018</b> , 8, 12046	4.9	15
65	Measuring genetic interactions in human cells by RNAi and imaging. <i>Nature Protocols</i> , <b>2014</b> , 9, 2341-53	18.8	15
64	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , <b>2011</b> , 12, R101	18.3	15



63	Estimating node degree in bait-prey graphs. <i>Bioinformatics</i> , <b>2008</b> , 24, 218-24	7.2	15
62	Top-down standards will not serve systems biology. <i>Nature</i> , <b>2006</b> , 440, 24	50.4	15
61	Timer-based proteomic profiling of the ubiquitin-proteasome system reveals a substrate receptor of the GID ubiquitin ligase. <i>Molecular Cell</i> , <b>2021</b> , 81, 2460-2476.e11	17.6	15
60	gscrend: modelling asymmetric count ratios in CRISPR screens to decrease experiment size and improve phenotype detection. <i>Genome Biology</i> , <b>2020</b> , 21, 53	18.3	14
59	A genetic interaction map of cell cycle regulators. <i>Molecular Biology of the Cell</i> , <b>2016</b> , 27, 1397-407	3.5	13
58	Extracting quantitative genetic interaction phenotypes from matrix combinatorial RNAi. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 342	3.6	12
57	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , <b>2012</b> ,		11
56	CellH5: a format for data exchange in high-content screening. <i>Bioinformatics</i> , <b>2013</b> , 29, 1580-2	7.2	11
55	Developmental Gene Expression Differences between Humans and Mammalian Models. <i>Cell Reports</i> , <b>2020</b> , 33, 108308	10.6	11
54	Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 308	3.6	10
53	TimerQuant: a modelling approach to tandem fluorescent timer design and data interpretation for measuring protein turnover in embryos. <i>Development (Cambridge)</i> , <b>2016</b> , 143, 174-9	6.6	9
52	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> , <b>2010</b> , 107, E175-E175	11.5	9
51	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. <i>Bioinformatics</i> , <b>2008</b> , 24, 1100-1	7.2	9
50	Contributions of the EMERALD project to assessing and improving microarray data quality. <i>BioTechniques</i> , <b>2011</b> , 50, 27-31	2.5	9
49	Orchestrating Single-Cell Analysis with Bioconductor		9
48	Transformation and Preprocessing of Single-Cell RNA-Seq Data		9
47	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , <b>2019</b> , 79, 3125-3138	3.8	8
46	Energy metabolism is co-determined by genetic variants in chronic lymphocytic leukemia and influences drug sensitivity. <i>Haematologica</i> , <b>2019</b> , 104, 1830-1840	6.6	8

45	Research Techniques Made Simple: Bioinformatics for Genome-Scale Biology. <i>Journal of Investigative Dermatology</i> , <b>2017</b> , 137, e163-e168	4.3	8
44	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , <b>2012</b> ,		8
43	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , <b>2020</b> , 11, 5783	17.4	8
42	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , <b>2020</b> , 11, 3400	17.4	7
41	Dissection of CD20 regulation in lymphoma using RNAi. <i>Leukemia</i> , <b>2016</b> , 30, 2409-2412	10.7	7
40	High-throughput flow cytometry-based assay to identify apoptosis-inducing proteins. <i>Journal of Biomolecular Screening</i> , <b>2007</b> , 12, 510-20		6
39	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , <b>2021</b> ,	2.2	6
38	A clash of cultures in discussions of the P value. <i>Nature Methods</i> , <b>2016</b> , 13, 607	21.6	6
37	Survey of ex vivo drug combination effects in chronic lymphocytic leukemia reveals synergistic drug effects and genetic dependencies. <i>Leukemia</i> , <b>2020</b> , 34, 2934-2950	10.7	5
36	Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. <i>Bioinformatics</i> , <b>2009</b> , 25, 1056-622		5
35	Data-driven hypothesis weighting increases detection power in multiple testing		5
34	Adaptive penalization in high-dimensional regression and classification with external covariates using variational Bayes. <i>Biostatistics</i> , <b>2021</b> , 22, 348-364	3.7	5
33	Upregulation of SPS100 gene expression by an antisense RNA via a switch of mRNA isoforms with different stabilities. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 11144-11158	20.1	4
32	The Bioconductor channel in F1000Research. <i>F1000Research</i> , <b>2015</b> , 4, 217	3.6	4
31	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation		4
30	Biological Plasticity Rescues Target Activity in CRISPR Knockouts		4
29	Miniaturized Drug Sensitivity and Resistance Test on Patient-Derived Cells Using Droplet-Microarray. <i>SLAS Technology</i> , <b>2021</b> , 26, 274-286	3	4
28	Covariate powered cross-weighted multiple testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , <b>2021</b> , 83, 720-751	3.9	4

27	Analysis of Microarray Gene Expression Data <b>2004</b> ,		3
26	Fast Monte Carlo algorithm for nonequilibrium systems. <i>Physical Review E</i> , <b>1996</b> , 53, 4232-4235	2.4	3
25	Asymptomatic Multiple Myeloma - Background of Progression, Evolution, and Prognosis. <i>Blood</i> , <b>2016</b> , 128, 235-235	2.2	3
24	The Bioconductor channel in F1000Research. <i>F1000Research</i> , <b>2015</b> , 4, 217	3.6	3
23	SomaticSignatures: Inferring Mutational Signatures from Single Nucleotide Variants		3
22	Single cell 3DTR analysis identifies changes in alternative polyadenylation throughout neuronal differentiation and in autism		3
21	Mutational landscape and complexity in CLL. <i>Blood</i> , <b>2015</b> , 126, 2078-9	2.2	2
20	h5vc: scalable nucleotide tallies with HDF5. <i>Bioinformatics</i> , <b>2014</b> , 30, 1464-6	7.2	2
19	glmGamPoi: Fitting Gamma-Poisson Generalized Linear Models on Single Cell Count Data		2
18	Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins		2
17	Multi-omics reveals clinically relevant proliferative drive associated with mTOR-MYC-OXPPOS activity in chronic lymphocytic leukemia. <i>Nature Cancer</i> , <b>2021</b> , 2, 853-864	15.4	2
16	DRUG PERTURBATION BASED STRATIFICATION OF LYMPHOPROLIFERATIVE DISORDERS. <i>Hematological Oncology</i> , <b>2017</b> , 35, 56-56	1.3	1
15	Large error models for microarray intensities <b>2005</b> ,		1
14	Systematic Investigation of Microenvironmental Drug Resistance Mechanisms in Chronic Lymphocytic Leukemia. <i>Blood</i> , <b>2019</b> , 134, 3363-3363	2.2	1
13	Transcript isoform differences across human tissues are predominantly driven by alternative start and termination sites of transcription		1
12	The small non-coding vault RNA1-1 acts as a riboregulator of autophagy		1
11	Computational analysis of ligand dose range thermal proteome profiles		1
10	Control of PD-L1 expression in CLL-cells by stromal triggering of the Notch-c-Myc-EZH2 oncogenic signaling axis <b>2021</b> , 9,		1

9	Subgroup-specific gene expression profiles and mixed epistasis in chronic lymphocytic leukemia		1
8	An autologous culture model of nodal B-cell lymphoma identifies ex vivo determinants of response to bispecific antibodies. <i>Blood Advances</i> , <b>2021</b> , 5, 5060-5071	7.8	1
7	Pairwise effects between lipid GWAS genes modulate lipid plasma levels and cellular uptake. <i>Nature Communications</i> , <b>2021</b> , 12, 6411	17.4	0
6	THE LANDSCAPE OF DRUG PERTURBATION EFFECTS IN LEUKEMIA AND LYMPHOMA. <i>Hematological Oncology</i> , <b>2019</b> , 37, 127-127	1.3	
5	Analysis of Microarray Gene Expression Data <b>2008</b> , 201-230		
4	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. <i>Bioinformatics</i> , <b>2007</b> , 23, 771-3	7.2	
3	Authoring Bioconductor workflows with BiocWorkflowTools. <i>F1000Research</i> , <b>7</b> , 431	3.6	
2	Discovery of Novel Drug Sensitivities in T-Prolymphocytic Leukemia (T-PLL) By High-Throughput Ex Vivo Drug Testing and Genetic Profiling. <i>Blood</i> , <b>2014</b> , 124, 917-917	2.2	
1	Systematic Mapping Of Drug and Pathway Sensitivity In Chronic Lymphocytic Leukemia Identifies Synthetic Lethal Interactions Of Mutant p53. <i>Blood</i> , <b>2013</b> , 122, 173-173	2.2	