

# 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  | Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. <i>Genome Biology</i> , 2014, 15, 550.   | 8.8  | 58,325    |
| 2  | HTSeq—a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, 166-169.   | 4.1  | 17,270    |
| 3  | Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010, 11, R106.   | 8.8  | 13,707    |
| 4  | Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004, 5, R80.   | 9.6  | 10,796    |
| 5  | Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.  | 27.8 | 5,800     |
| 6  | Software for Computing and Annotating Genomic Ranges. <i>PLoS Computational Biology</i> , 2013, 9, e1003118.  | 3.2  | 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.  | 12.0 | 3,084     |
| 8  | Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.  | 19.0 | 3,070     |
| 9  | Variance stabilization applied to microarray data calibration and to the quantification of differential expression. <i>Bioinformatics</i> , 2002, 18, S96-S104.                                 | 4.1  | 2,012     |
| 10 | BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. <i>Bioinformatics</i> , 2005, 21, 3439-3440.   | 4.1  | 1,781     |
| 11 | Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012, 22, 2008-2017.  | 5.5  | 1,341     |
| 12 | Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013, 8, 1765-1786.   | 12.0 | 1,124     |
| 13 | arrayQualityMetrics—a bioconductor package for quality assessment of microarray data. <i>Bioinformatics</i> , 2009, 25, 415-416.  | 4.1  | 885       |
| 14 | Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009, 457, 1033-1037.  | 27.8 | 872       |
| 15 | Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010, 464, 721-727.  | 27.8 | 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. | 7.1  | 720       |
| 17 | Human haematopoietic stem cell lineage commitment is a continuous process. <i>Nature Cell Biology</i> , 2017, 19, 271-281.  | 10.3 | 709       |
| 18 | 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       |

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|----|---|------|-----------|
| 19 | EImageR an R package for image processing with applications to cellular phenotypes. <i>Bioinformatics</i> , 2010, 26, 979-981.  | 4.1  | 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.                  | 7.1  | 613       |
| 21 | High-resolution mapping of meiotic crossovers and non-crossovers in yeast. <i>Nature</i> , 2008, 454, 479-485.  | 27.8 | 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.                           | 14.5 | 526       |
| 23 | Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235.  | 12.6 | 521       |
| 24 | Gene expression across mammalian organ development. <i>Nature</i> , 2019, 571, 505-509.   | 27.8 | 490       |
| 25 | Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.  | 19.0 | 488       |
| 26 | Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. <i>Nature Methods</i> , 2016, 13, 577-580.   | 19.0 | 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. | 12.0 | 481       |
| 28 | Addressing Accuracy and Precision Issues in iTRAQ Quantitation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1885-1897.  | 3.8  | 471       |
| 29 | Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , 2018, 13, 530-550.  | 12.0 | 454       |
| 30 | Enhancer loops appear stable during development and are associated with paused polymerase. <i>Nature</i> , 2014, 512, 96-100.   | 27.8 | 450       |
| 31 | Model-based variance-stabilizing transformation for Illumina microarray data. <i>Nucleic Acids Research</i> , 2008, 36, e11-e11.  | 14.5 | 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.    | 11.1 | 439       |
| 33 | The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. <i>Nature Communications</i> , 2015, 6, 10127.   | 12.8 | 385       |
| 34 | Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018, 46, D246-D251.   | 14.5 | 365       |
| 35 | The Genomic and Transcriptomic Landscape of a HeLa Cell Line. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1213-1224.   | 1.8  | 355       |
| 36 | Directional tissue migration through a self-generated chemokine gradient. <i>Nature</i> , 2013, 503, 285-289.   | 27.8 | 320       |

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|----|---|------|-----------|
| 37 | A global map of human gene expression. <i>Nature Biotechnology</i> , 2010, 28, 322-324.   | 17.5 | 315       |
| 38 | RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 2015, 4, 1070.  | 1.6  | 304       |
| 39 | Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.                                       | 28.9 | 304       |
| 40 | SomaticSignatures: inferring mutational signatures from single-nucleotide variants. <i>Bioinformatics</i> , 2015, 31, 3673-3675.  | 4.1  | 284       |
| 41 | Analysis of cell-based RNAi screens. <i>Genome Biology</i> , 2006, 7, R66.  | 9.6  | 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.           | 10.3 | 262       |
| 43 | Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015, 12, 1129-1131.                                       | 19.0 | 244       |
| 44 | Tandem fluorescent protein timers for in vivo analysis of protein dynamics. <i>Nature Biotechnology</i> , 2012, 30, 708-714.  | 17.5 | 239       |
| 45 | Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.  | 27.8 | 233       |
| 46 | Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2012, 2, 1579-1592.                                       | 6.4  | 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. | 14.5 | 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.          | 7.0  | 194       |
| 49 | Protein quality control at the inner nuclear membrane. <i>Nature</i> , 2014, 516, 410-413.  | 27.8 | 188       |
| 50 | Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , 2019, 10, 1155.                          | 12.8 | 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.   | 19.0 | 173       |
| 53 | Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.                                      | 7.2  | 173       |
| 54 | Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.  | 19.0 | 159       |

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|----|--|------|-----------|
| 55 | Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , 2016, 61, 260-273.  | 9.7  | 155       |
| 56 | Ringo – an R/Bioconductor package for analyzing ChIP-chip readouts. <i>BMC Bioinformatics</i> , 2007, 8, 221.  | 2.6  | 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.                              | 14.5 | 148       |
| 58 | Clustering phenotype populations by genome-wide RNAi and multiparametric imaging. <i>Molecular Systems Biology</i> , 2010, 6, 370.   | 7.2  | 141       |
| 59 | Transcript mapping with high-density oligonucleotide tiling arrays. <i>Bioinformatics</i> , 2006, 22, 1963-1970.   | 4.1  | 134       |
| 60 | 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       |
| 61 | Parameter estimation for the calibration and variance stabilization of microarray data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article3.                           | 0.6  | 128       |
| 62 | The Small Non-coding Vault RNA1-1 Acts as a Riboregulator of Autophagy. <i>Cell</i> , 2019, 176, 1054-1067.e12.  | 28.9 | 125       |
| 63 | Genome-wide analysis of mRNA decay patterns during early <i>Drosophila</i> development. <i>Genome Biology</i> , 2010, 11, R93.   | 9.6  | 124       |
| 64 | Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.   | 8.2  | 124       |
| 65 | Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping. <i>Nature Methods</i> , 2013, 10, 427-431.   | 19.0 | 122       |
| 66 | glmGamPoi: fitting Gamma-Poisson generalized linear models on single cell count data. <i>Bioinformatics</i> , 2021, 36, 5701-5702.   | 4.1  | 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.  | 4.1  | 113       |
| 68 | Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020, 38, 303-308.   | 17.5 | 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.               | 5.5  | 109       |
| 70 | Graphs in molecular biology. <i>BMC Bioinformatics</i> , 2007, 8, S8.  | 2.6  | 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. | 12.1 | 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.  | 3.6  | 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.   | 4.1  | 100       |
| 75 | High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.  | 9.6  | 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.                            | 10.3 | 93        |
| 77 | Alternative polyadenylation diversifies post-transcriptional regulation by selective <i>scRNA</i> protein interactions. <i>Molecular Systems Biology</i> , 2014, 10, 719.                           | 7.2  | 91        |
| 78 | FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , 2015, 31, 3085-3091.  | 4.1  | 91        |
| 79 | Microarray data quality control improves the detection of differentially expressed genes. <i>Genomics</i> , 2010, 95, 138-142.  | 2.9  | 88        |
| 80 | Recurrent CDKN1B (p27) mutations in hairy cell leukemia. <i>Blood</i> , 2015, 126, 1005-1008.   | 1.4  | 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.             | 6.4  | 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.  | 2.8  | 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.  | 7.2  | 79        |
| 84 | A map of directional genetic interactions in a metazoan cell. <i>ELife</i> , 2015, 4, .   | 6.0  | 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.   | 7.2  | 75        |
| 86 | Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2506-2515.   | 3.8  | 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.                   | 0.6  | 72        |
| 88 | Assessing affymetrix GeneChip microarray quality. <i>BMC Bioinformatics</i> , 2011, 12, 137.  | 2.6  | 71        |
| 89 | Comparison of normalization methods for Illumina BeadChip HumanHT-12 v3. <i>BMC Genomics</i> , 2010, 11, 349.   | 2.8  | 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.                   | 7.0  | 64        |
| 92  | Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018, 7, 482-495.e10.  | 6.2  | 62        |
| 93  | In situ analysis of cross-hybridisation on microarrays and the inference of expression correlation. <i>BMC Bioinformatics</i> , 2007, 8, 461.  | 2.6  | 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. | 1.9  | 57        |
| 95  | Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007, 89, 580-587.  | 2.9  | 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.                     | 3.5  | 56        |
| 97  | RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 0, 4, 1070.  | 1.6  | 55        |
| 98  | Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.   | 2.2  | 54        |
| 99  | Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015, 11, 812.  | 7.2  | 52        |
| 100 | High-Content siRNA Screen Reveals Global ENaC Regulators and Potential Cystic Fibrosis Therapy Targets. <i>Cell</i> , 2013, 154, 1390-1400.  | 28.9 | 50        |
| 101 | Identifying splits with clear separation: a new class discovery method for gene expression data. <i>Bioinformatics</i> , 2001, 17, S107-S114.  | 4.1  | 49        |
| 102 | arrayMagic: two-colour cDNA microarray quality control and preprocessing. <i>Bioinformatics</i> , 2005, 21, 554-556.   | 4.1  | 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.  | 6.4  | 47        |
| 104 | Developmental Gene Expression Differences between Humans and Mammalian Models. <i>Cell Reports</i> , 2020, 33, 108308.   | 6.4  | 46        |
| 105 | Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , 2008, 91, 41-51.   | 2.9  | 45        |
| 106 | Quality Assessment and Data Analysis for microRNA Expression Arrays. <i>Nucleic Acids Research</i> , 2009, 37, e17-e17.  | 14.5 | 45        |
| 107 | From ORFeome to Biology: A Functional Genomics Pipeline. <i>Genome Research</i> , 2004, 14, 2136-2144.   | 5.5  | 44        |
| 108 | Systematic comparison of surface coatings for protein microarrays. <i>Proteomics</i> , 2005, 5, 4705-4712.   | 2.2  | 42        |

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|-----|---|------|-----------|
| 109 | Making the most of high-throughput protein-interaction data. <i>Genome Biology</i> , 2007, 8, 112.  | 9.6  | 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.                    | 3.8  | 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.               | 9.7  | 39        |
| 112 | Coverage and error models of protein-protein interaction data by directed graph analysis. <i>Genome Biology</i> , 2007, 8, R186.  | 9.6  | 37        |
| 113 | The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D415-D418.   | 14.5 | 36        |
| 114 | A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020, 11, 5783.                                   | 12.8 | 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.                           | 8.8  | 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.   | 3.8  | 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. | 4.8  | 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.              | 13.2 | 32        |
| 119 | matchprobes: a Bioconductor package for the sequence-matching of microarray probe elements. <i>Bioinformatics</i> , 2004, 20, 1651-1652.  | 4.1  | 31        |
| 120 | Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009, 5, 274.  | 7.2  | 31        |
| 121 | Covariate Powered Cross-Weighted Multiple Testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2021, 83, 720-751.                                   | 2.2  | 26        |
| 122 | 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        |
| 123 | A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.   | 12.8 | 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.                             | 9.6  | 22        |
| 125 | Genome-wide survey of post-meiotic segregation during yeast recombination. <i>Genome Biology</i> , 2011, 12, R36.   | 8.8  | 22        |
| 126 | A genetic interaction map of cell cycle regulators. <i>Molecular Biology of the Cell</i> , 2016, 27, 1397-1407.   | 2.1  | 22        |



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|-----|--|------|-----------|
| 127 | Drug-based perturbation screen uncovers synergistic drug combinations in Burkitt lymphoma. <i>Scientific Reports</i> , 2018, 8, 12046.   | 3.3  | 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.   | 0.9  | 19        |
| 130 | SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011, 12, R101.  | 9.6  | 19        |
| 131 | MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019, 79, 3125-3138.  | 0.9  | 19        |
| 132 | Analyzing ChIP-chip Data Using Bioconductor. <i>PLoS Computational Biology</i> , 2008, 4, e1000227.  | 3.2  | 17        |
| 133 | Estimating node degree in bait-prey graphs. <i>Bioinformatics</i> , 2008, 24, 218-224.   | 4.1  | 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.   | 3.5  | 17        |
| 136 | The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021, , .  | 1.4  | 17        |
| 137 | Top-down standards will not serve systems biology. <i>Nature</i> , 2006, 440, 24-24.   | 27.8 | 16        |
| 138 | Measuring genetic interactions in human cells by RNAi and imaging. <i>Nature Protocols</i> , 2014, 9, 2341-2353.   | 12.0 | 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.   | 7.2  | 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.  | 2.6  | 14        |
| 142 | Research Techniques Made Simple: Bioinformatics for Genome-Scale Biology. <i>Journal of Investigative Dermatology</i> , 2017, 137, e163-e168.  | 0.7  | 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. | 7.1  | 13        |

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|-----|---|------|-----------|
| 145 | Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. BMC Bioinformatics, 2013, 14, 308.   | 2.6  | 13        |
| 146 | CellH5: a format for data exchange in high-content screening. Bioinformatics, 2013, 29, 1580-1582.  | 4.1  | 13        |
| 147 | Dissection of CD20 regulation in lymphoma using RNAi. Leukemia, 2016, 30, 2409-2412.  | 7.2  | 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. | 2.5  | 12        |
| 149 | Miniaturized Drug Sensitivity and Resistance Test on Patient-Derived Cells Using Droplet-Microarray. SLAS Technology, 2021, 26, 274-286.  | 1.9  | 11        |
| 150 | Contributions of the EMERALD project to assessing and improving microarray data quality. BioTechniques, 2011, 50, 27-31.  | 1.8  | 11        |
| 151 | Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. Bioinformatics, 2008, 24, 1100-1101.   | 4.1  | 9         |
| 152 | A clash of cultures in discussions of the P value. Nature Methods, 2016, 13, 607-607.   | 19.0 | 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.                    | 5.2  | 9         |
| 154 | Adaptive penalization in high-dimensional regression and classification with external covariates using variational Bayes. Biostatistics, 2021, 22, 348-364.                       | 1.5  | 8         |
| 155 | Array-based genotyping in <i>S.cerevisiae</i> using semi-supervised clustering. Bioinformatics, 2009, 25, 1056-1062.  | 4.1  | 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.   | 1.6  | 6         |
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