

# Oliver Stegle

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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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.

176  
papers

29,431  
citations

63  
h-index

171  
g-index

209  
ext. papers

41,593  
ext. citations

20  
avg, IF

7.68  
L-index

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 176 | scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation.. <i>Genome Biology</i> , <b>2022</b> , 23, 8  | 18.3 | 0         |
| 175 | Cell2location maps fine-grained cell types in spatial transcriptomics.. <i>Nature Biotechnology</i> , <b>2022</b> ,   | 44.5 | 18        |
| 174 | Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO.. <i>Nature Methods</i> , <b>2022</b> ,   | 21.6 | 5         |
| 173 | MUON: multimodal omics analysis framework.. <i>Genome Biology</i> , <b>2022</b> , 23, 42  | 18.3 | 1         |
| 172 | Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases.. <i>Nature Genetics</i> , <b>2022</b> , 54, 251-262                  | 36.3 | 1         |
| 171 | Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses.. <i>Nature Communications</i> , <b>2022</b> , 13, 1779 | 17.4 | 2         |
| 170 | Subclone-specific microenvironmental impact and drug response in refractory multiple myeloma revealed by single-cell transcriptomics. <i>Nature Communications</i> , <b>2021</b> , 12, 6960 | 17.4 | 9         |
| 169 | The Organoid Cell Atlas. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 13-17  | 44.5 | 30        |
| 168 | Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. <i>Nature Genetics</i> , <b>2021</b> , 53, 313-321                       | 36.3 | 16        |
| 167 | Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , <b>2021</b> , 53, 304-312   | 36.3 | 37        |
| 166 | Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , <b>2021</b> , 372,   | 33.3 | 100       |
| 165 | Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. <i>Cell Reports</i> , <b>2021</b> , 35, 109032   | 10.6 | 3         |
| 164 | Computational principles and challenges in single-cell data integration. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1202-1215  | 44.5 | 33        |
| 163 | Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , <b>2021</b> , 12, 3545   | 17.4 | 14        |
| 162 | Dissecting indirect genetic effects from peers in laboratory mice. <i>Genome Biology</i> , <b>2021</b> , 22, 216  | 18.3 | 0         |
| 161 | IceR improves proteome coverage and data completeness in global and single-cell proteomics. <i>Nature Communications</i> , <b>2021</b> , 12, 4787   | 17.4 | 7         |
| 160 | Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. <i>Nature Medicine</i> , <b>2021</b> , 27, 1564-1575                            | 50.5 | 4         |

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| 159 | Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , <b>2021</b> , 53, 1300-1310 | 36.3 | 60  |
| 158 | MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. <i>Genome Biology</i> , <b>2020</b> , 21, 111  | 18.3 | 97  |
| 157 | Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. <i>Nature Communications</i> , <b>2020</b> , 11, 2928                               | 17.4 | 11  |
| 156 | Properties of structural variants and short tandem repeats associated with gene expression and complex traits. <i>Nature Communications</i> , <b>2020</b> , 11, 2927                       | 17.4 | 22  |
| 155 | Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , <b>2020</b> , 17, 414-421                                      | 21.6 | 17  |
| 154 | Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 747-755   | 44.5 | 142 |
| 153 | A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. <i>Cell Systems</i> , <b>2020</b> , 11, 25-41.e9         | 10.6 | 27  |
| 152 | Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , <b>2020</b> , 21, 31  | 18.3 | 274 |
| 151 | Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , <b>2020</b> , 11, 810                           | 17.4 | 76  |
| 150 | Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. <i>Genome Biology</i> , <b>2020</b> , 21, 36                                  | 18.3 | 57  |
| 149 | Pan-cancer analysis of whole genomes. <i>Nature</i> , <b>2020</b> , 578, 82-93   | 50.4 | 840 |
| 148 | Genomic basis for RNA alterations in cancer. <i>Nature</i> , <b>2020</b> , 578, 129-136  | 50.4 | 148 |
| 147 | Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , <b>2020</b> , 9,   | 8.9  | 16  |
| 146 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , <b>2020</b> , 182, 1214-1231.e11   | 56.2 | 96  |
| 145 | LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , <b>2020</b> , 587, 377-386  | 50.4 | 56  |
| 144 | Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. <i>Cell Stem Cell</i> , <b>2020</b> , 27, 470-481.e6                                      | 18   | 16  |
| 143 | A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , <b>2019</b> , 178, 1465-1477.e17   | 56.2 | 56  |
| 142 | Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. <i>Cell Reports</i> , <b>2019</b> , 29, 202-211.e6                                   | 10.6 | 57  |

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| 141 | Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, S114-S125      | 7.6  | 4   |
| 140 | The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 592-600                    | 44.5 | 69  |
| 139 | Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. <i>Genome Biology</i> , <b>2019</b> , 20, 27                        | 18.3 | 22  |
| 138 | Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. <i>Genome Biology</i> , <b>2019</b> , 20, 30                | 18.3 | 36  |
| 137 | Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. <i>Genome Biology</i> , <b>2019</b> , 20, 146 | 18.3 | 36  |
| 136 | Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. <i>ELife</i> , <b>2019</b> , 8,                      | 8.9  | 12  |
| 135 | Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. <i>Cell Reports</i> , <b>2019</b> , 26, 2078-2087.e3  | 10.6 | 16  |
| 134 | Vireo: Bayesian demultiplexing of pooled single-cell RNA-seq data without genotype reference. <i>Genome Biology</i> , <b>2019</b> , 20, 273                                 | 18.3 | 46  |
| 133 | Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , <b>2019</b> , 576, 487-491   | 50.4 | 137 |
| 132 | A linear mixed-model approach to study multivariate gene-environment interactions. <i>Nature Genetics</i> , <b>2019</b> , 51, 180-186                                       | 36.3 | 63  |
| 131 | DNA methylation defines regional identity of human intestinal epithelial organoids and undergoes dynamic changes during development. <i>Gut</i> , <b>2019</b> , 68, 49-61   | 19.2 | 73  |
| 130 | scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. <i>Nature Communications</i> , <b>2018</b> , 9, 781         | 17.4 | 303 |
| 129 | Generalized correlation measure using count statistics for gene expression data with ordered samples. <i>Bioinformatics</i> , <b>2018</b> , 34, 617-624                     | 7.2  | 7   |
| 128 | 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 |
| 127 | SpatialDE: identification of spatially variable genes. <i>Nature Methods</i> , <b>2018</b> , 15, 343-346  | 21.6 | 153 |
| 126 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , <b>2018</b> , 34, 211-224.e6   | 24.3 | 327 |
| 125 | Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. <i>Cell Systems</i> , <b>2018</b> , 7, 63-76.e12  | 6.12 | 44  |
| 124 | Reply. <i>Gastroenterology</i> , <b>2018</b> , 155, 230-231   | 13.3 |     |

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|-----|--|-------|-----|
| 123 | The germline genetic component of drug sensitivity in cancer cell lines. <i>Nature Communications</i> , <b>2018</b> , 9, 3385  | 17.4  | 24  |
| 122 | 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 |
| 121 | DNA Methylation and Transcription Patterns in Intestinal Epithelial Cells From Pediatric Patients With Inflammatory Bowel Diseases Differentiate Disease Subtypes and Associate With Outcome. <i>Gastroenterology</i> , <b>2018</b> , 154, 585-598 | 13.3  | 126 |
| 120 | Interactions between genetic variation and cellular environment in skeletal muscle gene expression. <i>PLoS ONE</i> , <b>2018</b> , 13, e0195788   | 3.7   | 9   |
| 119 | Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , <b>2017</b> , 18, 18   | 18.3  | 70  |
| 118 | Genomic Rearrangements in Considered as Quantitative Traits. <i>Genetics</i> , <b>2017</b> , 205, 1425-1441  | 4     | 15  |
| 117 | Single-cell RNA-seq and computational analysis using temporal mixture modelling resolves Th1/Tfh fate bifurcation in malaria. <i>Science Immunology</i> , <b>2017</b> , 2,   | 28    | 171 |
| 116 | Promoter shape varies across populations and affects promoter evolution and expression noise. <i>Nature Genetics</i> , <b>2017</b> , 49, 550-558   | 36.3  | 51  |
| 115 | DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. <i>Genome Biology</i> , <b>2017</b> , 18, 67   | 18.3  | 226 |
| 114 | Multi-tissue DNA methylation age predictor in mouse. <i>Genome Biology</i> , <b>2017</b> , 18, 68  | 18.3  | 220 |
| 113 | Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , <b>2017</b> , 546, 370-375   | 50.4  | 294 |
| 112 | Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. <i>Cell</i> , <b>2017</b> , 169, 807-823   | 36.19 | 200 |
| 111 | Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , <b>2017</b> , 100, 865-884  | 11    | 74  |
| 110 | Genetic variants regulating expression levels and isoform diversity during embryogenesis. <i>Nature</i> , <b>2017</b> , 541, 402-406   | 50.4  | 39  |
| 109 | Open Targets: a platform for therapeutic target identification and validation. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D985-D994   | 20.1  | 241 |
| 108 | easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. <i>Plant Cell</i> , <b>2017</b> , 29, 5-19  | 11.6  | 56  |
| 107 | The Human Cell Atlas <b>2017</b> ,   |       | 41  |
| 106 | Single-cell epigenomics: Recording the past and predicting the future. <i>Science</i> , <b>2017</b> , 358, 69-75   | 33.3  | 237 |

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| 105 | Genetic Variation in the Social Environment Contributes to Health and Disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006498   | 6    | 53  |
| 104 | f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. <i>Genome Biology</i> , <b>2017</b> , 18, 212   | 18.3 | 63  |
| 103 | Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , <b>2017</b> , 20, 2201-2214  | 10.6 | 64  |
| 102 | Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. <i>Nature Communications</i> , <b>2017</b> , 8, 1511                 | 17.4 | 37  |
| 101 | Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , <b>2017</b> , 8, 16058                                     | 17.4 | 30  |
| 100 | The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,  | 8.9  | 937 |
| 99  | Joint genetic analysis using variant sets reveals polygenic gene-context interactions. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006693   | 6    | 12  |
| 98  | GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , <b>2016</b> , 21, 189-197                                       | 15.1 | 85  |
| 97  | Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , <b>2016</b> , 167, 1369-1384.e19                          | 56.2 | 556 |
| 96  | Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , <b>2016</b> , 167, 1398-1414.e34  | 56.2 | 539 |
| 95  | Deep learning for computational biology. <i>Molecular Systems Biology</i> , <b>2016</b> , 12, 878  | 12.2 | 733 |
| 94  | Modelling local gene networks increases power to detect trans-acting genetic effects on gene expression. <i>Genome Biology</i> , <b>2016</b> , 17, 33                                  | 18.3 | 16  |
| 93  | Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , <b>2016</b> , 13, 229-232  | 21.6 | 430 |
| 92  | A high-content platform to characterise human induced pluripotent stem cell lines. <i>Methods</i> , <b>2016</b> , 96, 85-96  | 4.6  | 28  |
| 91  | Limited Contribution of DNA Methylation Variation to Expression Regulation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006141                          | 6    | 68  |
| 90  | GeneCodeq: quality score compression and improved genotyping using a Bayesian framework. <i>Bioinformatics</i> , <b>2016</b> , 32, 3124-3132   | 7.2  | 14  |
| 89  | Warped Matrix Factorisation for Multi-view Data Integration. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 789-804  | 0.9  | 1   |
| 88  | Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 155-60 | 44.5 | 778 |

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| 87 | Efficient set tests for the genetic analysis of correlated traits. <i>Nature Methods</i> , <b>2015</b> , 12, 755-8   | 21.6 | 70   |
| 86 | Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , <b>2015</b> , 85, 54-61   | 4.6  | 259  |
| 85 | Century-scale methylome stability in a recently diverged <i>Arabidopsis thaliana</i> lineage. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1004920  | 6    | 104  |
| 84 | A random forest approach to capture genetic effects in the presence of population structure. <i>Nature Communications</i> , <b>2015</b> , 6, 7432  | 17.4 | 50   |
| 83 | Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , <b>2015</b> , 348, 666-9  | 33.3 | 170  |
| 82 | A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74   | 50.4 | 8599 |
| 81 | An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , <b>2015</b> , 526, 75-81   | 50.4 | 1368 |
| 80 | Genome-wide studies of verbal declarative memory in nondemented older people: the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. <i>Biological Psychiatry</i> , <b>2015</b> , 77, 749-63 | 7.9  | 48   |
| 79 | Estimation of Free-Living Energy Expenditure by Heart Rate and Movement Sensing: A Doubly-Labelled Water Study. <i>PLoS ONE</i> , <b>2015</b> , 10, e0137206   | 3.7  | 86   |
| 78 | Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 133-45  | 30.1 | 736  |
| 77 | Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2015</b> , 44-55        | 1.3  | 4    |
| 76 | Personalized medicine: from genotypes, molecular phenotypes and the quantified self, towards improved medicine. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2015</b> , 342-6   | 1.3  | 12   |
| 75 | DNA methylation in <i>Arabidopsis</i> has a genetic basis and shows evidence of local adaptation. <i>ELife</i> , <b>2015</b> , 4, e05255   | 8.9  | 300  |
| 74 | Author response: DNA methylation in <i>Arabidopsis</i> has a genetic basis and shows evidence of local adaptation <b>2015</b> ,  |      | 2    |
| 73 | Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. <i>Nature Methods</i> , <b>2014</b> , 11, 817-820   | 21.6 | 673  |
| 72 | A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 903-14                       | 44.5 | 618  |
| 71 | Personalized medicine: from genotypes and molecular phenotypes towards therapy- session introduction. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2014</b> , 19, 224-8         | 1.3  | 1    |
| 70 | Warped linear mixed models for the genetic analysis of transformed phenotypes. <i>Nature Communications</i> , <b>2014</b> , 5, 4890  | 17.4 | 35   |

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| 69 | PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE <b>2014</b> ,   |      | 4    |
| 68 | Extensive cis-regulatory variation robust to environmental perturbation in Arabidopsis. <i>Plant Cell</i> , <b>2014</b> , 26, 4298-310   | 11.6 | 53   |
| 67 | Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , <b>2013</b> , 501, 506-514  | 51.4 | 1323 |
| 66 | A Lasso multi-marker mixed model for association mapping with population structure correction. <i>Bioinformatics</i> , <b>2013</b> , 29, 206-14  | 7.2  | 76   |
| 65 | Genotype-environment interactions reveal causal pathways that mediate genetic effects on phenotype. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003803   | 6    | 63   |
| 64 | Accurate detection of differential RNA processing. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 5189-98   | 20.1 | 30   |
| 63 | A Palaeolithic-type diet causes strong tissue-specific effects on ectopic fat deposition in obese postmenopausal women. <i>Journal of Internal Medicine</i> , <b>2013</b> , 274, 67-76           | 10.8 | 35   |
| 62 | Detecting regulatory gene-environment interactions with unmeasured environmental factors. <i>Bioinformatics</i> , <b>2013</b> , 29, 1382-9   | 7.2  | 10   |
| 61 | PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS COMPUTED THERAPY. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2013</b> , 18, 171-174  | 1.3  |      |
| 60 | Using probabilistic estimation of expression residuals (PEER) to obtain increased power and interpretability of gene expression analyses. <i>Nature Protocols</i> , <b>2012</b> , 7, 500-7       | 18.8 | 460  |
| 59 | Arabidopsis defense against Botrytis cinerea: chronology and regulation deciphered by high-resolution temporal transcriptomic analysis. <i>Plant Cell</i> , <b>2012</b> , 24, 3530-57            | 11.6 | 233  |
| 58 | Joint modelling of confounding factors and prominent genetic regulators provides increased accuracy in genetical genomics studies. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002330 | 5    | 74   |
| 57 | Patterns of cis regulatory variation in diverse human populations. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002639  | 6    | 361  |
| 56 | ShapePheno: unsupervised extraction of shape phenotypes from biological image collections. <i>Bioinformatics</i> , <b>2012</b> , 28, 1001-8  | 7.2  | 4    |
| 55 | Spontaneous epigenetic variation in the Arabidopsis thaliana methylome. <i>Nature</i> , <b>2011</b> , 480, 245-9   | 50.4 | 533  |
| 54 | Whole-genome sequencing of multiple Arabidopsis thaliana populations. <i>Nature Genetics</i> , <b>2011</b> , 43, 956-563   | 56.3 | 737  |
| 53 | Efficient branch-and-bound techniques for two-locus association mapping. <i>BMC Bioinformatics</i> , <b>2011</b> , 12,   | 3.6  | 1    |
| 52 | Multiple reference genomes and transcriptomes for Arabidopsis thaliana. <i>Nature</i> , <b>2011</b> , 477, 419-23  | 50.4 | 495  |



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|----|--|-----|-----|
| 51 | Joint genetic analysis of gene expression data with inferred cellular phenotypes. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001276   | 6   | 57  |
| 50 | A toolbox for predicting g-quadruplex formation and stability. <i>Journal of Nucleic Acids</i> , <b>2010</b> , 2010,   | 2.3 | 40  |
| 49 | A robust Bayesian two-sample test for detecting intervals of differential gene expression in microarray time series. <i>Journal of Computational Biology</i> , <b>2010</b> , 17, 355-67          | 1.7 | 67  |
| 48 | A Bayesian framework to account for complex non-genetic factors in gene expression levels greatly increases power in eQTL studies. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000770 | 5   | 295 |
| 47 | Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. <i>Nature Precedings</i> , <b>2010</b> ,  |     | 10  |
| 46 | Predicting and understanding the stability of G-quadruplexes. <i>Bioinformatics</i> , <b>2009</b> , 25, i374-82  | 7.2 | 81  |
| 45 | Inference algorithms and learning theory for Bayesian sparse factor analysis. <i>Journal of Physics: Conference Series</i> , <b>2009</b> , 197, 012002   | 0.3 | 3   |
| 44 | A Robust Bayesian Two-Sample Test for Detecting Intervals of Differential Gene Expression in Microarray Time Series. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 201-216            | 0.9 | 1   |
| 43 | Gaussian process robust regression for noisy heart rate data. <i>IEEE Transactions on Biomedical Engineering</i> , <b>2008</b> , 55, 2143-51   | 5   | 134 |
| 42 | FISHFactor: A Probabilistic Factor Model for Spatial Transcriptomics Data with Subcellular Resolution  |     | 1   |
| 41 | A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche   |     | 8   |
| 40 | Discovery and Quality Analysis of a Comprehensive Set of Structural Variants and Short Tandem Repeats  |     | 2   |
| 39 | Genomic properties of structural variants and short tandem repeats that impact gene expression and complex traits in humans  |     | 3   |
| 38 | SpatialDE2: Fast and localized variance component analysis of spatial transcriptomics  |     | 2   |
| 37 | LIMIX: genetic analysis of multiple traits   |     | 50  |
| 36 | Common genetic variation drives molecular heterogeneity in human iPSCs   |     | 7   |
| 35 | Accurate prediction of single-cell DNA methylation states using deep learning  |     | 14  |
| 34 | Temporal mixture modelling of single-cell RNA-seq data resolves a CD4+ T cell fate bifurcation   |     | 4   |

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| 33 | scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells              | 4  |
| 32 | SpatialDE - Identification of spatially variable genes  | 5  |
| 31 | Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types                                      | 10 |
| 30 | Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for twelve immune-mediated diseases   | 8  |
| 29 | Genetic Analyses of Blood Cell Structure for Biological and Pharmacological Inference                                       | 3  |
| 28 | The Polygenic and Monogenic Basis of Blood Traits and Diseases  | 3  |
| 27 | Identifying temporal and spatial patterns of variation from multi-modal data using MEFISTO                                  | 6  |
| 26 | Comprehensive mapping of tissue cell architecture via integrated single cell and spatial transcriptomics                    | 36 |
| 25 | De novo assembly of 64 haplotype-resolved human genomes of diverse ancestry and integrated analysis of structural variation | 3  |
| 24 | Germline determinants of the somatic mutation landscape in 2,642 cancer genomes   | 13 |
| 23 | Multi-Omics factor analysis - a framework for unsupervised integration of multi-omic data sets                              | 7  |
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